

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
12 September 2002 (12.09.2002)

PCT

(10) International Publication Number
WO 02/069900 A2

(51) International Patent Classification⁷: **A61K**

(21) International Application Number: PCT/US02/06518

(22) International Filing Date: 1 March 2002 (01.03.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/272,751 1 March 2001 (01.03.2001) US

(71) Applicant (for all designated States except US): **CONFORMA THERAPEUTICS CORP.** [US/US]; 9393 Towne Centre Drive, Suite 240, San Diego, CA 92121 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **FRITZ, Lawrence, C.** [US/US]; 9393 Towne Centre Drive, Suite 240, San Diego, CA 9212 (US). **BURROWS, Francis, J.** [US/US]; 9393 Towne Centre Drive, Suite 240, San Diego, CA 9212 (US).

(74) Agents: **KREUSSER, Edward, O.** et al.; Brobeck, Phleger & Harrison, LLP, 12390 El Camino Real, San Diego, CA 92121 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE DISORDERS WITH HSP90 INHIBITORS

Type of Aberration	Background Literature	Affected Gene(s)	Protein Domain	Fusion Protein	Disease
t(9; 22)(q34; q11)	de Klein, A. et al. Nature 300, 765-767 (1982)	<i>CABL</i> (9q34) <i>BCR</i> (22q11)	tyrosine kinase serine kinase	serine + tyrosine kinase	CML/ALL
inv14 (q11; q32)	Baer, R., Chen, K.-C., Smith, S. D. & Rabbitts, T. H. Cell 43, 705-713 (1985); Denny, C. T. et al. Nature 320, 549-551 (1986)	TCR- α (14q11) VH-(14q32)	TCR-C α Ig VH	VH-TCR-C α	T/B-cell lymphoma
t(1; 19)(q23; p13.3)	Kamps, M. P., Murre, C., Sun, X.-H. & Baltimore, D. Cell 60, 547-555 (1990); Nourse, J. et al. Cell 60, 535-545 (1990)	<i>PBX1</i> (1q23) <i>E2A</i> (19p13.3)	HD AD-b-HLH	AD + HD	pre-B-ALL
t(17; 19)(q22; p13)	Hunger, S. P., Ohyashiki, K., Toyama, K. & Clearly, M. L. Genes Dev. 6, 1608-1620 (1992); Inaba, T. et al. Science 257, 531-534 (1992)	<i>HLF</i> (17q22) <i>E2A</i> (19p13)	bZIP AD-b HLH	AD + bZIP	pro-B-ALL
t(15; 17)(q21-q11-22)	Gillard, E. F. & Solomon, E. Sem. Cancer Biol. 4, 359-368 (1993)	<i>PML</i> (15Q21) <i>RARA</i> (17q21)	Zinc-finger Retinoic acid receptor- α	Zinc-finger + RAR DNA and ligand binding	APL
t(11; 17)(q23; q21.1)	Chen, Z. et al. EMBO J. 12, 1161-1167 (1993)	<i>PLZF</i> (11q23) <i>RARA</i> (17q21)	Zinc-finger Retinoic acid receptor α	Zn-finger + RAR DNA and ligand binding	APL
t(4; 11)(q21; q23)	Djabali, M. et al. Nature Genet. 2, 113-118 (1992); Gu, Y. et al. Cell 71, 701-708 (1992)	<i>MLL</i> (11q23) <i>AF4</i> (4q21)	A-T hook/Zn-finger Ser-Pro rich	A-T hook + (Ser-pro)	ALL/preB-ALL/ ANLL
t(9; 11)(q21; q23)	Nakamura, T. et al. Proc. natn. Acad. Sci. U.S.A. 90, 4631-4635 (1993); Lida, S. et al. Oncogene 8, 3085-3092 (1993)	<i>MLL</i> (11q23) <i>AF9/MLLT3</i> (9p22)	A-T hook/Zn-finger Ser-Pro rich	A-T hook + (Ser-Pro)	ALL/preB-ALL/ ANLL
t(11; 19)(q23; p13)	Tkachuk, D. C., Kohler, S. & Cleary, M. L. Cell 71, 691-700 (1992); Yamamoto, K. et al. Oncogene 8, 2617-2625 (1993)	<i>MLL</i> (11q23) <i>ENL</i> (19p13)	A-T hook/Zn-finger Ser-Pro rich	A-T hook + Ser-Pro	pre-B-ALL/ T-ALL/ ANLL

(57) Abstract: The invention relates generally to methods of treating cell proliferative diseases with HSP90 inhibitors and, depending on the specific aspect and embodiment(s) claimed, to the treatment of proliferative diseases that are associated with fusion proteins, e.g., bcrabl, or mutant proteins or cellular protein isoforms, e.g., mutant forms of p53.



WO 02/069900 A2

Methods for Treating Genetically-Defined Proliferative Disorders with HSP90 Inhibitors

Field of the Invention

The field of the invention relates to chemotherapeutic treatments of proliferative disorders, including rheumatoid arthritis and neoplasias.

Background of the Invention

The following description includes information that may be useful in understanding the present invention. It is not an admission that any of the information provided herein is prior art, or relevant, to the presently claimed inventions, or that any publication specifically or implicitly referenced is prior art.

The eukaryotic heat shock protein 90s (HSP90s) are ubiquitous chaperone proteins that are involved in folding, activation and assembly of a wide range of proteins, including key proteins involved in signal transduction, cell cycle control and transcriptional regulation. HSP90 proteins are highly conserved in nature (see, e.g., NCBI accession # P07900 (SEQ ID NO: 318) and XM004515 (SEQ ID NOs: 319 and 320) (human α and β HSP90, respectively), P11499 (SEQ ID NO: 321) (mouse), AAB23369 (SEQ ID NO: 322) (rat), P46633 (SEQ ID NO: 323) (chinese hamster), JC1468 (SEQ ID NO: 324) (chicken), AAF69019 (SEQ ID NO: 325) (fleshfly), AAC21566 (SEQ ID NO: 326) (zebrafish), AAD30275 (SEQ ID NO: 327) (salmon), AAC48718 (SEQ ID NO: 328) (pig), NP 015084 (SEQ ID NO: 329) (yeast), and CAC29071 (SEQ ID NO: 330) (frog).

Researchers have reported that HSP90 chaperone proteins are associated with important signaling proteins, such as steroid hormone receptors and protein kinases, including many that are implicated in tumorigenesis, e.g., Raf-1, EGFR, v-Src family kinases, Cdk4, and ErbB-2 (Buchner J., 1999, *TIBS*, 24:136-141; Stepanova, L. *et al.*, 1996, *Genes Dev.* 10:1491-502; Dai, K. *et al.*, 1996, *J. Biol. Chem.* 271:22030-4). *In vivo* and *in vitro* studies indicate that certain co-chaperones, e.g., Hsp70, p60/Hop/Sti1, Hip, Bag1, HSP40/Hdj2/Hsj1, immunophilins, p23, and p50, may assist HSP90 in its function (Caplan, A., 1999, *Trends in Cell Biol.*, 9: 262-68).

Ansamycins are antibiotics derived from *Streptomyces hygroscopicus* which are known to inhibit HSP90s. These antibiotics, e.g., herbimycin A (HA) and geldanamycin (GM), as well as other HSP90 inhibitors such as radicicol, bind tightly to an N-terminal pocket in HSP90 (Stebbins, C. *et al.*, 1997, *Cell*, 89:239-250). This pocket is highly conserved and has weak

homology to the ATP-binding site of DNA gyrase (Stebbins, C. *et al.*, *supra*; Grenert, J.P. *et al.*, 1997, *J. Biol. Chem.*, 272:23843-50). ATP and ADP have been shown to bind this pocket with low affinity, and HSP90 itself has been shown to have weak ATPase activity (Proromou, C. *et al.*, 1997, *Cell*, 90: 65-75; Panaretou, B. *et al.*, 1998, *EMBO J.*, 17: 4829-36). *In vitro and in vivo* studies have demonstrated that occupancy of the N-terminal pocket of HSP90 by ansamycins and other inhibitors alters HSP90 function and inhibits client protein folding. At high concentrations, ansamycins and other HSP90 inhibitors have been shown to prevent binding of client protein substrates to HSP90 (Scheibel, T., H. *et al.*, 1999, *Proc. Natl. Acad. Sci. U S A* 96:1297-302; Schulte, T. W. *et al.*, 1995, *J. Biol. Chem.* 270:24585-8; Whitesell, L., *et al.*, 1994, *Proc. Natl. Acad. Sci. U S A* 91:8324-8328). Ansamycins have also been demonstrated to inhibit the ATP-dependent release of chaperone-associated protein substrates (Schneider, C., L. *et al.*, 1996, *Proc. Natl. Acad. Sci. U S A*, 93:14536-41; Sepp-Lorenzino *et al.*, 1995, *J. Biol. Chem.* 270:16580-16587), and some of these substrates have been shown to be degraded by a ubiquitin-dependent process in the proteasome (Schneider, C., L., *supra*; Sepp-Lorenzino, L., *et al.*, 1995, *J. Biol. Chem.*, 270:16580-16587; Whitesell, L. *et al.*, 1994, *Proc. Natl. Acad. Sci. USA*, 91: 8324-8328).

This substrate destabilization occurs in tumor and nontransformed cells alike and has been shown to be especially effective on a subset of signaling regulators, *e.g.*, Raf (Schulte, T. W. *et al.*, 1997, *Biochem. Biophys. Res. Commun.* 239:655-9; Schulte, T. W., *et al.*, 1995, *J. Biol. Chem.* 270:24585-8), nuclear steroid receptors (Segnitz, B., and U. Gehring. 1997, *J. Biol. Chem.* 272:18694-18701; Smith, D. F. *et al.*, 1995, *Mol. Cell. Biol.* 15:6804-12), *v-src* (Whitesell, L., *et al.*, 1994, *Proc. Natl. Acad. Sci. U S A* 91:8324-8328) and certain transmembrane tyrosine kinases (Sepp-Lorenzino, L. *et al.*, 1995, *J. Biol. Chem.* 270:16580-16587) such as EGF receptor (EGFR) and Her2/Neu (Hartmann, F., *et al.*, 1997, *Int. J. Cancer* 70:221-9; Miller, P. *et al.*, 1994, *Cancer Res.* 54:2724-2730; Mimnaugh, E. G., *et al.*, 1996, *J. Biol. Chem.* 271:22796-801; Schnur, R. *et al.*, 1995, *J. Med. Chem.* 38:3806-3812). The ansamycin-induced loss of these proteins leads to the selective disruption of certain regulatory pathways and results in growth arrest at specific phases of the cell cycle (Muisse-Heimericks, R. C. *et al.*, 1998, *J. Biol. Chem.* 273:29864-72), and apoptosis of cells so treated (Vasilevskaya, A. *et al.*, 1999, *Cancer Res.*, 59:3935-40).

Growth arrest of this sort, provided it can be made selective, has important ramifications for the treatment of certain proliferative disorders, including cancer. Whereas cancer treatments have thus far been limited to traditional surgical removal, radiation, and/or chemotherapy, and

whereas these procedures have been more or less successful, a need remains to develop additional therapies with increased efficacy and decreased side-effects that can be used alone or in combination with existing therapies. There particularly remains a need for cancer treatments that target specific cancer types. The present invention satisfies these needs and provides related advantages as well.

Summary of the Invention

Applicants report that many proliferative disorders are associated with aberrant proteins that exhibit a dependence on HSP90. In some cases this dependence manifests as a heightened sensitivity to HSP90 inhibitors such that affected cells can be selectively treated using a dosage that is effective against the aberrant cells but which is ineffective or less effective against normal cells. The aberrant proteins may also exhibit increased proteosome-dependent degradation when in the presence of HSP90 inhibitors. While the invention is not limited by mechanism, increased dependence, sensitivity, and /or disposition to preferential degradation may advantageously be used to treat corresponding proliferative diseases according to the methods of the invention.

Among others, the invention targets two groups of aberrant proteins in particular and the corresponding proliferative disorders they are associated with. Within the first group are fusion proteins generated as a result of non-random chromosomal aberrations (such as translocations, deletions and inversions) that juxtapose parts of the coding sequences of two normal cellular proteins (Rabbitts, T., 1994, *Nature* 372:143-149). Duplication of genetic material within a chromosome resulting in a augmented or semi-duplicative transcripts is also a possibility. Within the second group are mutants and isoforms of cellular proteins that override, dominate, or otherwise obscure the natural gene products and their function. For example, mutants and isoforms of p53 family proteins and other tumor suppressor gene products can act as dominant-negative inhibitors of the corresponding normal protein in heterozygous tumor cells (Blagosklonny, M., *et al*, 1995, *Oncogene*, 11:933-939. Other examples include virally-encoded species of certain kinases, such as v-src and other dominantly-acting mutant oncogene products (Uehara, Y. *et al.*, 1985, *supra*).

Accordingly, in a first aspect the invention features a method of treating a patient having a genetically-defined proliferative disease characterized by a non-random chromosomal aberration. This aberration produces or is capable of producing an oncogenic fusion protein. The method in its broadest embodiment includes (a) providing a

cell, tissue, or fluid sample of a patient suspected of having a genetically-defined proliferative disease; (b) identifying in the cell, tissue, or fluid sample one or more characteristics indicative of the proliferative disease; and (c) administering to the patient a pharmaceutically effective amount of an HSP90-inhibiting compound.

5 The patient may be any organism that can manifest a proliferative disease characterized by an oncogenic fusion protein, which disease is responsive to HSP90 inhibitors. Preferably, but not necessarily, the organism is an animal, more preferably a mammal, and most preferably a human.

10 In preferred embodiments, the inhibitory compound is an ansamycin including but not limited to, *e.g.*, geldanamycin, the geldanamycin derivative, 17-AAG, herbimycin A, and/or macbecin. Most preferably, the ansamycin is 17-AAG. These and other ansamycins and methods of preparing them are well-known in the art. *See, e.g.*, US Patents 3,595,955, 4,261,989, 5,387,584, and 5,932,566. Although preferably the compound is an ansamycin, the method may make use of any compound, synthetic or
15 nonsynthetic, that can inhibit HSP90. Preferably, the inhibitor binds the ATP-binding site of HSP90, or an HSP90 homolog. Radicicol is a nonsynthetic example of a compound useful in the invention described and claimed herein. Libraries of small molecules, synthetic and/or nonsynthetic exist or can be made according to routine, well-known methods and screened for HSP90 binding and/or inhibitory activity. These molecules with
20 HSP90 binding and/or inhibitory activity are also useful in the methods of the invention.

 In the identifying step of the invention, which is carried out prior to diagnosis where/when there is no previous diagnosis, any technique can be used that can identify or predict a proliferative disorder targetable by HSP90 inhibitors. Especially preferred are antibody-based and nucleic acid hybridization and/or amplification techniques.
25 Immunoprecipitation, western blotting, and immunoblotting are illustrative examples of antibody-based methods. The antibodies may be monoclonal and/or polyclonal. Illustrative examples of nucleic acid hybridization-based techniques involve Southern blotting, northern blotting, and dot-blotting. Illustrative examples of nucleic acid amplification include standard polymerase chain reactions and variations thereof, *e.g.*,
30 reverse transcriptase-PCR (RT-PCR). The latter is especially useful for identifying levels of gene expression. Other techniques such as the ligase chain reaction (LCR) are also

well-known and have the ability to distinguish an aberrant gene (and indirectly a protein product produced therefrom) from a normal one, or at least predict genotype and/or phenotype. Other methods of identification include ligand-binding assays and gel-retardation assays that display characteristic binding affinities and/or mobility profiles for normal and variant proteins. Where the fusion protein is also an enzyme, one can establish and/or measure aberrance by enzymatic activity (or lack thereof). Conventional and derivative karyotyping and cytochemical techniques can also be used to identify a proliferative disorder of the invention prior to administration of HSP90-inhibitors. One such method is fluorescent *in situ* hybridization (FISH).

In some embodiments, the proliferative disease is a hematopoietic disorder including but not limited to one selected from the group consisting of T or B cell lymphomas, chronic myeloid leukemias (CMLs), acute promyelocytic leukemias (APLs), acute lymphoid or lymphoblastic leukemias (ALLs), acute myeloid leukemias (AMLs), non-Hodgkin lymphomas (NHLs), and chronic myelomonocytic leukemias (CMMLs). In other embodiments, the disease is characterized by a solid tumor, preferably including but not limited to papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma, synovial sarcoma. The embodiments are not necessarily mutually exclusive of one another, and treatment of multiple distinct diseases may simultaneously be effected in a given patient, as the invention has broad-spectrum merit against a variety of different proliferative disorders.

Targeted fusion proteins may contain one or more functional domains or portions thereof, e.g., kinases, DNA binding motifs, etc. Such domains are well-known in the art. Figure 1 illustrates several types of these domains, and the specific fusion proteins, genes, and diseases they can be associated with.

Administration may be by a variety of means. In some preferred embodiments, administration is made *ex vivo*, e.g., removing and treating blood or tissue that is thereafter administered back into the patient. Alternatively, or in combination, administration may be intralésional, e.g., administered to the site of a solid tumor, and/or parenteral. These constitute just some of the many different modes of administration that can be used.

Others are described herein.

In other embodiments, the HSP90-inhibiting compound has an IC_{50} that is higher (preferably two-fold, more preferably five-fold, and most preferably ten-fold) for cells that do not have characteristics indicative of the proliferative disorder as compared with those cells that do have such characteristics.

5 In other embodiments, the patient may be tested pre- and/or post-administration for sensitivity and or effect of one or more HSP90 inhibitors. This may be done *in vitro* or *in vivo*.

Numerous non-random chromosomal aberrations exist that are associated with proliferative disorders. These include but are not limited to chromosomal translocations, inversions, and deletions. Duplications also account for some aberrant chromosomes and aberrant resulting gene products. All aberrations can be targeted in various aspects of the invention. Illustrative examples of specific aberrations include those listed in Figure 1, which is adapted from Table 1 of Rabbitts, Nature 372:143-149 (1994), and others including but not limited to: inv14 (q11; q32), t(9; 22)(q34; q11), t(1; 19)(q23; p13.3), t(17; 19)(q22; p13), t(15; 17)(q21-q11-22), t(11; 17)(q23; q21.1), t(4; 11)(q21; q23), t(9; 11)(q21; q23), t(11; 19)(q23; p13), t(X; 11)(q13; q23), t(1; 11)(p32; q23), t(6; 11)(q27; q23), t(11; 17)(q23; q21), t(8; 21)(q22; q22), t(3; 21)(q26; q22), 5(16; 21)(p11; q22), t(6; 9)(p23; q34), 9; 9?, t(4; 16)(q26; p13), inv(2; 2)(p13; p11.2-14), inv(16)(p13q22), t(5; 12)(q33; p13), t(2; 5)(2p23; q35), t(9; 12)(q34; p13), del(12p), t(9; 22), +8, +Ph, i(17q), t(15; 17)(q22; q12), t(11; 17)(q23; q12), t(16; 16)(p13; q22), inv(16)(p13; q22), t(9; 11)(p22; q23), t(1; 22)(p13; q13), t(3; 3)(q21; q26), inv(3)(q21q26), t(3; 5)(q21; q31), t(3; 5)(q25; q34), t(7; 11)(p15; p15), t(8; 16)(p11; p13), t(9; 12)(q34; p13), t(12; 22)(p13; q13), del(5q), del(7q), del(20q), t(11q23), t(12; 21)(p13; q22), t(5; 12)(q31; p13), t(1; 12)(q25; p13), t(12; 15)(p13; q25), t(1; 12)(q21; p13), t(12; 21)(q13; p32), and t(5; 7)(q33; q11.2). These are merely a sampling of the many chromosomal aberrations well-known in the art that give rise to particular proliferative disorders treatable according to the invention. For these and others, *see, e.g.*, the National Center for Biotechnology Information (NCBI) databases, including, *e.g.*, the Online Mendelian Inheritance in Man (OMIM) database and related links to nucleotide and protein sequences. For purposes of the present invention, the underlying genetic sequences affected are for the most part known and/or may be deduced using techniques routine in the art.

Targeted in particularly preferred embodiments of the invention are chromosomal aberrations corresponding to t(9; 22)(q34; q11) that give rise to bcr-abl fusion proteins, chronic myelogenous leukemia (CML) and, in some cases, acute lymphoid or lymphoblastic leukemia (for ALL, *see, e.g.,* Erikson et al., *Heterogeneity of chromosome 22 breakpoint in Philadelphia-positive (Ph⁺) acute lymphocytic leukemia*, Proc. Nat. Acad. Sci. 83: 1807-1811 (1986))).

In a second aspect, the invention features a method of treating cancerous cells in a heterogeneous population of cells. The heterogeneous population includes both cancerous and noncancerous cells, and the cancerous cells are further characterized by fusion proteins that are not produced in the noncancerous cells. The method includes administering to the heterogeneous population a pharmaceutically effective amount of an HSP90-inhibiting compound. The population may be tested by separation of samples from each population into separate subpopulations, cancerous or noncancerous, *e.g.,* where cultured cells of each are tested in parallel for response and/or susceptibility to an HSP90-inhibitor or candidate inhibitor molecule. Alternatively, the population may be mixed, *e.g.,* in an *ex vivo* procedure in which cells of a patient, *e.g.,* blood, are treated and administered back to the patient or to another individual. This method otherwise tracks the various described and/or claimed embodiments and/or combinations of embodiments of the first aspect.

In a third aspect, the invention features a method of treating a patient having a proliferative disease associated with a mutant protein or cellular protein isoform dependent on HSP90, or which disease is otherwise sensitive to HSP90 inhibitors. The method includes (a) providing a cell, tissue, or fluid sample of a patient suspected of having said proliferative disease; (b) identifying in the cell, tissue, or fluid sample one or more characteristics indicative of a mutant or cellular protein isoform; and (c) administering to the patient a pharmaceutically effective amount of an HSP90-inhibiting compound.

In preferred embodiments, the mutant protein or cellular protein isoform is selected from the group consisting of src, RET, p53, p51, p63, and p73. Most preferably selected are isoforms of p53 selected from N239S, C176R, and R213*, Y236delta, C174Y, M133T, G245D, E258K, 1-293delta, G245C, R248W, E258K, R282W, R175H, R280K,

V143A, R175H, P177S, H178P, H179R, R181P, 238-9delta, G245S, G245D, M246R, R248Q, R249S, R273H, R273C, R273L, and D281Y.

In another preferred embodiment, the proliferative disease to be treated is rheumatoid arthritis.

5 In some embodiments, the mutant protein or cellular protein isoform may give rise to a dominant negative phenotype. In other embodiments, the mutant or cellular protein isoform may give rise to a dominant positive mutant. In either embodiment, the patient may be heterozygous for the normal cellular gene. Other embodiments track those listed for the preceding aspects.

10 In a fourth aspect, the invention features a method of selectively treating cells that express a mutant protein or cellular protein isoform associated with a proliferative disorder and which mutant/isoform is dependent on HSP90, or which disease is otherwise sensitive to HSP90 inhibitors. The method includes (a) providing a population of cells in which at least some of the population express a mutant protein or cellular protein isoform that is
15 dependent on HSP90 or which are otherwise sensitive to HSP90 inhibitors. The method further includes administering to the population a pharmaceutically effective amount of an HSP90-inhibiting compound. The embodiments for this aspect may otherwise track preceding embodiments.

The foregoing aspects contemplate treatment of existing cell proliferative
20 disorders. It is expected that the invention may also find use in prophylactic prevention of various proliferative disorders of the invention. Further, and where appropriate, each of the embodiments discussed above and different combinations thereof, including subgenus and sub-Markush groups, may cross-apply to each of the different aspects of the invention. Further, where sequence listings are provided, the invention may in some aspects
25 contemplate subsequences of the primary sequence listings. Any subsequence within such primary listing is also contemplated for the invention, as well as all allelic variants, and mutant variants and isoforms thereof, as well as corresponding homologs from other organisms and species. Sequences contiguous with and/or in addition to the listed sequences and their above equivalents are also contemplated.

Advantages of the invention include broad-acting treatment or prophylaxis directed to a variety of different proliferative disorders. Other advantages include the efficient and rapid diagnosis and care of patients suffering from proliferative disorders, with minimal apparent adverse effects. Still other advantages, aspects, and embodiments will be
5 apparent from the figures, the detailed description, and the claims.

Brief Description of the Drawings

Figure 1 illustrates various genetically defined diseases characterized by non-random chromosomal aberrations that give rise to oncogenic fusion proteins. These illustrative aberrations, diseases, and fusion proteins are targeted in various embodiments
10 of the invention. Other targeted aberrations, diseases, and fusion proteins may be found in the specification and in sources commonly known in the art, e.g., the NCBI and GenBank databases, and journal literature.

Detailed Description of the Invention

Definitions

15 As used herein and in the claims the following terms have the following meanings:

A “genetically-defined disease” is one with a basis in DNA. Genetically defined diseases of the invention include “cell proliferative disorders” wherein unwanted cell proliferation of one or more subset(s) of cells in a multicellular organism occurs, resulting in harm, for example, pain or decreased life expectancy to the organism. “Cell proliferative disorders” refer to disorders
20 wherein unwanted cell proliferation of one or more subset(s) of cells in a multicellular organism occurs, resulting in harm, for example, pain or decreased life expectancy to the organism. Cell proliferative disorders include, but are not limited to, cancers, tumors, benign tumors, blood vessel proliferative disorders, autoimmune disorders and fibrotic disorders. These disorders are not necessarily independent. For example, fibrotic disorders may be related to, or overlap with,
25 blood vessel disorders, *e.g.*, atherosclerosis (which is characterized herein as a blood vessel disorder that is associated with the abnormal formation of fibrous tissue).

A “non-random chromosomal aberration” is one that occurs with a nonrandom frequency or is selected for in a population of individuals. Chromosomal aberrations of the invention include translocations, *i.e.*, relocation of a fragment of one chromosome onto another

chromosome; inversions, *i.e.*, wherein pieces of a chromosome rotate within the same chromosome, and deletions, *i.e.*, wherein fragments of a chromosome are lost thereby juxtaposing pieces of DNA that previously did not reside immediately beside each other.

An “oncogenic fusion protein” is a protein that is non-natural in and of itself but that may contain one or more pieces of other proteins that may or may not naturally occur within a cell. The fusion protein functions by improperly stimulating cell growth, directly or indirectly. In the context of the invention, the term is also associated with a cellular proliferative disease and is preferably encoded by a nucleic acid found in the cell, *e.g.*, as part of a non-random chromosomal aberration. An oncogenic fusion protein may contain domains or portions thereof, *e.g.*, kinases and/or DNA binding proteins that are well known in the art, or else predicted from their structure to behave as such.

A “fusion” may relate to, as appropriate to a given context, a fusion chromosome, an abnormal mRNA transcribed from the fused portion of the chromosome, or a polypeptide product translated from the abnormal mRNA that is transcribed from the fusion chromosome. These fusions may result from chromosomal deletions, insertions, and/or translocations. Domains or portions of different genes and gene products are frequently, although not necessarily always, brought together as a consequence of the fusion event. For example, an intragenic deletion can result in an intragenic fusion and give rise to an abnormal protein lacking a component from a second gene. More frequently it occurs that two genes or portions thereof are juxtaposed more or less, transcribed together as a single transcript, and translated together as a fusion protein bearing contributions from multiple genes or other chromosomal DNA pieces. In such fusions, reading frames can be preserved, *e.g.*, as in preserved functional domains or portions thereof coming from two or more different genes, or else the reading frame can be disrupted, *e.g.*, as in the case of a “missense” or “nonsense” event as these terms are known in the art.

By “providing a cell, tissue, or fluid sample of a patient suspected of having said genetically-defined disease” and “identifying one or more characteristics indicative of said disease in or on said cell, tissue, or fluid sample” can mean, although is not limited to the situation where, the sample is withdrawn from the patient in order to perform the analysis or analyses. Many invasive and noninvasive procedures exist, *e.g.*, NMR, ultrasound and other imaging techniques, that can be used to diagnose, at least in part, an illness and its cause. For example, “tagged” antibodies or other ligands with affinity for a fusion protein or chromosomal aberrancy or

aberrancy product of the invention can be used to make the diagnosis and/or assist in treatment according to methods of the invention.

“Characteristics indicative of said disease” may embrace phenotypes or genotypes and may be measured qualitatively or quantitatively by a variety of techniques. The characteristics may be observed with the naked eye or else through the assistance of a machine or other diagnostic technique(s). Exemplary techniques of measurement include but are not limited to immunoreactivity and/or precipitation, PCR, LCR, karyotyping, and fluorescence activated cell sorting (“FACS”) as those terms are known and understood in the art.

“Administering” can be by direct means, *e.g.*, intralesional or by parenteral or peripheral administration to a patient, or else by indirect means, *e.g.*, as by withdrawing a patient’s cells, treating them, and then re-introducing them back into the patient. The latter constitutes an “*ex vivo*” technique.

An “HSP90-inhibiting compound” is one that disrupts the expression, structure, and/or function of an HSP90 chaperone protein and/or a protein that is dependent on HSP90. HSP90 proteins are highly conserved in nature (see, *e.g.*, NCBI accession #'s P07900 and XM 004515 (human α and β HSP90, respectively), P11499 (mouse), AAB2369 (rat), P46633 (chinese hamster), JC1468 (chicken), AAF69019 (flesh fly), AAC21566 (zebrafish), AAD30275 (salmon), O02075 (pig), NP 015084 (yeast), and CAC29071 (frog). There are thus many different HSP90s, all with anticipated similar effect and similar inhibition capabilities. The HSP90 inhibitor used in the methods of the invention may be specifically directed against an HSP90 of the specific host patient or may be identified based on reactivity against an HSP90 homolog from a different species, or an artificial HSP90 variant. The inhibitors used may be ring-structured antibiotics, *e.g.*, benzoquinone ansamycins, or other types of molecules, *e.g.*, antisense nucleic acids and molecules such as radicicol.

An “ansamycin” includes but is not limited to geldanamycin, 17-AAG, herbimycin A, and mabeccin. The specific ansamycin 17-AAG stands for 17-allylamino-17-demethoxygeldanamycin. This and other ansamycins that can be used are well-known in the art. See, *e.g.*, U.S. Patent Nos. 3,595,955, 4, 261, 989, 5,387,584, and 5,932,566. Ansamycins may be synthetic, naturally-occurring, or else derivatives of naturally occurring ansamycins that are prepared using standard chemical derivatization techniques.

A "pharmaceutically effective amount" means an amount which is capable of providing a therapeutic or prophylactic effect. The specific dose of compound administered according to this invention to obtain therapeutic and/or prophylactic effects will, of course, be determined by the particular circumstances surrounding the case, including, for example, the specific compound
5 administered, the route of administration, the condition being treated, the individual being treated, and the tissue or cell type targeted (or not targeted). A typical daily dose (administered in single or divided doses) will contain a dosage level of from about 0.01 mg/kg to about 100 and more preferably 50 mg/kg of body weight of an active compound of this invention. Preferred daily doses generally will be from about 0.05 mg/kg to about 20 mg/kg and ideally from about 0.1 mg/kg to
10 about 10 mg/kg.

A preferred therapeutic effect is the inhibition to some extent of the growth of cells causing or contributing to a cell proliferative disorder. A therapeutic effect will also normally, but need not, relieve to some extent one or more of the symptoms of a cell proliferative disorder other than cell growth or size of cell mass. In reference to the treatment of a cancer, a therapeutic effect
15 refers to one or more of the following: 1) reduction in the number of cancer cells; 2) reduction in tumor size; 3) inhibition (*i.e.*, slowing to some extent, preferably stopping) of cancer cell infiltration into peripheral organs; 3) inhibition (*i.e.*, slowing to some extent, preferably stopping) of tumor metastasis; 4) inhibition, to some extent, of tumor growth; and/or 5) relieving to some extent one or more of the symptoms associated with the disorder.

20 In reference to the treatment of a cell proliferative disorder other than a cancer, a therapeutic effect refers to either: 1) the inhibition, to some extent, of the growth of cells causing the disorder; 2) the inhibition, to some extent, of the production of factors (*e.g.*, growth factors) causing the disorder; and/or 3) relieving to some extent one or more of the symptoms associated with the disorder.

25 With respect to viral infections, the preferred therapeutic effect is the inhibition of a viral infection. More preferably, the therapeutic effect is the destruction of cells which contain the virus.

A "cancer" refers to one or more various types of benign or malignant neoplasms. In the case of the latter, these may invade surrounding tissues and may metastasize to different sites, as
30 defined in Stedman's Medical Dictionary 25th edition (Hensyl ed. 1990).

The term "IC₅₀" is defined as the concentration of an HSP90 inhibitor required to achieve killing or other growth inhibition of 50% of the cells of a homogenous cell type population, or of a particular cell type, *e.g.*, cancerous versus noncancerous, over a period of time. The IC₅₀ is preferably, although not necessarily, greater for normal cells than for cells exhibiting a
5 proliferative disorder.

The term "mutant or isoform cellular protein" refers to a variation of a wild-type protein that occurs in a cell and has a particular function. The mutant or isoform cellular protein of the invention preferably associates with or gives rise to a proliferative disorder, *e.g.*, a cancer, whereas the wild-type protein ordinarily does not.

10 General

As described and claimed herein, ansamycins and other HSP90 inhibitors can be used to treat two important classes of tumor-promoting (oncogenic) human proteins.

1. Oncogenic Fusion Proteins

The first class of target proteins of the invention are fusion proteins generated as a result
15 of non-random chromosomal aberrations (such as translocations, deletions and inversions) that juxtapose parts of the coding sequences of two normal cellular proteins (Rabbitts, T., 1994, *Nature* 372:143-149) leading to the lineage-specific expression of a mutant fusion protein that has biological activities derived from both parent proteins (Barr, F, 1998, *Nat. Genet.* 19:121-124). Without being limiting of the invention, Applicants have discovered that these fusion proteins
20 have a heightened dependence on HSP90 chaperone activity, and/or decreased stability in the presence of HSP90 inhibitors, thus making them selective targets for treatment with HSP90 inhibitors.

a. Bcr-abl as an example

One example of heightened HSP90 dependence and inhibitor sensitivity is observed when
25 chronic myelogenous leukemia (CML) cells harboring the fusion oncoprotein p210-bcr-abl are treated with HSP90 inhibitors. This fusion protein is degraded faster and more completely than wild type c-abl protein (An, W *et al*, 2000, *Cell Growth and Differentiation* 11: 355-360). Further experimental evidence that bcr-abl expressing leukemia cells are more sensitive to HSP90 inhibitors than are closely related bcr-abl-negative leukemia lines is found in Honma, Y *et al*,

1995, *Int. J. Cancer* 60:685-688, where it is reported that the IC₅₀ of herbimycin A in six bcr-abl expressing leukemia cell lines averaged 29.3 nM as compared to a mean IC₅₀ of 399.3 nM in a panel of four bcr-abl-negative leukemia lines. Illustrative protein and nucleic acid sequences corresponding to embodiments of bcr-abl fusions of the invention include but are not limited to those found in SEQ ID NOs 1-26 and subsequences thereof, which are further discussed below, along with corresponding NCBI accession numbers.

The normal Bcr gene occupies a region of about 135 kb on chromosome 22. It is expressed as mRNAs of 4.5- and 6.7-kb, which apparently encode for the same cytoplasmic 160-kD protein, and contains 23 exons as well as an unusual inverted repeat flanking the first exon. The BCR protein reportedly contains a unique serine/threonine kinase activity and at least two SH2 binding sites encoded in its first exon and a C-terminal domain that functions as a GTPase activating protein for p21(rac) (Diekmann et al., *Nature* 351: 400-402 (1991). Chisoe et al., *Genomics* 27: 67-82 (1995), sequenced the complete BCR gene and greater than 80% of the human ABL gene, which are both involved in the t(9;22) translocation (Philadelphia chromosome) associated with more than 90% of chronic myelogenous leukemia, 25 to 30% of adult and 2 to 10% of childhood acute lymphoblastic leukemia, and rare cases of acute myelogenous leukemia. Comparison of the gene with its cDNA sequence revealed the positions of 23 BCR exons and putative alternative BCR first and second exons. From the sequence of four newly studied Philadelphia chromosome translocations and a review of several other previously sequenced breakpoints, Chisoe et al. found a variety of breakpoints and recombinations sites possible within the genes. Thus, despite the normal chromosomes and genes each being known (9 and 12; bcr and abl), and the fact that combinations of these genes are known to lead to forms of CML and ALL, the precise genetic breakpoint/recombination junctions that lead to these diseases can vary.

This heterogeneity likely also applies to some non bcr-abl chromosomal aberrations of the invention as well. Nevertheless, because the genes and/or chromosomes involved are known to have a part in the disorders, the disorders are said to be "genetically defined."

b. Other oncogenic fusion proteins

Oncogenic fusion proteins in general are thought to be inherently unstable. To the extent these unstable oncogenic fusion proteins make use of HSP90, they are susceptible of the methods claimed herein. Because the fusion genes and their protein products exert overtly oncogenic activity (Deininger, M *et al*, 2000, *Cancer Res.* 60:2049-2055), preferential degradation of these labile proteins induced by HSP90 inhibitors will have therapeutic value in diseases where the fusion protein is expressed. The present invention thus includes treatment of patients with tumors that are dependent upon other oncogenic fusion proteins that arise from non-random genetic aberrations. An illustrative but nonexhaustive list of these tumors is included in Figure 1, adapted from Table 1 of Rabbitts, T., 1994, *Nature* 372:143-149. The list may be supplemented by additional information found, *e.g.*, in Rowley, J, 1999, *Semin. Hematol.* 36:59-72 and other publications known in the art, as well as discussion below.

Myeloid cancers in particular are within the scope of the invention and include chromosomal abnormalities that give rise to oncogenic fusion proteins that drive the growth of chronic myeloid leukemia (CML), chronic myelomonocytic leukemia (CMML), acute myeloid leukemia (AML), acute promyelocytic leukemia (APL), and acute lymphoblastic leukemia (ALL). The following chromosomal aberrancies give rise to some illustrative fusions implicated in various forms of ALL:

t(1:19)(q23:p13) Pro-pre-B acute lymphoblastic leukemia

t(12:21)(p13;q32) Pro-pre-B acute lymphoblastic leukemia

t(9:22)(q34;q11) B or B-myeloid acute lymphoblastic leukemia

t(9:12)(q34:p13) Acute B-lymphoblastic leukemia

del(12p) Acute B-lymphoblastic leukemia

Specific genes and proteins thereof implicated in various ALL forms include the *MLL* gene and the *TEL* gene, which are commonly rearranged in tumors. Rowley, J, *supra*. Each has numerous fusion partners. ETV6 denotes the name of the *TEL* gene product. Fusion of *TEL*/ETV6 to an acyl CoA synthetase, ACS2, results from a t(5;12)(q31;p13) AML event (Yagasaki, F *et al*, 1999, *Genes Chromosomes Cancer* 26:192-202); fusion of *TEL*/ETV6 to ABL-related gene (*ARG*)

results from a t(1;12)(q25;p13) AML event (Iijima, Y *et al*, 2000, *Blood* 95:2126-2131); fusion of TEL/ETV6 to the neurotrophin-3 receptor TRKC results from a t(12;15)(p13;q25) AML event and gives rise to congenital fibrosarcoma (Liu, Q *et al*, 2000, *EMBO J.* 19:1827-1838, Eguchi, M *et al*, 1999, *Blood* 93:1355-1363); fusion of TEL/ETV6 to the aryl hydrocarbon receptor ARNT results from a t(1;12)(q21;p13) event and gives rise to acute myeloblastic leukemia (AML-M2) (Salomon-Nguyen, F *et al*, 2000, *Proc. Natl. Acad. Sci.* 97:6757-6762); and fusion of TEL/ETV6 to AML-1, the DNA-binding subunit of the AML-1/CBF β transcription factor results from a (12;21)(q13;p32) event that can give rise to acute lymphoblastic leukemia (ALL, Shurtleff, SA *et al*, 1995, *Leukemia* 9:1985-1989) and, in some cases, non-Hodgkin's lymphoma (NHL).

Another illustrative fusion within the scope of the invention is the EWS/FLI-1 hybrid protein that is the hallmark of Ewing's sarcoma and the primitive neuroectodermal tumor family (Silvany, *et al*, 2000, *Oncogene* 19:4523-4530).

Yet another illustrative family of fusion proteins within the scope of the invention is the group of fusion proteins arising from chromosomal rearrangements involving the *RET* gene in thyroid cancer (Kolibaba, K, *et al*, 1997, *Biochem. Biophys. Acta* 1333:F217-F248). Rearrangements of *RET*, resulting in juxtaposition of the RET tyrosine kinase domain with one of three 5' sequences (RET-PTC-1, -2 and -3) generate fusion proteins comprising the kinase domain of RET fused to parts of the genes *H4* (RET-PTC-1), *R1a* of cAMP-dependent protein kinase A (RET-PTC-2) and *ELF-1* (RET-PTC-3).

The scope of the present invention also includes cancers and other proliferative diseases, e.g., rheumatoid arthritis, now known or discovered in the future to be characterized by specific chromosomal aberrations giving rise to fusion proteins.

In at least some cases, heterogeneity of breakpoints within the affected chromosomes is possible, thus providing for the possibility of many different DNA fusions and amino acid sequence variations than those specifically listed in the SEQ ID NOs provided, and which can also be formed by the chromosomal rearrangements, e.g., translocations, inversions, deletions, insertion/duplications, etc., so designated. For example, many different *abl-bcr* gene combinations and corresponding fusion proteins can be designated by the t(9; 22)(q34; q11) translocation event, and all—not just those listed below—are included within the purview of the designation, t(9;22)(q34;q11).

Aberrant proteins of the invention, at least in some instances, feature one or more properties of the individual normal parent genes' gene products (normal polypeptide gene product(s), including e.g., functional and structural domains and subportions thereof resulting from transcription and translation of normal parent genes on normal
5 chromosomes) but otherwise lack exact identity and function with the parent genes' protein products. Chromosomal aberrations may give rise to in-frame fusions or frame-shifts, the latter of which can account for missense or nonsense translation of at least a portion of the mRNA, and thereby result in aberrant polypeptide product(s).

Of the SEQ ID NOs discussed herein, some reflect fusion genes, some reflect
10 fusion gene products, e.g., mRNAs and peptides, and some reflect portions of such entities. Still some others reflect recombination "hot spots" in the normal genes that have a general propensity to form a chromosomal aberration. Each of the above sequences may be useful as diagnostic markers in appropriate embodiments of the invention and/or may be characteristic of a given proliferative disorder (or patient exhibiting such and,
15 accordingly, a candidate for treatment according to some methods of the invention.

While the specific sequences discussed are predominantly human in origin, it is understood that other animal "homologs" of the corresponding human sequences are known in the art and are intended to be within the purview of various aspects of the invention. Because HSP90s are also found in plants, plants and plant cells and tissues
20 exhibiting fusion protein products that give rise to undesirable traits may also be treatable in some aspects and embodiments of the invention. The NCBI nucleotide and protein databases are an example of where such sequences can be found. It is also appreciated that the complete human genome and other genomes have been sequenced, and continue to be sequenced at a high rate, thus facilitating the identity of sequences contiguous with
25 those listed herein and homologs thereto.

Further, some of the sequences listed herein may contain errors associated with the logistical complexities of compiling such extensive data, and the true sequences should be interpreted to be within the scope of the invention, either literally or under the doctrine of equivalents, as they are known in the art.

30 As those of ordinary skill will appreciate, allelic variations and different isotype proteins are also possible for some genes, e.g., the product of differential splicing events in

mRNA, and these are likewise considered within the scope of the invention. Further, some of the NCBI and SEQ ID NOs listed below are for wild-type genes, and are included to give an indication of the different chimeric possibilities for the fused counterpart during a chromosomal aberration according to the invention. Should any of the sequences listed below be in error, such should be construed consistent with what is commonly understood in the art—irrespective of how presented in the application.

c. Further Discussion of Illustrative Chromosomal Aberrancies

Convention: where two or more SEQ ID NOs are provided per NCBI accession #, peptide(s) shall be listed first where applicable, followed by corresponding mRNA/cDNA and/or genomic sequence as the case may be. The terms “nucleotide” and “nucleotides” are interchangeable with, and may be symbolized by, “nt.”

t(9; 22)(q34; q11)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # S72478, corresponding to SEQ ID NOs 1 and 2, illustrates one aberrant polypeptide/mRNA in a patient having CML and another patient having ALL. The junction for the nucleic acid sequence between the BCR and ABL genes is stated to reside between nucleotides 100 and 101., with 1-100 derived from BCR and 101-140 derived from ABL.

NCBI #M19695 (SEQ ID NO 3) illustrates a nucleic acid sequence identified from a human myelocytic chimeric bcr/chromosome 9 fusion (CML K562 cell line).

NCBI #M30829 (SEQ ID NOs 4 and 5) illustrates a partial bcr/abl fusion protein mRNA.

NCBI #M13096 (SEQ ID NO 6) illustrates a human chimeric bcr/c-abl fusion protein gene characteristic of cell line K562.

NCBI #M30832 (SEQ ID NOs 7 and 8) corresponds to a human bcr/abl fusion protein, partial cds, clone E3 from cell line EM2.

NCBI # AJ131466 (SEQ ID NOs 9 and 10) corresponds to a partial human bcr/abl (major breakpoint) fusion peptide and the underlying nucleic acid encoding it. Nucleotides 1-373 are said to derive from exons 11-14 of the bcr gene, and nucleotides 374-997 are said to derive from exons 2-4 of the abl gene.

5 NCBI # AF192533 (SEQ ID NOs 11 and 12) corresponds to a partial human bcr/abl (major breakpoint) fusion mRNA. Nucleotides 1-289 are said to come from the bcr gene of chromosome 22 and nucleotides 290-305 from the abl gene of chromosome 9.

10 NCBI # AF321981 (SEQ ID NO 13) corresponds to a BCR-ABL fusion transcript e15a2 mRNA sequence. This particular fusion is stated to result from results from a translocation between the 3' portion of the c-ABL oncogene on chromosome 9 and exon 15 of the BCR gene on chromosome 22; t(9;22).

15 NCBI # M17543 (SEQ ID NO 14) corresponds to at least a portion of a Philadelphia chromosome breakpoint cluster region associated with one embodiment of a bcr abl fusion gene. Nucleotides 1-31 are said to be exon 1 and nucleotides 32-63 are said to be intron A.

NCBI # M17542 (SEQ ID NOs 15 and 16) corresponds to a human bcr/abl fusion protein mRNA (product of translocation t(22q11; 9q34)), exons 1 and 2. Nucleotides 1-31 are stated to denote exon 1 and nucleotides 32-63 are stated to denote exon 2.

20 NCBI # M17541 (SEQ ID NOs 17 and 18) corresponds to a human bcr/abl fusion protein mRNA (product of translocation t(22q11; 9q34)), exons 1 and 2. Nucleotides 1-31 are stated to denote exon 1 and nucleotides 32-63 are stated to denote exon 2.

25 NCBI # AB069693 (SEQ ID NOs 19 and 20) denotes a human partial mRNA corresponding to a bcr/abl e8a2 fusion protein. BCR exons 7 (nucleotides 1-53) and 8 (nucleotides 54-194) are joined to ABL intron 1b inverted (nucleotides 195-249) and ABL exon a2 (nucleotides 250-423).

NCBI # AJ131467 (SEQ ID NOs 21 and 22) correspond to a human partial BCR/ABL chimeric fusion peptide and corresponding mRNA. Nucleotides 1-117 denote exon 1 of the bcr gene, nucleotides 118-193 and 194-298 denote exons 12 and 13 of the

bcr gene, and nucleotides 299-472, 473-768, and 769-922 respectively denote exons 2-4 of the abl gene.

NCBI # AF113911 (SEQ ID NOs 23 and 24) correspond to a partial BCR-ABL minor breakpoint peptide (BCR-ABL fusion) mRNA. Nucleotides 1-455 are stated to be
 5 from chromosome 22 and nucleotides 456-1079 from chromosome 9.

NCBI # AF251769 (SEQ ID NOs 25 and 26) correspond to a human partial bcr/abl e1-a3 chimeric fusion protein (BCR/ABL_{e1-a3}) mRNA. Nucleotides 1-455 are stated to be from chromosome 22 and nucleotides 456-1079 from chromosome 9.

inv14 (q11; q32)

10 This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # X82240 (SEQ ID NOs 27 and 28) correspond to at least a portion of an mRNA for the gene TCL1, which is disrupted in aberrations of the type noted.

NCBI # NM_021966 (SEQ ID NOs 29 and 30) relate to a human T-cell
 15 leukemia/lymphoma 1A (TCL1A), mRNA.

NCBI # X82241 (SEQ ID NO 31) relates to a 5' portion of a human TCL1 gene. Nucleotides 496-560 are said to correspond to exon 1.

NCBI # M14198 (SEQ ID NOs 32 and 33) relate to a human chromosome 14 paracentric inversion producing an heavy chain/T-cell receptor J-alpha fusion protein.

20 NCBI # X03752 (SEQ ID NOs 34 and 35) relate to a human gene for rearranged Ig V(H) are said to encode the IgVH region (108 aa) and nucleotides 324 to 377 are said to encode 18 amino acids of the TCR-J-alpha protein.

NCBI # M12071 (SEQ ID NOs 36 and 37) relates to a human Ig heavy-chain V-region gene (VII family) rearranged to T-cell receptor alpha-chain D-J-sp region (IgT) in
 25 an inv(14)(q11; q32), SUP-T1 cell line. Nucleotides 121-166 are said to derive from exon 1 of the IgH gene, nucleotides 167-248 from intron 1 of the IgH gene, nucleotides 249-623 from exon 2 of the IgH gene, and nucleotides 624-675 from intron 2 of the IgH gene.

NCBI # S45947 (SEQ ID NOs 38 and 39) relate to an IgT=T cell specific exon ET-immunoglobulin VH-T cell receptor J alpha fusion [human, T cell lymphoma cell line SUP-T1, mRNA Mutant, 508 nt]. Nucleotides 34-507 are stated to be IgT coding sequence.

5 NCBI # S45207 (SEQ ID NOs 40 and 41) relate to an IgT=T cell specific exon ET-exon EX-immunoglobulin VH-T cell receptor J alpha fusion [human, T cell lymphoma cell line SUP-T1, mRNA Mutant, 616 nt]. Nucleotides 130-616 are stated to be IgT coding sequence.

t(1; 19)(q23; p13.3)

10 This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # M31522 (SEQ ID NOs 42 and 43) relate to a human translocation (t1;19) fusion protein (E2A/PRL) mRNA, 3' end.]. Nucleotides 1-1653 are stated to encode a portion of an E2A/PRL fusion protein.

15 **t(17; 19)(q22; p13)**

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # M95586 (SEQ ID NOs 44 and 45) relate to a human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds. Nucleotides 31-1755 are said to be coding
20 sequence.

t(15; 17)(q21-q11-22)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # S50916 (SEQ ID NOs 46 and 47) relate to a PML-RAR fusion gene
25 {fusion transcript} [human, mRNA Partial, 1284 nt]. . Nucleotides 1-1251 are said to be coding sequence.

NCBI # M73779 (SEQ ID NOs 48 and 49) relate to a human PML-RAR protein (PML-RAR) mRNA, complete cds; coding sequence: nucleotides 67-2460.

NCBI # AJ417079 (SEQ ID NOs 50 and 51) relate to a human partial mRNA for PML/RARA fusion protein (PML/RARA gene); Nucleotides 1-109 derive from exon 6 of PML, nucleotides 110-172 from intron 2 of RARA, and nucleotides 173-296 from exon 3 of RARA.

t(11; 17)(q23; q21.1)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # AAB29813 (SEQ ID NO 52) relates to a retinoic acid receptor alpha, RAR alpha(PLZF=zinc finger protein, PLZF-RAR alpha isoform A=fusion protein) {translocation} [human, acute promyelocytic leukemia patient, Peptide Mutant, 858 aa].

NCBI # AAB29814 (SEQ ID NO 53) relates to a PLZF=zinc finger protein(retinoic acid receptor alpha, RAR alpha, RAR alpha 1-PLZF isoform B=fusion protein) {translocation} [human, acute promyelocytic leukemia patient, Peptide Mutant, 277 aa].

t(4; 11)(q21; q23)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # L22179 (SEQ ID NOs 54 and 55) relate to a human MLL-AF4 der(11) fusion protein mRNA, complete cds. Nucleotides 5-6940 are said to be coding sequence.

NCBI # S67825 (SEQ ID NOs 56 and 57) relate to a human ALL1-AF4 fusion protein mRNA, partial cds. Nucleotides 1-585 are said to derive from chromosome 11 and nucleotides 586-832 from chromosome 4.

NCBI # AF024541 (SEQ ID NOs 58 and 59) relate to a human MLL-AF4 fusion protein mRNA, partial cds. The codons are said to start with nucleotide 3.

NCBI # AF031404 (SEQ ID NOs 60 and 61) relate to a human MLL-AF4 fusion protein mRNA, partial cds. Nucleotides 1-305 are said to derive from chromosome 11 and nucleotides 306-741 from chromosome 4. Codons begin with nucleotide 3.

5 NCBI # L04731 (SEQ ID NO 63) relates to a human translocation T(4;11) of the human ALL-1 gene to chromosome 4.

NCBI # AF177237 (SEQ ID NOs 64 and 65) relate to human cell-line MV4-11, MLL/AF4 fusion protein (MLL/AF4) mRNA, partial cds. Nucleotides 1-62 derive from exon 6 of the MLL gene on chromosome 11, and nucleotides 63-450 from exon 5 of the AF4 gene on chromosome 4.

10 NCBI # AF177236 (SEQ ID NOs 66 and 67) relate to a human A1 MLL/AF4 fusion protein (MLL/AF4) mRNA, partial cds. Nucleotides 1-63 are stated to derive from exon 6 of the MLL gene on chromosome 11, and nucleotides 64-450 from exon 5 of the AF4 gene on chromosome 4.

15 NCBI # AF031403 (SEQ ID NO 68) relates to a human MLL/AF4 translocation breakpoint t(4;11)(q21;23). Nucleotides 1-105 are said to derive from exon 5 of MLL, nucleotides 435-508 from exon 6 of MLL, nucleotides 2195-2326 from exon 7 of MLL, nucleotides 2874-2987 from exon 8 of MLL, and nucleotides 3645-6983 from AF4.

20 NCBI # AF177238 (SEQ ID NOs 69 and 70) relate to a human A1 AF4-MLL fusion protein (AF4-MLL) mRNA, partial cds. Nucleotides 1-484 are said to derive from exon 3 of AF4 and nucleotides 485-596 from exon 7 of MLL.

NCBI # AF177239 (SEQ ID NOs 71 and 72) relate to a human cell-line MV4-11 AF4-MLL fusion protein (AF4-MLL) mRNA, partial cds. Nucleotides 1-484 are said to derive from exon 3 of AF4 and nucleotides 485-596 from exon 7 of MLL

25 NCBI # AF397907 (SEQ ID NO 73) relates to a human AF4/MLL translocation breakpoint region. Nucleotides 1-437 are said to derive from intron 3 of AF6, nucleotides 440-631 from intron 6 of MLL, and nucleotides 632-747 from exon 7 of MLL. The breakpoint is approximately nucleotide 438-439, which was undetermined due to GC compressions.

NCBI # AF024543 (SEQ ID NO 74) relates to a human MLL/AF4 translocation breakpoint t(4;11)(q21;q23).

t(9; 11)(q21; q23)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # S82034 (SEQ ID NO 75) relates to an MLL-AF9=fusion gene {fusion site} [human, peripheral blood, acute myeloid leukemia FAB type M1 patient UPN 427, mRNA Partial, 60 nt].

t(11; 19)(q23; p13)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # S81007 (SEQ ID NO 76) relates to an MLL/ENL=fusion gene {rearranged derivative 11 junction region} [human, leukemic lymphoblasts, T-cell acute lymphoblastic leukemia patient RUPN2, Genomic Mutant, 74 nt]. The authors indicated that the first 34 nt derived from MLL intron 8 on 11q23, and nt 35-74 from the ENL-distal region on 19p13.3

NCBI # S81008 (SEQ ID NO 77) relates to an ENL {rearranged derivative 19 junction region} [human, leukemic lymphoblasts, T-cell acute lymphoblastic leukemia patient RUPN2, Genomic Mutant, 84 nt]. The authors indicated that nt 55-84 derived from MLL gene 3' region on 11q23.

t(X; 11)(q13; q23)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # NM_005938 (SEQ ID NOs 78 and 79) relate to a human myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7 (MLLT7), mRNA. Nucleotides 183-1688 denote an MLLT7 coding

region, with nucleotides 465-719 and 480-749 corresponding to a forkhead and forkhead domain, and G and C allelic variations possible at nucleotide 1435.

NCBI # X93996 (SEQ ID NOs 80 and 81) relate to a human mRNA for AFX protein. Nucleotides 183-1688 are said to be AFX coding sequence.

5 **t(1; 11)(p32; q23)**

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # AF331760 (SEQ ID NO 82) relates to human clone UPN5379L mRNA sequence (bone marrow acute lymphoblastic FAB L2 type).

10 **t(6; 11)(q27; q23)**

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # S82519 (SEQ ID NOs 83 and 84) relate to a human MLL-AF6 fusion protein mRNA, partial cds, identified in a leukemic patient, and with the breakpoint stated
15 to be approximately between nt 26 and 27.

NCBI # S82521 (SEQ ID NOs 85 and 86) relate to a an MLL-AF6=fusion gene {breakpoint region, clone b} [human, blood, leukemic patient 2, mRNA Partial, 69 nt]. The breakpoint here is said to reside between nt 24 and 25.

NCBI # S82517 (SEQ ID NOs 87 and 88) relate to an MLL-AF6=fusion gene
20 {breakpoint region} [human, blood, leukemia patient 1, mRNA Partial, 69 nt]. The breakpoint here is said to reside between nt 24 and 25.

t(11; 17)(q23; q21)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

25 NCBI # S72604 (SEQ ID NOs 89 and 90) relate to an AF17...ALL-1 {reciprocal translocation} [human, acute myeloid leukemia patient, mRNA Partial Mutant, 3 genes,

228 nt]. Nucleotides 1-88 are said to derive from AF17 and nucleotides 89-228 from ALL-1.

NCBI # (SEQ ID NOs 91 and 92) relate to a human myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*); translocated to, 6 (MLLT6), mRNA.

- 5 Nucleotides approximating 22-168 are said to encode a PHD zinc finger motif and nucleotides 2185-2292 (amino acids 729-764) are said to encode a leucine zipper motif, with A and G allelic variations at nt 592 possible.

t(8; 21)(q22; q22)

- 10 This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # (SEQ ID NOs 93 and 94) relate to a human mRNA for AML1-MTG8 fusion protein, complete cds. The coding sequence is said to be nucleotides 1579-3837 and the breakpoint is said to be between nt 2110 and 2111.

- 15 NCBI # S78158 (SEQ ID NOs 95 and 96) relate to a human AML1-ETO fusion protein (AML1-ETO) mRNA, partial cds. Nucleotides 1-1767 are said to denote the coding sequence.

NCBI # S78159 (SEQ ID NOs 97 and 98) relate to a human AML1-ETO fusion protein (AML1-ETO) mRNA, partial cds. . Nucleotides 1-696 are said to denote the coding sequence and nucleotides 40 and 41 are said to represent the junction point.

- 20 NCBI # D14822 (SEQ ID NOs 99 and 100) relate to a human chimeric partial mRNA derived from AML1 and MTG8(ETO) gene sequences. Nucleotides 1-101 are said to derive from the AML1 gene on chromosome 21 and nucleotides 102-799 from the MTG8 (ETO) gene on chromosome 8.

- 25 NCBI # S45790 (SEQ ID NO 101) relates to a AML1/ETO=acute myelogenous leukemia {translocation breakpoint} [human, Genomic Mutant, 237 nt].

NCBI # Z35296 (SEQ ID NO 102) relates to a human AML1/ETO alternative fusion transcript mRNA, 276bp. Nucleotides 1-117 are said to derive from AML1 and 186-276 are said to derive from ETO.

NCBI # D14823 (SEQ ID NOs 103 and 104) relate to a human chimeric mRNA derived from AML1 gene and MTG8(ETO) gene, partial sequence. Nucleotides 1-101 are said to be derived from the AML1 gene on chromosome 21 and nucleotides 102-1446 are said to be derived from the MTG8(ETO) gene on chromosome 8, with the coding
 5 sequence denoted nt 1-757.

t(3; 21)(q26; q22)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # S69002 (SEQ ID NOs 105 and 106) relate to a AML1-EVI-1=AML1-
 10 EVI-1 fusion protein {rearranged translocation} [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]. The author indicated the boundary between AML1 and EVI-1 to be between nt 2138 and 2139, with the coding sequence being 1603-5790.

NCBI # L21756 (SEQ ID NOs 107 and 108) relate to a human acute myeloid leukemia associated protein (AML1/EAP) mRNA, complete cds. Nucleotides 1-786 are
 15 said to denote the coding sequence.

NCBI # S76343 (SEQ ID NO 109) relates to AML1...EAP {translocation breakpoint} [human, chronic myelogenous leukemia in blast crisis patient, Genomic Mutant, 3 genes, 470 nt]. Nucleotides 1-125 are said to derive from AML1 and nucleotides 126-470 are said to derive from EAP.

20 **t(16; 21)(p11; q22)**

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # S71718 (SEQ ID NOs 110 and 111) relate to a TLS/FUS...ERG {translocation} [human, myeloid leukemia patient, peripheral blood, bone marrow cells,
 25 mRNA Partial Mutant, 3 genes, 55 nt]. Nucleotides 46-55 are said to derive from ERG, with the codon start beginning with nt 3.

NCBI # S71805 SEQ ID NOs 112 and 113) relate to a TLS/FUS...ERG {translocation} [human, myeloid leukemia patient, peripheral blood, bone marrow cells,

mRNA Partial Mutant, 3 genes, 99 nt]. Nucleotides 1-89 are said to derive from TLS/FUS and nucleotides 90-99 from ERG, with the codon start beginning with nt 3.

NCBI # Y10001 (SEQ ID NO 114) relates to a DNA fragment containing fusion point of FUS gene and ERG gene, translocation t(16;21)(p11;q22).

5 **t(6; 9)(p23; q34)**

NCBI # X64229 (SEQ ID NOs 115 and 116) relate to a human dek mRNA. The coding sequence is said to be nt 34-1161.

inv(9;9)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # X63689 (SEQ ID NO 117) relates to a human translocation breakpoint in the “can” gene sequence. The translocation breakpoint is said to be 174..175.

NCBI # M93651 (SEQ ID NOs 118 and 119) relate to a human set gene, complete cds. The coding sequence is said to be 4-837.

15 **t(4; 16)(q26; p13)**

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # Z14955 (SEQ ID NOs 120 and 121) relate to a human mRNA encoding the interleukin 2/BCM fusion protein. Nucleotides 1-321 derive from exons 1-3 of IL-2 and nucleotides 322-864 from the BCM gene.

20 **inv(16)(p13q22)**

This inversion is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # AF251768 (SEQ ID NOs 122 and 123) relate to a human
25 PCBFB/MYH11E chimeric fusion protein (CBFB/MYH11) mRNA, partial cds.

Nucleotides 1-41 correspond to exon 5 of CBFB and nucleotides 42-78 to exon 7 of MYH11.

NCBI # AF249898 (SEQ ID NOs 124 and 125) relate to a human PCBFbeta/MYH11A chimeric fusion protein (CBFbeta/MYH11A) mRNA, partial cds.

5 Nucleotides 1-41 correspond to exon 5 of CBFB and nucleotides 42-102 to exon 12 of MYH11.

NCBI # AF249897 (SEQ ID NOs 126 and 127) relate a human PCBFb-MYH11d chimeric fusion protein (CBFB/MYH11D) mRNA, partial cds. Nucleotides 1-41 correspond to exon 5 of CBFB and nucleotides 42-109 to exon 8 of MYH11.

10 NCBI # AF390860 (SEQ ID NO 128) relates to a human isolate UPN2 CBFB/MYH11 translocation breakpoint region sequence.

NCBI # AF390859 (SEQ ID NO 129) relates to a human isolate UPN1 CBFB/MYH11 translocation breakpoint region sequence.

15 NCBI # AF202996 (SEQ ID NOs 130 and 131) relate to human core binding factor beta-smooth muscle myosin heavy chain fusion protein (CBFB-MYH11) mRNA, partial cds. Nucleotides 1-46 are said to correspond to 16q22 and nucleotides 47-89 to 16p13. Nucleotide 50 is said to be a "t" in some cases.

t(5; 12)(q33; p13)

20 This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # NM_001987 (SEQ ID NOs 132 and 133) relate to a human ets variant gene 6 (TEL oncogene) (ETV6), mRNA. Nucleotides 25-1383 are said to correspond to coding sequence, of which nt 136-393 are said to correspond to a sterile alpha motif (SAM) pointed domain, nt 1036-1290 to an erythroblast transformation-specific (Ets)-
25 domain, and wherein allelic variations including "c"s and "t"s at each of nt 798, nt 1541, and nt 1598, and an "a"s and "c"s at each of nt 1822 and 1881.

NCBI # U11732 (SEQ ID NOs 134 and 135) relate to a human ets-like gene (tel) mRNA, complete cds. The coding sequence is said to be from nt 25-1383, and the translocation breakpoint said to occur after nt 487.

t(2; 5)(2p23; q35)

5 This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI #14: AF032882 (SEQ ID NO 136) relates to a human anaplastic lymphoma kinase receptor (ALK) and nucleophosmin (NPM) truncated genes at a t(2;5) translocation breakpoint. Nucleotides 1-46 are said to be ALK sequence that is truncated at 3' due to
10 translocation, and nucleotides 1370-1451 are said to be NPM sequence that is truncated at 5' due to translocation.

NCBI # S82740 (SEQ ID NO 137) relates to a NPM/ALK=fusion gene {translocation breakpoint} [human, lymphoma cells SUP-M2, Genomic, 1565 nt].

NCBI # S82725 (SEQ ID NO 138) relates to a NPM/ALK=fusion gene
15 {translocation breakpoint} [human, lymphoma cells SU-DHL-1, Genomic, 1679 nt].

NCBI # U04946 SEQ ID NOs 139 and 140) relate to a human nucleophosmin-anaplastic lymphoma kinase fusion protein (NPM/ALK) mRNA, complete cds. The recombination junction is said to occur at nt 353.

t(11; 22) (q24; q12)

20 This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # AJ229320 (SEQ ID NO 141) relates to a human translocation t(11;22) DNA in ewings's tumor derivative 22 (isolate: EWTUM64/ MIC). Nucleotides 1-88 are said to denote EWS sequence and nucleotides 89-180 FLI-1 sequence.

25 NCBI # AJ229311 SEQ ID NO 142) relates to a human translocation t(11;22) DNA in ewings's tumor derivative 22 (isolate: EWTUM56/ EW20). Nucleotides 1-114 are said to denote EWS sequence and nucleotides 115-180 FLI-1 sequence.

NCBI # AF177752 (SEQ NO 143) relates to a human clone Jugo Ewing's sarcoma-specific EWS-FLI1 chimera target sequence.

NCBI # AF177751 (SEQ ID NO 144) relates to a human Juyon Ewing's sarcoma-specific EWS-FLI1 chimera target sequence.

5 NCBI # AF177750 (SEQ ID NO 145) relates to a human clone Iti Ewing's sarcoma-specific EWS-FLI1 chimera target sequence.

NCBI # AF327066 SEQ ID NOs 146 and 147) relate to a human Ewings sarcoma EWS-Fli1 (type 1) oncogene mRNA, complete cds.

10 NCBI # XM_060745 (SEQ ID NOs 148 and 149) relate to a human similar to EWS/FLI1 activated transcript 2 (H. sapiens) (LOC127935), mRNA. Nucleotides 10-225 and 13-195 are said to denote src homology 2 (SH2) domains.

NCBI # AF403479 SEQ ID NOs 150 and 151) relate to a human EWS/FLI1 activated transcript 2 protein mRNA, complete cds.

15 NCBI # AF020264 (SEQ ID NOs 152 and 153) relate to a human EWS/FLI1 activated transcript 2 homolog (EAT-2) gene, partial cds.

NCBI # AF020263 (SEQ ID NOs 154 and 155) relate to a Mus musculus EWS/FLI1 activated transcript 2 (EAT-2) mRNA, complete cds.

20 NCBI # S72620 SEQ ID NOs 156 and 157) relate to a EWS...Fli1 [human, T93-113 tumor, mRNA Partial Mutant, 3 genes, 229 nt]. Nucleotides 1-85 are said to denote partial EWS gene sequence and nt 86-229 are said to denote partial FLI-1 sequence.

NCBI # S64709 (SEQ ID NO 158) relates to EWS...Fli-1 {translocation} [human, IARC-EW11 Ewing's tumor-derived cells, mRNA Mutant, 3 genes, 100 nt]. Nucleotides 1-18 are said to denote partial EWS gene sequence and nt 19-100 are said to denote partial FLI-1 sequence.

25 NCBI # S62665 (SEQ ID NOs 159 and 160) relate to a type 4 EWS-FLI1 fusion {translocation} [human, primitive neuroectodermal tumor cell line TC-32, mRNA Partial Mutant, 60 nt]. Positions 1-31 are said to be from the 5' portion of EWS on chromosome

22 and positions 32-60 are said to be from the 3' (DNA-binding) region of FLI1 on chromosome 11.

inv(10)(q11.2; q21)

This aberration is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # AF395885 (SEQ ID NO 161) relates to a human H4/RET fusion mRNA, partial sequence. tyrosine kinase domain of the ret. Nt 1-83 are said to derive from H4, nt 84-142 from an unidentified insertion sequence, and nt 143-447 from ret. The tyrosine kinase domain in the ret portion is said be constitutively active in the fusion product.

NCBI # NM_005436 (SEQ ID NOs 162 and 163) relate to a human DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1, (D10S170), mRNA. Nt 37-1794 are said to represent coding sequence, nt 202-996 said to encode a myosin tail, nt 610-999 an Ezrin/radixin/moesin family (ERM) region, with "a" and "c" allelic variation possible at nts 979, 1080, and 1445, and "a" and "g" possible at nt 1362, and "t" and "c" possible at nts 1996 and 2642.

NCBI # S77910 (SEQ ID NO 164) relates to H4= gene frequently rearranged with the ret proto-oncogene {promoter} [human, Genomic, 447 nt]. Nt 442-447 are said to correspond to the coding sequence, "MA".

NCBI # S72869 (SEQ ID NOs 165 and 166) relate to H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]. Nt 37-1794 are said to correspond to coding sequence.

NCBI # X65617 (SEQ ID NO 167) relates to a human ret proto-oncogene DNA. Nt 1-54 are said to replace sequences from the H4 gene, nt 55-787 are said to correspond to an intron between the transmembrane and tyrosine kinase domain, and nt 788-808 said to correspond to an exon coding for a tyrosine kinase domain.

t(12;22)(q13;q12)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # NM_005171 (SEQ ID NOs 168 and 169) relate to a human activating transcription factor 1 (ATF1), mRNA. Nt 157-252 are said to correspond to a pKID domain and nt 631-795 are said to correspond to a bZIP transcription factor region.

NCBI # AF047022 (SEQ ID NOs 170 and 171) relate to a human RNA binding
 5 protein-activating transcription factor-1 fusion protein (EWS-ATF1) mRNA, partial cds. Nt 1-65 are said to correspond to chromosome 22 and nt 66-353 to chromosome 12, with nt 66^67 said to represent the fusion junction between the EWS and ATF1 genes.

t(12; 16(q13; p11))

This translocation is generally addressed in Figure 1. Illustrative embodiments
 10 include but are not limited to events comprising the sequences:

NCBI # AJ301614 (SEQ ID NO 172) relates to a human t(12;16)(q13;p11) translocation breakpoint (CHOP/FUS chimaeric genomic DNA). Nt 1-225 are said to correspond to the CHOP gene (chromosome 12) and nt 226-500 to the FUS gene (chromosome 16).

15 NCBI # AJ301613 (SEQ ID NO 173) relates to a human t(12;16)(q13;p11) translocation breakpoint (FUS/CHOP chimaeric genomic DNA). Nt 1-317 are said to correspond to the FUS gene (chromosome 16) and nt 318-521 to the CHOP gene (chromosome 12).

NCBI # AJ301612 (SEQ ID NOs 174 and 175) relate human partial mRNA for
 20 FUS/CHOP chimaeric fusion protein (type 9 transcript variant). Nt 1-118 are said to originate from chromosome 16 and nt 119-225 are said to originate from chromosome 12.

NCBI # AJ301611 (SEQ ID NOs 176 and 177) relate to a human partial mRNA for FUS/CHOP chimaeric fusion protein (type 8 transcript variant). Nt 1-128 are said to originate from chromosome 16 and nt 129-235 are said to originate from chromosome 12.

25 NCBI # NM_004960 (SEQ ID NOs 178 and 179) relate to a human fusion protein derived from t(12;16) malignant liposarcoma (FUS), mRNA. Nt 79-1659 are said to denote the coding sequence. Allelic variation is stated to be possible at nts 225 (a/c), 369 (c/t), and 1586 (a/g). Nt 937-1173 are said to denote an RNA recognition motif

(RRM), and nt 1354-1425 are said to denote a zinc finger domain in a Ran binding proteins (zf-Ranbp).

NCBI # S75762 (SEQ ID NOs 180 and 181) relate to a FUS...CHOP [human, myxoid liposarcoma specimens, mRNA Partial Mutant, 3 genes, 652 nt]. Nucleotides 1-272 are said to derive from FUS.

NCBI # X71427 (SEQ ID NOs 182 and 183) relate to a human mRNA for FUS-CHOP protein fusion. Nucleotides 70-1458 are said to denote the fusion coding sequence.

NCBI # X71428 (SEQ ID NOs 184 and 185) relate to a human mRNA for FUS glycine rich protein. Nucleotides 73-1650 are said to denote the coding sequence.

NCBI # Y10004 (SEQ ID NO 186) relates to a human DNA fragment containing fusion point of FUS gene and CHOP gene, translocation t(12;16)(q13;p11). The sequence is said to contain 5'-FUS intron 7 sequence and intron 1 3' sequence from CHOP.

NCBI # Y10003 (SEQ ID NO 187) relates to a human DNA fragment containing fusion point of FUS gene and CHOP gene, translocation t(12;16)(q13;p11). The sequence is said to contain 5'-FUS intron 7 sequence and intron 1 3' sequence from CHOP.

NCBI # Y10002 (SEQ ID NO 188) relates to a human DNA fragment containing fusion point of FUS gene and CHOP gene, translocation t(12;16)(q13;p11). The sequence is said to contain 5'-FUS intron 7 sequence and intron 1 3' sequence from CHOP.

NCBI # S75763 (SEQ ID NOs 189 and 190) relate to a FUS...CHOP [human, myxoid liposarcoma specimens, mRNA Partial Mutant, 3 genes, 377 nt]. Nt 1-272 are said to derive from FUS and nt 273-377 from CHOP.

t(2; 13)(q35;q14)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # U02308 (SEQ ID NOs 191 and 192) relate a human PAX-3-FKHR gene fusion mRNA, partial cds. Nt 1-2070 are said to be coding sequence.

t(x; 18)(p11.2; q11.2)

This translocation is generally addressed in Figure 1. Illustrative embodiments include but are not limited to events comprising the sequences:

NCBI # S79894 (SEQ ID NOs 193 and 194) relate to a SYT...SSX {translocation
5 breakpoint} [human, synovial sarcoma patient, tumor, mRNA Mutant, 3 genes, 165 nt].
Nt 1-18 are said to derive from SYT and nt 22-165 from SSX.

NCBI # X86175 (SEQ ID NOs 195 and 196) relate to a human mRNA for SSX2 protein. Nt 92-658 are said to be coding sequence.

The following chromosomal aberrations are not discussed in Figure 1 and will now
10 be discussed in more detail:

t(12:21)(p13;q32)

The TEL (ETV6)-AML1 (CBFA2) gene fusion is the most common reciprocal chromosomal rearrangement in childhood cancer, occurring in approximately 25% of the most predominant subtype of leukemia- common acute lymphoblastic leukemia. Ford et
15 al., Proc. Natl. Acad. Sci. U.S.A. 95 (8), 4584-4588 (1998), reported characterization of the translocation event responsible for one TEL-AML1 genomic sequence in a pair of monozygotic twins diagnosed at ages 3 years, 6 months and 4 years, 10 months with common acute lymphoblastic leukemia. The twins shared an identical rearranged IgH allele. These data have implications for the etiology and natural history of childhood
20 leukemia.

Other articles of interest on this subject include: Wiemels et al., *Protracted and variable latency of acute lymphoblastic leukemia after TEL-AML1 gene fusion in utero*, Blood. 1999 Aug 1;94(3):1057-62; Rubnitz et al., *The role of TEL fusion genes in pediatric leukemias*, Leukemia, 1999 Jan;13(1):6-13. Review; Romana et al., *The t(12;21)
25 of acute lymphoblastic leukemia results in a tel-AML1 gene fusion*, Blood. 1995 Jun 15;85(12):3662-70; Seeger et al., *TEL-AML1 fusion in relapsed childhood acute lymphoblastic leukemia*, Blood. 1999 94(1):374-6; Bayar et al., *Monozygotic twins with congenital acute lymphoblastic leukemia (ALL) and t(4;11)(q21;q23)*, Cancer Genet Cytogenet. 1996 Jul 15;89(2):177-80; Kobayashi et al., *Detection of the Der (21)t(12;21)*

chromosome forming the *TEL-AML1* fusion gene in childhood acute lymphoblastic leukemia, *Leuk Lymphoma*. 1997 Dec;28(1-2):43-50; and Shurtleff et al., *TEL/AML1 fusion resulting from a cryptic t(12;21) is the most common genetic lesion in pediatric ALL and defines a subgroup of patients with an excellent prognosis*, *Leukemia*, 1995 (12):1985-9.

NCBI# AF044317 (SEQ ID NO 197) relates to a human TEL/AML1 fusion gene, partial sequence. This was derived from an ALL infant. Nts 1-407 are said to derive from TEL and nts 408-548 from AML-1.

NCBI # AF231770 (SEQ ID NO 198) relates to a human ETV6/AML1 translocation breakpoint region.

t(9;12)(q34; p13)

In human leukemia, activation of the ABL proto-oncogene locus on chromosome 9 most commonly occurs as a result of its fusion to the BCR locus on chromosome. Papadopoulos et al., *Cancer Res.* 55 (1), 34-38 (1995), reported a t(9;12) event—a chimeric ABL protein displaying an elevated tyrosine kinase activity fused to a TEL protein from chromosome 12. Like BCR, TEL is fused in-frame with ABL and produces a fusion protein with an elevated tyrosine kinase activity when assayed in an immune complex. The amino-terminal sequences of TEL encodes a helix-loop-helix motif which may mediate dimerization. 43: *See also* Okuda et al., *Oncogene*. 1996 Sep 19;13(6):1147-52.

NCBI # Z36279 (SEQ ID NO 199) relates to a human (9TX) breakpoint position DNA for the tel-abl fusion identified by Papadopoulos et al. The translocation breakpoint is said to reside between nt 567 and 568.

del(12p)

Revy et al., *Cell* 102:565-575 (2000), reported hyper IgM immunodeficiencies associated with deletions of 19 and 9 bases at cDNA positions 21 and 175 respectively of the activation-induced cytidine deaminase (AID) gene. The former results in a 6 amino acid deletions and a phe15 to ter premature nonsense codon. The latter results in a 3-amino acid deletion and leu59-to -phe substitution.

NCBI # AB040430 (SEQ ID NOs 200 and 201) relate to a human AID gene for activation-induced cytidine deaminase, complete cds.

NCBI # AB040431 (SEQ ID NO 202 and 203) relate to a human AID mRNA for activation-induced cytidine deaminase, complete cds. Nt 77-673 is said to be coding
5 sequence.

NCBI # NM_020661 (SEQ ID NOs 204 and 205) relate to a human activation-induced cytidine deaminase (AICDA), mRNA. Nt 77-673 is said to be coding sequence. Allelic variation (a/g) is said to occur at nt 541.

t(15;17)(q22;q12)

10 de The et al., Cell 1991 Aug 23;66(4):675-84, reported a PML-RAR alpha fusion mRNA generated by a t(15;17) translocation associated with acute promyelocytic leukemia (APL). The gene product contained a novel zinc finger motif common to several DNA-binding proteins and the mRNA encoded a predicted 106 kd chimeric protein
15 containing most of the PML sequences fused to a large part of RAR alpha, including its DNA- and hormone-binding domains. In transient expression assays, the hybrid protein exhibited altered transactivating properties if compared with the wild-type RAR alpha progenitor. Identical PML-RAR alpha fusion points were found in several patients, suggesting that in APL the t(15;17) translocation generates an RAR mutant that could contribute to leukemogenesis through interference with promyelocytic differentiation.

20 NCBI # S50916 (SEQ ID NOs 206 and 207) relate to a PML-RAR fusion gene {fusion transcript} [human, mRNA Partial, 1284 nt]. Nt 1-1251 is said to be coding sequence.

NCBI # M73779 (SEQ ID NOs 208 and 209) relate to a human PML-RAR protein (PML-RAR) mRNA, complete cds. Nt 67-2460 is said to be coding sequence.

25 NCBI # AJ417079 (SEQ ID NOs 210 and 211) relate to a human partial mRNA for PML/RARA fusion protein (PML/RARA gene). Nt 1-109 are said to derive from exon 6 of PML and nts 110-172 and 173-296 are said to derive from intron 2 and exon 3 of RARA.

t(11;17)(q23;q12)

Chen et al., EMBO J., 12 (3), 1161-1167 (1993), reported a fusion between a novel Kruppel-like zinc finger gene and the retinoic acid receptor-alpha locus due to a variant t(11;17) translocation associated with acute promyelocytic leukaemia (APL). Chen et al identified mRNAs containing the coding sequences of the new gene, fused in-frame either upstream of the RAR alpha B region or downstream from the unique A1 and A2 regions of the two major RAR alpha isoforms. The new gene, which Chen et al. termed PLZF (for promyelocytic leukaemia zinc finger), encodes a potential transcription factor containing nine zinc finger motifs related to the Drosophila gap gene Kruppel and is expressed as at least two isoforms which differ in the sequences encoding the N-terminal region of the protein. Within the haematopoietic system the PLZF mRNAs are detected in the bone marrow, early myeloid cell lines and peripheral blood mononuclear cells, but not in lymphoid cell lines or tissues. In addition, the PLZF mRNA levels were down-regulated in NB-4 and HL-60 promyelocytic cell lines in response to retinoic acid-induced granulocytic differentiation and were very low in mature granulocytes, suggesting an important role for PLZF as well as retinoic acid and its receptors in myeloid maturation.

NCBI # NM_006006 (SEQ ID NOs 212 and 213) relate to a human zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia) (ZNF145), mRNA. Nt 76-2097 are said to be coding sequence.

NCBI # Z19002 (SEQ ID NOs 214 and 215) relate to a human PLZF gene encoding kruppel-like zinc finger protein. Nt 76-2097 are said to be coding sequence.

t(16;16)(p13;q22) and inv(16)

Springall et al., Leukemia 12 (12), 2034-2035 (1998), identified a novel CBFβ-MYH11 fusion transcript in a patient with AML and attributed it to an inversion/translocation of chromosome 16. *See also*, Krauter et al., Genes Chromosomes Cancer. 2001 Apr;30(4):342-8, *Detection and quantification of CBFβ/MYH11 fusion transcripts in patients with inv(16)-positive acute myeloblastic leukemia by real-time RT-PCR.*; Martinelli et al., Haematologica. 2000 May;85(5):552-5, *Long-term disease-free acute myeloblastic leukemia with inv(16) is associated with PCR undetectable CBFβ/MYH11 transcript*; and Dierlamm et al., Genes Chromosomes Cancer. 1998

Jun;22(2):87-94. Review, *FISH identifies inv(16)(p13q22) masked by translocations in three cases of acute myeloid leukemia.*

NCBI # AF202996 (SEQ ID NOs 216 and 217) relate to a human core binding factor beta-smooth muscle myosin heavy chain fusion protein (CBFB-MYH11) mRNA, partial cds. Nt 1-46 are said to originate from 16q22 and nt 47-89 are said to originate from 16p13. Nt 50 is said to be a "t" in some reports.

NCBI # AF251768 (SEQ ID NOs 218 and 219) relate to human PCFBF/MYH11E chimeric fusion protein (CBFB/MYH11) mRNA, partial cds. Nt 1-42 are said to derive from exon 5 of CBFB and nts 42-78 from exon 7 of MYH11.

NCBI # AF249898 (SEQ ID NOs 220 and 221) relate to a human PCFBbeta/MYH11A chimeric fusion protein (CBFBbeta/MYH11A) mRNA, partial cds. Nt 1-42 are said to derive from exon 5 of CBFB and nts 42-78 from exon 12 of MYH11.

NCBI # AF249897 (SEQ ID NOs 222 and 223) relate to a human s PCFBf-MYH11d chimeric fusion protein (CBFB/MYH11D) mRNA, partial cds.

NCBI # AF390860 (SEQ ID NO 224) relates to a human UPN2 CBFB/MYH11 translocation breakpoint region sequence.

NCBI # AF390859 (SEQ ID NO 225) relates to a human isolate UPN1 CBFB/MYH11 translocation breakpoint region sequence.

t(9;11)(p22;q23)

Tkachuk et al., Cell 71: 691-700, (1992), showed that the gene involved in recurring 11q23 leukemogenic translocations codes for an unusually large protein that is a homolog of Drosophila 'trithorax' and is involved in homeotic gene regulation (MLL; aka ALL1). In studies of a t(11;19) translocation, they identified a chimeric protein containing the amino-terminal 'AT-hook' motifs of the MLL gene on chromosome 11 fused to a previously undescribed protein from chromosome 19. The nucleotide sequence determinations demonstrated an open reading frame that coded for a predicted 62-kD protein, which Tkachuk et al. named ENL.

Nakamura et al., Proc. Nat. Acad. Sci. 90: 4631-4635, (1993), showed that the gene on chromosome 19 that is fused to the MLL gene in patients with leukemia and translocation t(11;19)(q23;p13) shows high sequence homology to the genes on chromosome 4 and chromosome 9 that are fused with the ALL1 gene in patients with translocation t(4;11)(q21;q23) and t(9;11)(p22;q23), respectively. The 3 protein gene products contained nuclear targeting sequences as well as serine-rich and proline-rich regions. The results suggested that the different proteins fused to ALL1 polypeptides. These leukemias provide similar functional domains.

Negrini et al., Cancer Res 1993 Oct 1;53(19):4489-92, reported potential topoisomerase II DNA-binding sites at the breakpoints of a t(9;11) chromosome translocation in acute myeloid leukemia. The event examined was a t(9;11)(p22;q23) chromosome translocation and the breakpoints on the two chromosomes occurred within introns of the involved genes: AF-9 on chromosome 9, and ALL-1 on chromosome 11. Sequence analysis identified heptamers flanking the breakpoints on both chromosomes 9 and 11, suggesting that the V-D-J recombinase was involved in the translocation. See also Cimino et al., Cancer Res. 1991 Dec 15;51(24):6712-4, *Cloning of ALL-1, the locus involved in leukemias with the t(4;11)(q21;q23), t(9;11)(p22;q23), and t(11;19)(q23;p13) chromosome translocations.*

Poirel et al., Blood 87 (6), 2496-2505 (1996), reported an MLL-AF9=fusion gene {fusion site} [human, peripheral blood, acute myeloid leukemia FAB type M1 patient UPN 427, mRNA Partial, 60 nt]; NCBI # S82034 (SEQ ID NO 226), and indicated the breakpoint to be at nucleotide 29.

t(1;22)(p13;q13)

Nakamura et al., Proc Natl Acad Sci U S A 1993 May 15;90(10):4631-5, correlated aberrations on chromosomes 4, 9, and 19 involved in 11q23 abnormalities in acute leukemia with shared sequence homology and/or common motifs, including fusions of the ENL gene with ALL-1 in (11;19) translocations. ENL proteins contain nuclear targeting sequences as well as serine-rich and proline-rich regions. Stretches abundant in basic amino acids are also present.

NCBI # AF364037 (SEQ ID NOs 227 and 228) relate to a human megakaryoblastic leukemia-1 protein/RNA-binding motif protein 15s + ae fusion protein (MKL1/RBM15 fusion) mRNA, complete cds. Ma et al., Nat. Genet. 28 (3), 220-221 (2001) identified this with an acute megakaryoblastic leukemia patient. Nt 144-221 are said to be coding sequence, with nts 1-150 deriving from chromosome 22 and nts 151-300 deriving from chromosome 1.

t(3;3)(q21;q26) or inv(3)(q21q26)

Ogawa et al., Oncogene 1996 Jul 4;13(1):183-91 showed that overexpression of the Evi-1 gene appears to be a consistent feature of the 3q21q26 syndrome, an association of myeloid leukemias/myelodysplastic syndrome with a specific chromosomal aberration involving both 3q21 and 3q26, such as t(3;3)(q21;q26) or inv(3)(q21q26). The rearrangement in 3q26 has been reported to occur near the Evi-1 locus, implicating that it is the critical gene deregulated in the 3q21q26 syndrome. Ogawa identified a structural abnormality of Evi-1 protein in a case with the 3q21q26 syndrome. That case carried the typical inv(3)(q21q26), in which the 3q26 breakpoint is located within an intron of the Evi-1 gene, and resulted in overexpression of a normally unexpressed, aberrant form of Evi-1 protein, in which the C-terminal 44 amino acids of wild-type Evi-1 protein were truncated and replaced by five amino acids. The truncated Evi-1 protein was shown to increase AP1 activity when expressed in NIH3T3 cells as its wild-type counterpart. The origin of this peculiar type of rearrangement of the Evi-1 gene was shown not to be an artifact during establishment of the cell line, but rather an event that occurred in the primary leukemic cells, and consistent with 3q21q26 syndrome.

NCBI # S82592 (SEQ ID NOs 229 and 230) relate to an Evi-1=Evi-1 protein {3' region, deletion region} [human, megakaryoblastoid cell line MOLM-1, chronic myelocytic leukemia patient, mRNA Partial Mutant, 916 nt]. Nt 1-132 are said to represent a partial coding sequence.

t(3;5)(q25;q34)

Yoneda-Kato et al., Oncogene 12: 265-275 (1996), showed that t(3;5)(q25.1;q34) of myelodysplastic syndrome and acute myeloid leukemia produces a novel fusion gene, NPM-MLF1, which results from an in-frame fusion between the 5-prime coding region of

the nucleophosmin gene on chromosome 5 and a gene on chromosome 3, designated MLF1 (myeloid leukemia factor-1). The translocation was identified in 3 t(3;5)-positive cases of AML. Expression of the mRNA was widespread but highest in testis, ovary, skeletal muscle, heart, kidney and colon. Antibodies to MLF1 detected a 31-kD protein in K562 and HEL erythroleukemia cell lines

NCBI # L49054 (SEQ ID NOs 231 and 232) relate to a t(3;5)(q25.1;p34) fusion gene NPM-MLF1 mRNA, complete cds. Nt 109-915 are said to be coding sequence.

NCBI # BC007045 (SEQ ID NOs 233 and 234) relate to a human myeloid leukemia factor 1, clone MGC:12449, mRNA, complete cds. Nt 107-913 are said to be coding sequence.

NCBI # L49054 (SEQ ID NOs 235 and 236) relate to a human t(3;5)(q25.1;p34) fusion gene NPM-MLF1 mRNA, complete cds. Nt 109-915 are said to be coding sequence.

t(7;11)(p15;p15)

Borrow et al., Nat. Genet. 1996 Feb;12(2):159-67, reported a t(7;11)(p15;p15) translocation in acute myeloid leukaemia that fused the genes for nucleoporin NUP98 and class I homeoprotein HOXA9.

NCBI # U41814 (SEQ ID NOs 237 and 238) relate to human NUP98-HOXA9 fusion protein mRNA, partial cds. Nt 46^47 are said to represent a NUP98-HOXA9 in-frame junction and nt 138^139 are said to be an alternative splice site within HOXA9

NCBI # NM_002142 (SEQ ID NOs 239 and 240) relate to a human homeo box A9 (HOXA9), mRNA. Nts 67 and 213 are said to have allelic variation possible (c/g), and nt 397-567 and 397-576 are said to respectively represent a homeobox domain and a homeodomain (HOX region).

NCBI # U81511 (SEQ ID NOs 241, 242, and 243) relate to a human HOXA-9A and HOXA-9B (HOXA-9) gene, alternatively spliced, complete cds. Nts 145-502, 4327-4894, and 5893-6131 are said to be exon (coding) sequences, with introns present at 503-5892 and 4895-5892. Alternative splicing events are said to account for the overlap.

t(8;16)(p11;p13)

Panagopoulos et al., Genes Chromosomes Cancer. 2000 Aug;28(4):415-24, used RT-PCR analysis to identify MOZ-CBP and CBP-MOZ chimeric transcripts in acute myeloid leukemias with t(8;16)(p11;p13) translocations.

5 NCBI # AJ251844 (SEQ ID NOs 244 and 245) relate to human partial mRNA for MOZ/CBP chimeric transcript type II. Nt 1-188 are said to derive from chromosome 8 and nts 189-415 from chromosome 16.

NCBI # AJ251845 (SEQ ID NOs 246 and 247) relate to a human partial mRNA for CBP/MOZ chimeric transcript. Nt 1-110 are said to derive from chromosome 16 and nts
10 111-229 from chromosome 8.

NCBI # AJ251843 (SEQ ID NOs 248 and 249) relate to human partial mRNA for MOZ/CBP chimeric transcript type I. Nt 1-188 are said to derive from chromosome 8 and nts 189-1128 from chromosome 16.

NCBI # U47742 (SEQ ID NOs 250 and 251) relate to human monocytic leukaemia
15 zinc finger protein (MOZ) mRNA, complete cds.

NCBI # U85962 (SEQ ID NOs 252 and 253) relate to a human CREB-binding protein mRNA, complete cds. Nt 814-8147 are said to contain coding sequence and nts 819-1124 are said to encode a nuclear receptor binding domain.

t(9;12)(q34;p13)

20 Papadopoulos et al., Cancer Res. 1995 Jan 1;55(1):34-8, reported activation of ABL by fusion to an ets-related gene, TEL.

NCBI # Z35761 (SEQ ID NOs 254 and 255) relate to a human TEL/ABL fusion protien. Nt 1-463 are said to contain a partial TEL sequence and nt 464-549 are said to contain ABL sequence.

25 NCBI # Z36279 (SEQ ID NO 256) relates to human (9TX) breakpoint position DNA. The breakpoint position is said to reside at 567..568.

NCBI # Z36278 (SEQ ID NO 257) relates to human (boucher) breakpoint position DNA. The breakpoint position is said to reside at 567..568.

t(12;22)(p13;q13)

5 Buijs et al., *Oncogene*. 1995 Apr 20;10(8):1511-9, reported that a t(12;22) (p13;q11) event resulted in a myeloproliferative disorders characterized by the fusion of the ETS-like TEL gene on 12p13 to the MN1 gene on 22q11.

NCBI # X85024 (SEQ ID NOs 258 and 259) relate to a human mRNA for TEL-MN1 fusion gene (type II). Nt 22..23 is said to be the fusion site.

10 NCBI # X85026 (SEQ ID NOs 260 and 261) relate to a human mRNA for a TEL-MN1 fusion gene (type I). Nt 22..23 is said to be the fusion site.

NCBI # X85027 (SEQ ID NOs 262 and 263) relate to a human mRNA for a MN1-TEL fusion gene (type II). Nt 22..23 is said to be the fusion site.

NCBI # X85025 (SEQ ID NOs 264 and 265) relate to a human mRNA for a MN1-TEL fusion gene (type I). Nt 22..23 is said to be the fusion site.

15 **del(5q)**

Jaju et al., *Blood* 1999 Jul 15;94(2):773-80, reported a recurrent translocation, t(5;11)(q35;p15.5), associated with a del(5q) in childhood acute myeloid leukemia. Partial deletion of the long arm of chromosome 5, del(5q), is the cytogenetic hallmark of the 5q-syndrome, a distinct subtype of myelodysplastic syndrome-refractory anemia (MDS-RA).
20 Deletions of 5q also occur in the full spectrum of other de novo and therapy-related MDS and acute myeloid leukemia (AML) types, most often in association with other chromosome abnormalities. However, the loss of genetic material from 5q is believed to be of primary importance in the pathogenesis of all del(5q) disorders.

Lindgren et al., *Am J Hum Genet* 1992 May;50(5):988-97, reported phenotypic,
25 cytogenetic, and molecular studies of three patients with constitutional deletions of chromosome 5 in the region of the gene for familial adenomatous polyposis, APC, affiliated with colon cancer and polyps. High-resolution banding studies indicated that some deletions spans the region 5q21-q22..

Other potential deletion aberrations at the 5q locus include but are not limited to deletions at positions 5q13.3, corresponding to the RASA1 gene encoding the GAP RAS p21 protein activator 1 (GTPase activating protein), aberrancies of which are known to associate with basal cell carcinoma; 5q21, corresponding to the PST gene encoding PST1 Polysialyltransferase; 5q21-q22, corresponding to the APC gene, aberrancies of which correlate with colorectal cancer; 5q31, corresponding to the FACL6 gene encoding ACS2 Fatty-acid-Coenzyme A ligase, a long-chain 6 (long-chain acyl-CoA synthetase 2), aberrancies of which give rise to myelodysplastic syndrome and acute myelogenous leukemia; 5q31, encoding the GRAF GTPase regulator associated with the focal adhesion kinase, aberrancies of which give rise to juvenile myelomonocytic leukemia; 5q31.1, encoding IRF1, a MAR Interferon regulatory factor-1, aberrancies of which give rise to macrocytic anemiam myelodysplastic syndrome (preleukemic), acute myelogenous leukemia, gastric cancer, and nonsmall cell lung cancer; 5q33.2-q33.3, corresponding to CSF1R, FMS Colony-stimulating factor-1 receptor, aberranceis of which have been associated with oncogene FMS (McDonough feline sarcoma), and predisposition to myeloid malignancy; 5q35, encoding NPM1 Nucleophosmin 1 (nucleolar phosphoprotein B23, numatrin), aberrancies of which are known to associate with acute promyelocytic leukemia; 5q35.3, encoding gene FLT4, VEGFR3, encoding PCL fins-related tyrosine kinase-4 (vascular endothelial growth factor receptor, aberrancies of which contribute to hereditary lymphedema.

NCBI # NM_002387 (SEQ ID NOs 266 and 267) relate to a human gene that is found mutated in colorectal cancers(MCC) mRNA. Nt 221-2710 are said to represent coding sequence. Allelic variation is said to exist at nt 2869 (c/t).

del(7q)

Schwartz et al., Cytogenet. Cell Genet. 51: 152-153 (1991) reported deletion mapping of plasminogen activator inhibitor, type I (PLANH1) and beta-glucuronidase (GUSB) in 7q21-q22. Wedemeyer et al., Genomics 46: 313-315 (1997) reported the proximity of the human HIP1 gene close to the elastin (ELN) locus on 7q11.23. Dridi et al., Am. J. Med. Genet. 87: 134-138 (1999), reported skin elastic fibers in Williams syndrome and Dutly et al., Am. J. Med. Genet. 87: 134-138 (1999), reported unequal interchromosomal rearrangements corresponding to deletions in these genes, and affiliated

with Williams-Beuren syndrome. Naritomi et al., Hum. Genet. 80: 201-202 (1988), reported a microdeletion of the proximal long arm of chromosome 7 affiliated with Zellweger syndrome. Horiike et al., Leukemia. (1999) Aug;13(8):1235-42, reported distinct genetic involvement of the TP53 gene in therapy-related leukemia and myelodysplasia, with chromosomal 7 losses and their possible relationship to replication error phenotype and the development of therapy-related AML/MDS. Wong et al., Cancer Genet Cytogenet. 1995 Jul 1;82(1):70-2, reported biclonal acute monoblastic leukemia associated with del(7q). Particular sites of interest include 7q11.23, encoding PTPN12, PTPG1 Protein tyrosine phosphatase, nonreceptor-type, known to associate with colon cancer; 7q21-q22, encoding PEX1, ZWS1 Peroxisome biogenesis factor-1, associate with Zellweger syndrome-1, neonatal adrenoleukodystrophy and infantile Refsum disease; 7q22-q31.1, encoding SLC26A3, DRA, CLD Solute carrier family 26 (sulfate transporter), member 3, associated with colon cancer; 7q31-q32 SMOH, SMO Smoothed, Drosophila, homolog of 601500, associated with sporadic basal cell carcinoma.

del(20q)

A deletion in the long arm of chromosome 20 is a recurring abnormality in malignant myeloid disorders. Its occurrence suggests that the loss of genetic material on 20q provides a proliferative advantage to myeloid cells, possibly through the loss of a tumor-suppressor gene. Roulston et al., Blood 82: 3424-3429 (1993), examined a series of patients with the del(20q) using fluorescence in situ hybridization with unique sequence probes that map along the length of 20q and delineated a segment that is deleted in 95% of all patients they examined (18 of 19). In addition, they showed that the deletions are interstitial rather than terminal. The region of deletion extended from 20q11.2 to 20q12 and was flanked by RPN2 (180490) proximally and D20S17 distally. The SRC (190090) and ADA (102700) genes were found to be located within the commonly deleted segment.

Stoffel et al. (1996) generated a YAC contig map of 20q11.2-q13.1 in a region spanning about 18 Mb and representing about 40% of the physical length of 20q. The map contains the chromosomal regions deleted in MODY1 (125850) and in myeloid leukemia. Using this physical map, they refined the location of a myeloid tumor suppressor-related gene to an 18-cM interval (approximately 13 Mb) between RPN2 and D20S17.

Stoffel et al., Proc. Nat. Acad. Sci. 93: 3937-3941 (1996), correlated the occurrence of del(20q) in a broad spectrum of myeloid disorders, suggesting that the loss of genetic material on 20q could provide a proliferative advantage to myeloid cells, possibly through the loss of a tumor-suppressor gene. Stoffel et al. examined a series of patients with the del(20q) using fluorescence in situ hybridization (FISH) with unique sequence probes that map along the length of 20q, delineated a segment that is deleted in 95% of all patients examined (18 of 19), and showed that the deletions are interstitial rather than terminal. This region of deletion extends from 20q11.2 to q12, and is flanked by the RPN2 (proximal) and D20S17 loci (distal). The SRC and ADA genes are located within the commonly deleted segment.

t(11q23)

Shiah et al., Leukemia, (2002) 16(2):196-202, reported clinical and biological implications of partial tandem duplication of the MLL gene in acute myeloid leukemia without chromosomal abnormalities at 11q23. The clinical and biological features of acute myeloid leukemia (AML) with 11q23/MLL translocations are well known, but the characteristics of AML with partial tandem duplication of the MLL gene have not been explored comprehensively. Sheah et al analyzed MLL duplication in 81 AML patients without chromosomal abnormalities at 11q23, using Southern blotting, genomic DNA polymerase chain reaction (PCR), reverse-transcription PCR and complementary DNA sequencing. Nine patients showed partial tandem duplication of the MLL gene, including eight (12%) of the 68 with normal karyotype. Seven patients showed fusion of exon 6/exon 2 (e6/e2), one, combination of differentially spliced transcripts e7/e2 and e6/e2, and the remaining one, combination of e8/e2 and e7/e2. Among the patients with normal karyotype, children aged 1 to 15 showed a trend to higher frequency of MLL duplication than other patients (2/5 or 40% vs 6/62 or 10%, $P = 0.102$). The patients with tandem duplication of the MLL gene had a significantly higher incidence of CD11b expression on leukemic cells than did those without in the subgroup of patients with normal karyotype (75% vs 28%, $P = 0.017$). There were no significant differences in the expression of lymphoid antigens or other myeloid antigens between the two groups of patients. In adults, the patients with MLL duplication had a shorter median survival time than those without (4.5 months vs 12 months, $P = 0.036$). In conclusion, partial tandem duplication of the MLL gene is associated with increased expression of CD11b on leukemic blasts and

implicates poor prognosis in adult AML patients. The higher frequency of MLL duplication in children older than 1 year, than in other age groups, needs to be confirmed by further studies.

Ono et al., Cancer Res. 2002 Jan 15;62(2):333-7, reported that SEPTIN6, a human
5 homologue to mouse Septin6, is fused to MLL in infant acute myeloid leukemia with complex chromosomal abnormalities involving 11q23 and Xq24.

Borkhardt et al., Genes Chromosomes Cancer. 2001 Sep;32(1):82-8, reported an ins(X;11)(q24;q23) that fuses the MLL and the Septin 6/KIAA0128 gene in an infant with AML-M2.

10 Luo et al., Mol Cell Biol. 2001 Aug;21(16):5678-87, reported that ELL-associated factor 1 interaction domain is essential for MLL-ELL-induced leukemogenesis.

Kuwada et al., Cancer Res. 2001 Mar 15;61(6):2665-9, reported a t(11;14)(q23;q24) that generates an MLL-human gephyrin fusion gene along with a de facto truncated MLL in acute monoblastic leukemia.

15 Garcia-Cuellar et al., Oncogene. 2000 Mar 30;19(14):1744-51, reported that ENL, the MLL fusion partner in t(11;19), binds to the c-Abl interactor protein 1 (ABI1) that is fused to MLL in t(10;11)+.

Akao et al., Genes Chromosomes Cancer. 2000 Apr;27(4):412-7, reported an analysis of the rearranged genome and chimeric mRNAs caused by a t(6;11)(q27;q23)
20 chromosome translocation involving MLL in an infant acute monocytic leukemia.

Hayashi et al., Cancer Res. 2000 Feb 15;60(4):1139-45, reported a leukemic cell line, SN-1, associated with a t(11;16)(q23;p13).

So et al., Cancer Genet Cytogenet. 2000 Feb;117(1):24-7, analysed MLL-derived transcripts in an infant acute monocytic leukemia having a complex translocation
25 (1;11;4)(q21;q23;p16).

Kourlas et al., Proc Natl Acad Sci U S A. 2000 Feb 29;97(5):2145-50, identified a gene at 11q23 encoding a guanine nucleotide exchange factor that fuses with MLL in acute myeloid leukemia.

Taki et al., Proc Natl Acad Sci U S A. 1999 Dec 7;96(25):14535-40, reported that AF5q31, an AF4-related gene, is fused to MLL in infant acute lymphoblastic leukemia with an ins(5;11)(q31;q13q23).

Taki et al., Cancer Res. 1999 Sep 1;59(17):4261-5, reported that AF17q25, a putative septin family gene, fuses with the MLL gene in acute myeloid leukemia associated with a t(11;17)(q23;q25).

Busson-Le Coniat et al., Leukemia. 1999 Feb;13(2):302-6, reported MLL-AF1q fusion resulting from t(1;11) in an acute leukemia.

Slany et al., Mol Cell Biol. 1998 Jan;18(1):122-9, reported on the oncogenic capacity of HRX-ENL that requires the transcriptional transactivation activity of ENL and the DNA binding motifs of HRX.

Other articles of interest include, Super et al., Genes Chromosomes Cancer. 1997 Oct;20(2):185-95, *Identification of complex genomic breakpoint junctions in the t(9;11) MLL-AF9 fusion gene in acute leukemia*; Taki et al., Blood. 1997 Jun 1;89(11):3945-50, *The t(11;16)(q23;p13) translocation in myelodysplastic syndrome fuses the MLL gene to the CBP gene*; Taki et al., *Fusion of the MLL gene with two different genes, AF-6 and AF-5alpha, by a complex translocation involving chromosomes 5, 6, 8 and 11 in infant leukemia*, Oncogene. 1996 Nov 21;13(10):2121-30. Tanabe et al., *AF10 is split by MLL and HEAB, a human homolog to a putative Caenorhabditis elegans ATP/GTP-binding protein in an inv(10;11)(p12;q23q12)*, Blood. 1996 Nov 1;88(9):3535-45; Ma et al., *LAF-4 encodes a lymphoid nuclear protein with transactivation potential that is homologous to AF-4, the gene fused to MLL in t(4;11) leukemias*, Blood. 1996 Jan 15;87(2):734-45; Prasad et al., *Domains with transcriptional regulatory activity within the ALL1 and AF4 proteins involved in acute leukemia*, Proc Natl Acad Sci U S A. 1995 Dec 19;92(26):12160-4. Baffa et al., *Involvement of the ALL-1 gene in a solid tumor*, Proc Natl Acad Sci U S A. 1995 May 23;92(11):4922; Mitani, *Cloning of several species of MLL/MEN chimeric cDNAs in myeloid leukemia with t(11;19)(q23;p13.1) translocation*, Blood. 1995 Apr 15;85(8):2017-24; Tse et al., *A novel gene, AF1q, fused to MLL in t(1;11)(q21;q23), is specifically expressed in leukemic and immature hematopoietic cells*, Blood. 1995 Feb 1;85(3):650-6; Chen et al., *Acute promyelocytic leukemia: from clinic to molecular biology*, Stem Cells. 1995 Jan;13(1):22-31. Review; Rubnitz et al., *ENL, the*

- gene fused with HRX in t(11;19) leukemias, encodes a nuclear protein with transcriptional activation potential in lymphoid and myeloid cells, *Blood*. 1994 Sep 15;84(6):1747-52; Prasad et al., *Leucine-zipper dimerization motif encoded by the AF17 gene fused to ALL-1 (MLL) in acute leukemia*, *Proc Natl Acad Sci U S A*. 1994 Aug 16;91(17):8107-11;
- 5 Meerbach et al., *Molecular cloning of a novel 11q23 breakpoint associated with non-Hodgkin's lymphoma*, *Oncogene*. 1994 Mar;9(3):893-8; Gauwerky et al., *Chromosomal translocations in leukaemia*, *Semin Cancer Biol*. 1993 Dec;4(6):333-40. Review; Hunger et al., *HRX involvement in de novo and secondary leukemias with diverse chromosome 11q23 abnormalities*, *Blood*. 1993 Jun 15;81(12):3197-203; Morrissey et al., *A*
- 10 *serine/proline-rich protein is fused to HRX in t(4;11) acute leukemias*, *Blood*. 1993 Mar 1;81(5):1124-31; Tkachuk et al., *Involvement of a homolog of Drosophila trithorax by 11q23 chromosomal translocations in acute leukemias*, *Cell*. 1992 Nov 13;71(4):691-700.

t(5;12)(q31;p13)

- Yagasaki et al. described a fusion of LACS to a TEL/ETV6 gene in an acute
- 15 myeloblastic leukemia case having a t(5;12) chromosomal translocation. The human mRNA fusion sequence may be found in NCBI # AF102845 (SEQ ID NO 268). Nt 1-40 are said to derive from the TEL gene on chromosome 12 and nt 41-1172 are said to derive from the LACS gene on chromosome 5.

t(1;12)(q25;p13)

- Cazzaniga et al., *Blood* 94: 4370-4373 (1999), reported an instance of the tyrosine kinase Abl-related gene ARG fused to ETV6 in an AML-M4Eo patient having a
- t(1;12)(q25;p13) translocation, and cloned reciprocal chimeric transcripts associated with the event. The ETV6/TEL gene is rearranged in most patients with 12p13 translocations fused to a number of different partners. One of the chimeric proteins consisted of the
- 25 helix-loop-helix oligomerization domain of ETV6 and the SH2, SH3, and protein tyrosine kinase domains of ABL2. The reciprocal transcript ABL2-ETV6 was also detected in the patient's RNA by RT-PCR, although at a lower expression level.

t(12;15)(p13;q25)

Wai et al., *Oncogene*. 2000 Feb 17;19(7):906-15, reported an ETV6-NTRK3 gene fusion associated with such translocation.

Eguchi et al., *Blood*. 1999 Feb 15;93(4):1355-63, reported a similar fusion of ETV6 to neurotrophin-3 receptor TRKC in acute myeloid leukemia with t(12;15)(p13;q25).

Knezevich et al., *Nat Genet*. 1998 Feb;18(2):184-7; reported an ETV6-NTRK3 gene fusion in congenital fibrosarcoma.

NCBI # AF125808 (SEQ ID NOs 269 and 270) relate to a human ETS related protein-neurotrophic receptor tyrosine kinase fusion protein (ETV6-NTRK3 fusion) mRNA, partial cds. Nt 12-64 are said to derive from chromosome 12 and nt 65-980 from chromosome 15.

NCBI # AF041811 (SEQ ID NOs 271 and 272) relate to a human ETS related protein-growth factor receptor tyrosine kinase fusion proteins (ETV6-NTRK3 fusion) mRNA, partial cds. . Nt 1-336 are said to derive from chromosome 12 and nt 337-1403 from chromosome 15.

t(1;12)(q21;p13)

Salomon-Nguyen et al., *Proc Natl Acad Sci U S A*. (2000) 97(12):6757-62, reported a t(1;12)(q21;p13) translocation observed in a case of acute myeloblastic leukemia (AML-M2). At the protein level, the untranslocated TEL copy and, as a result of the t(1;12) translocation, a fusion protein containing the amino-terminal part of TEL and essentially all of the ARNT gene (126110), were expressed. The TEL/ETV6 gene is located at 12p13 and encodes a member of the ETS family of transcription factors. Translocated ETS leukemia (TEL) is frequently involved in chromosomal translocations in human malignancies, usually resulting in the expression of fusion proteins between the amino-terminal part of TEL and either unrelated transcription factors or protein tyrosine kinases. ARNT (aryl hydrocarbon receptor nuclear translocator) belongs to a subfamily of the "basic region helix-loop-helix" (bHLH) protein that shares an additional region of similarity called the PAS (Per, ARNT, SIM) domain. ARNT is the central partner of

several heterodimeric transcription factors, including those containing the aryl hydrocarbon (dioxin) receptor (AhR) and the hypoxia-inducible factor 1alpha (HIF1alpha). Interference with the activity of AhR or HIF1alpha may contribute to leukemogenesis.

2. Mutant Protein or Cellular Protein Isoforms

The second group of target proteins are mutants or isoforms (*e.g.* splice variants) of normal cellular proteins (usually the products of tumor suppressor genes) that, due to their mutant nature, exhibit a heightened dependence on HSP90 chaperone functions or else increased sensitivity, *i.e.*, instability, due to HSP90 inhibitors. The mutant or isoform proteins either (a) have become overtly oncogenic (a “dominant-positive” (DP) effect), or (b) exert a “dominant-negative” (DN) effect on their normal counterpart, thus preventing the normal protein’s tumor suppressor activity, and resulting in a net oncogenic effect. The examples are largely illustrated with respect to human sequences, although the person of ordinary skill will appreciate that homologs in other organisms are likewise included within the purview of the invention.

a. v-src

One such example of a mutant or isoform protein is human v-src (NCBI #s NM_005417; SEQ ID NOs 273 and 274), which counterpart, c-src (NCBI # XM_044659 (SEQ ID NOs 275 and 276), corresponds to the normal cellular gene product. As described above, proteins with a heightened dependence on HSP90 can be identified by their enhanced sensitivity to degradation induced by HSP90 inhibitors, such as the ansamycin antibiotic geldanamycin. Ansamycins and other HSP90 inhibitors were originally isolated on the basis of their ability to revert v-src transformed fibroblasts (Uehara, Y. *et al.*, 1985, *Supra*, 76: 672-675) and this reversal was correlated with the functional inactivation of the v-src protein (Uehara, Y. *et al.*, 1986, *Mol. Cell. Biol.*, 6: 2198-2206). This effect was subsequently reported to be caused by the ubiquitin/proteasome-dependent degradation of the transforming v-src protein as a result of inhibition of HSP90 function by geldanamycin (Whitesell, L., *et al.*, 1994, *supra*). Finally, a recent study compared the rate and potency of degradation of v-src and c-src proteins after treatment of Rous sarcoma virus-transformed 3T3 fibroblasts with the ansamycin geldanamycin. In this study, the oncogenic mutant v-src protein was almost 100% degraded within 6 hours (An, W *et al.*, 2000, *supra*, see Figure 2), whereas the normal cellular counterpart, c-src, was largely unaffected even after 20 hours of the same treatment (An, W *et al.*, 2000, *supra*, see Figure 4).

HSP90 inhibitors can selectively induce degradation of a wide range of mutated or otherwise aberrant proteins that cause or exacerbate a disease, and that have an apparent heightened dependence on HSP90.

b. RET

5 An example of a dominant proto-oncogene encoding a signaling protein that is mutated in certain human cancers giving rise to constitutively active structurally abnormal cellular proteins is the *RET* proto-oncogene (NCBI # P07949; SEQ ID NO 277) in multiple endocrine neoplasia Type 2 (MEN-2). *RET* encodes a receptor tyrosine kinase whose ligand is presently unidentified (Kolibaba, K, *et al*, 1997, *Supra*). The germline mutations found in MEN-2A patients (Cys634→
10 Arg/Tyr, similar mutations at Cys609, 611, 618 and 620) alter the tertiary structure of the protein resulting in homodimerization and activation of the kinase domain. The commonly observed mutation in MEN-2B, Met918→Thr, alters the kinase domain structure, causing activation directly. Both of these pathways involve alterations in protein conformation, which again implicates HSP90 and underscores the broad utility of the invention.

15 c. p53

Another example of a mutant, oncogenic variant group of a normal cellular protein is tumor suppressor antigen p53. The wild-type protein and mRNA sequences for p53 are found in NCBI accession # M14695 (SEQ ID NOs 278 and 279). However, numerous mutations in p53 are known to occur and represent the most common molecular genetic defects found in human
20 cancers (Harris, C *et al*, 1993, *N. Engl. J. Med.* 329:1318-1327). A mutant p53 protein was reportedly degraded in cells following treatment with geldanamycin, but wild type p53 exhibited no such, or only minimal, degradation (Blagosklonny, M *et al*, 1995, *Oncogene*, 11:933-939). Unlike the situation described above for v-src, most p53 mutations are “loss of function” effects, *i.e.*, the mutation results in the inability of the protein to perform one or more of its normal
25 functions. Thus, in a tumor cell that has an intact p53 allele and a loss of function mutant allele, simply causing the mutant form to be degraded will not change cellular behavior. However, if the mutant protein by some mechanism inhibits the action of its coexpressed normal counterpart inside tumor cells, then degrading it will affect cellular behaviour.

This “dominant-negative” (DN) effect has been shown to occur in cells harboring certain
30 p53 mutants, and by several different mechanisms. For example, a mutant may afford tighter

DNA binding without transactivation (Chene, P, *et al*, 1999, *Int. J. Cancer*. 82:17-22). This type of p53 mutant does not exhibit “classical” DN activity unless the mutation confers an increased affinity for DNA, because the mutant stoichiometrically competes with the wild type (WT) protein for binding to DNA. Another example is inhibition of tetramerization by incorporation of one or more mutant p53s into a complex with WT proteins (Deb, D *et al*, 1999, *Int. J. Oncol.* 15:413-422, Rollenhagen, C *et al*, 1998, *Int. J. Cancer* 78:372-376). Yet a third example concerns “prion-like” activity, in which a mutant protein forces a WT protein into a mutant conformation that then impairs its ability to bind to DNA and/or transactivate p53 target genes (Chene, P, 1998, *J. Mol. Biol.* 281:205-209)

Increased stability of mutants relative to WT proteins causes them to accumulate and override normal p53 biology. This is counterintuitive given the fact that p53 has a built-in negative feedback loop on its own transcription (via induction of the mdm-2 protein, which subsequently targets p53 for degradation). If the increased stability of a given mutant were due solely to failure to transactivate mdm-2, then accumulation of the mutant would not occur in the presence of a WT allele (Blagosklonny, M, 2000, *FASEB J.* 14:1901-1907) because this protein would initiate negative feedback mechanisms that would be expected to act on both WT and mutant p53.

On the other hand, an independent mechanism favoring mutant accumulation (*e.g.* protection by association with HSP90 (Smith, D, *et al*, 1998, *supra*; Sepehrnia, B, *et al*, 1996, *J. Biol. Chem.* 271:15084-15090) would permit a “recessive” mutant to become in sufficient excess of the transactivating form to result in progressive inhibition of the negative feedback pathways. In this situation, the mutant would have a net DN effect due to progressive accumulation of a stoichiometric antagonist, and selective degradation of that mutant by inhibition of HSP90 activity would be expected to restore normal p53 function. Thus, in most or all cases, a DN phenotype produced by mutant p53 is secondary to the activity of HSP90 and inhibition of HSP90 function with 17-AAG or other HSP90 ATP binding site antagonists would prevent the expression of the DN phenotype and so rescue normal p53 function.

i. Dominant negative p53 mutants

A list of exemplary p53 mutations, including examples of structurally-abnormal proteins, dominant-negative proteins, prion-like proteins, and mutants with various combinations of these properties, follows:

Chene *et al*, 1999, *Int. J. Cancer*. 82:17-22; Y236delta (deletion of codon 236) resulted in a conformationally altered & dominant-negative phenotype.

Preuss *et al*, 2000, *Int. J. Cancer* 88:162-171); C174Y (Cys→Tyr) (rat) is dominant-negative, non-transactivating. The same mutation at position 176 is predicted to have a similar effect in humans, as the respective homologs have close correlative structural similarities at these positions.

Srivastava *et al*, 1993, *Oncogene* 8:2449-2456); M133T (Met→Thr), G245D (Gly→Asp), and E258K (Glu→Lys) all display conformationally altered, dominant-negative, prion-like displaying activity, in that co-incubation with WT p53 converts it into the mutated conformation.

Deb *et al*, 1999, *Int. J. Oncol.* 15:413-422); 1-293delta (deletion of codons 1-293) exhibited dominant negative DNA binding characteristics without transactivating activity.

Frebourg *et al*, 1992, *Proc. Natl. Acad. Sci.* 89:6413-6417; G245C (Gly→Cys), R248W (Arg→Trp), E258K (Glu→Lys), and R282W (Arg→Try) all independently display conformationally altered, dominant-negative activity.

Brachmann *et al*, 1996, *Proc. Natl. Acad. Sci.* 93:4091-4095; novel yeast assay used to identify dominant-negative p53 mutants that have also been found in human tumors, specifically implicating codons 132, 135, 151, 158, 176, 179, 236, 241, 242, 244, 245, 246, 248, 257, 265, 273, 277, 278, 279, 280, and 281. Of particular interest because they exhibited the greatest dominant-negative activity were mutants at codons 241, 242, 244, 245, 246, 248, 277, 278, 279, 280, and 281.

Blagosklonny *et al*, 1995, *Oncogene* 11:933-939); p53s mutated at the following codons exhibited disrupted conformations were dominant negative, and sensitive to geldanamycin: R175H (Arg→His), 194, 213, 223, 248, 274, R280K (Arg→Lys).

Aurelio *et al*, 2000, *Mol. Cell. Biol.* 20:770-778; without identifying conformational status, the following mutants were identified as dominant-negative for transactivation of apoptotic signals (Bax), but not growth arrest signals (p21^{WAF}): V143A (Val→Ala), R175H (Arg→His), G245C (Gly→Cys), R248W (Arg→Trp), R273H (Arg→His), K305M (Lys→Met), G325V (Gly→Val).

Marutani *et al*, 1999, *Cancer Res.* 59:4765-4769; yeast-based transdominance assay used to identify dominant-negative mutations at 16 codons : R156H (Arg→His), R175H (Arg→His), P177S (Pro→Ser), H178P (His→Pro), H179R (His→Arg), R181P (Arg→Pro), 238-9delta (deletion of codons 238 & 239), G245S (Gly→Ser), G245D (Gly→Asp), M246R (Met→Arg),
 5 R248Q (Arg→Gln), R249S (Arg→Ser), R273H (Arg→His), R273C (Arg→Cys), R273L (Arg→Leu), D281Y (Asp→Tyr).

ii. Dominant positive p53 mutants

In addition to dominant-negative mutations, some p53 mutations actually transactivate inappropriate gene expression, contributing to oncogenesis; *i.e.* a positive tumor promoting effect.
 10 See Park *et al*, 1994, *Oncogene* 9:1899-1906. This type of mutation is particularly suited to the approach embodied in the present invention because, unlike in the dominant-negative situation, the presence or absence of a normal allele of the tumor suppressor gene is irrelevant to the therapeutic utility of the HSP90 inhibitor. In other words, because the mutant p53 itself contributes to the malignant process, destruction of the mutant protein by inhibition of HSP90 is
 15 expected to have direct therapeutic value. A good example is C176Y (Cys→Tyr), as reported by Preuss, U *et al*, 2000, *Int. J. Cancer* 88:162-171. This mutant induces rather than represses the cellular fos promoter, resulting in activation of oncogenic signaling pathways. The biology of “dominant-positive” p53 mutants is reviewed in van Oijen *et al*, 2000, *Clin. Cancer Res.* 6:2138-2145. Other examples of mutations of p53 that give rise to tumorigenic phenotypes include, but
 20 are not limited to, Phe-132, Val-135, Ala-143, His-175, His-179, Trp-248, Ser-249, Leu-273, His-273 and Gly-281. Of particular interest, because these mutant proteins have been shown to be disrupted conformationally, are Ala-143, His-175, His-179 and Gly-281 (van Oijen, M, *et al*, 2000, *supra*). Particular subsets of the above list of tumor-promoting mutants have been shown to exert their oncogenic effects via transactivation of one or more of the growth promoting genes
 25 *bFGF*, *IGF-1*, *EGF-R*, and *c-myc*. Alternatively or conjunctively, some gain-of-function mutants, including Ala-143, His-175, Trp-248, Ser-249, His-273, and Gly-281, contribute to tumor resistance to chemotherapeutic drugs by transactivating the *MDR* gene.

As described above, in the case of this type of mutant, in heterozygous cells, selective degradation of that mutant by inhibition of HSP90 activity will restore normal p53 function.
 30 Furthermore, in cases of loss of heterozygosity (LOH), where the tumor has progressed further and the second, normal p53 allele has become mutated or lost, selective degradation of the

mutated protein by inhibition of HSP90 chaperoning will result in a therapeutic effect. In this case the p53 mutant is behaving as an oncoprotein, as in the bcr-abl and v-src examples described above.

d. Other tumor suppressor variant proteins

5 In addition to p53 itself, additional members of the p53 family of tumor suppressor proteins have also been implicated in human cancer progression. Although p53 itself is a fairly ubiquitous protein, other family members have more restricted tissue distributions. In particular tissues and tumors derived therefrom, closely related non-p53 proteins serve the same role as p53 itself. In these tumors, a truncated variant, termed deltaN,
10 predominates over the full-length form. The truncated and/or deletent isoform is able to compete with the full length form for DNA binding, but does not itself have any transactivating activity. Thus, the deltaN form inhibits the tumor suppressor activity of the full length form, so that if the variant is degraded as a result of inhibition of HSP90 activity, an antitumor effect or drug-sensitizing effect will result. The deltaN isoform will
15 have a heightened dependence on HSP90.

The following three examples concern the specific tumor suppressor proteins p51, p63, and p73. p51 and p63 are each produced from a common 15 exon gene, p73L/p63/p51/p40/KET, and all three proteins exhibit various isoforms, including deltaN isoforms that lack N-terminal transactivation (TA) domains and which are implicated in
20 various carcinomas treatable according to methods of the invention. The many isotypes possible for these gene products are attributable, at least in part, to complex alternative splicing events and, in the case of p63, multiple promoters. For each, it is understood that isoforms may exist and specific isoform expression patterns may vary as between different tissue types, and as between normal versus carcinomic or neoplastic tissues.

i. deltaN p51

25 Osada et al. described the cloning and functional analysis of human p51, which structurally and functionally resembles p53. Nature Med. 4: 839-843 (1998). Two major splicing variant gene products have been detected in normal cells, p51A and p51B. p51A (aka TAp63gamma; NCBI #s AB016072 (SEQ ID NOs 280 and 281) is a 448-amino-acid protein with
30 a molecular weight of 50.9 kDa; and p51B (aka TAp63alpha; AB016073 (SEQ ID NOs 282 and

283) is a 641-amino-acid protein with a molecular weight of 71.9 kDa. Other encoded isoforms have also been observed, including, e.g., those denoted in the following list: p51 delta (NCBI # AF116771 (SEQ ID NOs 284 and 285), delNdelta (NCBI # AAF43493 (SEQ ID NOs 286 and 287), delNbeta (NCBI # AAF43492 (SEQ ID NOs. 288 and 289), delNalpha (NCBI # AAF43491 (SEQ ID NOs. 290 and 291), delNgamma (NCBI # AAF43490; SEQ ID NOs 292 and 293), TAp63delta (NCBI # AAF43489; SEQ ID NOs 294 and 295), TAp63beta (NCBI # AAF43488 (SEQ ID NOs 296 and 297), TAp63alpha (NCBI # AAF43487 (SEQ ID NOs 298 and 299), and TAp63gamma (NCBI # AAF43486 (SEQ ID NOs 300 and 301). The TA isoforms contain a transactivation domain (encoded by exon 3') for transactivating p53; the deltaN forms do not.

The absence of the TA domain is thought to render those particular isoforms nonfunctional, thereby contributing to carcinoma etiology at least when those isoforms are expressed in abnormally high amounts. Normal expression patterns of the various isoforms is known to vary as between different tissue types. In lung cancer specimens, for example, multiple deltaN ("TA-less") forms of the p51 protein were found to be overexpressed in 34 of 44 lung cancer specimens analysed (77%). (Tani, M *et al*, 1999, *Neoplasia* 1:71-79).

ii. deltaN p63

In certain bladder and nasopharyngeal carcinomas, various isoforms of the p53 family member p63 are expressed, and one or more of the deltaN forms, e.g., deltaN p63beta (NCBI #AF075433; SEQ ID NOs 302 and 303), deltaN p63gamma (NCBI #AF075429; SEQ ID NOs 304 and 305), and deltaN p63 alpha (NCBI #AF075431 (SEQ ID NOs 306 and 307) predominate and dominantly inhibit the transactivating activity of the full length TA-containing forms. (Park, B *et al*, 2000, *Cancer Res.* 60:3370-3374). The TA-containing isoforms are TA p63 beta (NCBI #AF075432; SEQ ID NOs 308 and 309) and TA p63 alpha (NCBI #AF075430; SEQ ID NOs 310 and 311). In nasopharyngeal carcinoma, the deltaN isoform predominance is even more pronounced (Crook, T *et al*, 2000, *Oncogene* 19:3439-3444). The p63 protein is also important in UV-B-induced skin cancer. Overexpression of the deltaN isoform of p63 in transgenic mouse epidermis was found to block apoptosis induced by WT p53 in response to UV-B irradiation (Liefer, K, *et al*, 2000, *Cancer Res.* 60:4016-4020). Mutations in the *p63* gene have also been reported in epidermal carcinomas. See, e.g., Osada *et al*, 1998, *Nat. Med.* 4:839-843 and NCBI #NM003722 (SEQ ID NOs 312 and 313).

iii. deltaN p73

The p73 protein is important in ovarian carcinoma – when compared to primary cultures of normal ovarian epithelial cells, 57% of ovarian carcinoma cell lines, 71% of invasive tumors and 92% of borderline tumor tissues were found to express elevated levels of deltaN p73 (Ng, S *et al.*, 2000, *Oncogene* 19:1885-1890). Full-length p73 and isoforms thereof are displayed in NCBI # Y11416 (SEQ ID NOs 314, 315, 316, and 317), along with splice and allelic variations, including splice variations responsible for the deltaN isoform.

Applicants expect that all of the foregoing truncated p53 family members are structurally unstable, dependent on HSP90 and/or exhibit increased sensitivity to HSP90 inhibitors relative to their wild-type counterparts. Applicants further anticipate that other isomeric/aberrant forms of proteins may exhibit similar behavior(s).

The methods of the present invention may be used on mammals, preferably humans, either alone or in combination with other therapies or methods useful for treating a particular cell proliferative disorder or viral infection.

The use of the present invention is facilitated by first identifying whether the cell proliferation disorder or viral infection is accompanied by cells which contain expression of a fusion oncoprotein or a mutated cellular protein with heightened dependence on HSP90 (or a fusion protein or mutant protein that, by one skilled in the art, would be predicted to have heightened dependence on HSP90). Once such disorders are identified, patients suffering from such a disorder can be identified by analysis of their symptoms by procedures well known to medical doctors. Such patients are treated as described herein.

3. Representative assays for diagnosing proliferative disorders

Many different types of methods are known in the art that can be used to diagnose a proliferative disorder characterized by an aberrant protein, *e.g.*, those that involve determining protein concentrations and measuring or predicting the level of proteins within cells, tissues, and fluid samples. Indirect techniques include nucleic acid hybridization and amplification using, *e.g.*, polymerase chain reaction (PCR). These techniques are known to the person of skill and are discussed, *e.g.*, in Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, Second Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., Ausubel, *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, 1994. Because the nucleic acid sequence is

known, and because the aberrant proteins have a foundational basis in the nucleic acid sequence, the specific sequences found for aberrant proteins can also be used to generate primers and probes that span the novel junction (in the case of fusion proteins), *e.g.*, using RT-PCR and other procedures. For non-fusion proteins, as well as fusion proteins,
5 stringent hybridization and/or PCR can be used diagnostically.

Polyclonal or monoclonal antibodies can also be generated based on the specific sequence of the aberrant protein (in the case of fusion proteins, preferably the novel amino acid junction itself) using routine techniques. See Harlow *et al.*, *Antibodies: A Laboratory Manual*, 2nd Ed; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988).

10 Examples of diagnostic methods of that can be used with the invention include those reviewed in Slominski, A *et al*, 1999, *Arch. Pathol. Lab. Med.* 123:1246-1259, O'Connor *et al*, 1999, *Leuk. Lymphoma* 33:53-63, and Scarpa, A *et al*, 1997, *Leuk. Lymphoma* 26 Suppl. 1:77-82. A further list of methods that is intended to be exemplary but not to limit the scope of the invention, follows.

15 O'Connor *et al* , 1997, *Br. J. Haematol.* 99:597-604 described that the t(15;17)(q22;q21) translocation found in APL produces a PML-RAR fusion protein that can be specifically detected with the 5E10 Mab by fluorescence activated cell sorting (FACS).

Le *et al* , 1998, *Eur. J. Haematol.* 60:217-225 reported that the AML-ETO fusion protein that arises in t(8;21) AML can be identified in tumor cells with ETO-specific polyclonal
20 antibodies using western blotting. The normal ETO protein (70kD) can be distinguished from the AML-ETO fusion protein (94kD) on the basis of their differing mobilities in the gel.

Viswanatha *et al* , 1998, *Blood* 91:1882-1890 found that the CBFB-SMMHC fusion protein present in Inv(16)(p13q32) and t(16;16)(p13;q32) AML can be specifically detected with a polyclonal antibody specific for a junctional epitope using FACS of permeabilized cells.

25 In the case of dominantly-acting mutant proteins, such as mutant RET or gain-of-function mutants of p53, the presence of the specific point mutations known to give rise to the dominant mutant may be identified by the molecular genetic techniques listed above in reference to fusion proteins. Numerous reviews of germline and acquired p53 mutations detected in human cancers have been published (*see, e.g.*, Hainuit, P, *et al*, 2000, *Adv. Cancer Res.* 77:81-137).

In the case of dominant-negative p53 mutations, several other diagnostic criteria may be employed to identify patients susceptible of treatment with the current invention. First, molecular genetic methodologies such as Southern Blotting or PCR can be used to detect the presence of a specific point mutation known to give rise to a dominant-negative version of p53. Similarly, FISH
5 may be employed to detect specific point mutations known to confer conformational changes and/or dominant-negative activity (Villadsen R *et al*, 2000, *Cancer Genet. Cytogenet.* 116:28-34). Other methods include allele-specific PCR (AS-PCR) and chromosome flow cytometry (Villadsen *et al*, *Supra*).

Alternatively, if the mutation in question has not previously been shown to generate a
10 dominant-negative p53 mutant, a cell-based transdominance assay may be used to determine the phenotype (Frebourg, T *et al*, 1992, *Proc. Natl. Acad. Sci.* 89:6413-6417). In this assay, p53-null SAOS-2 cells are co-transfected with WT p53 and the test mutant. The normal p53 protein causes the cells to undergo apoptosis, from which fate they can be rescued by a p53 mutant that has a dominant negative activity. In these cases, further genetic analyses may be performed to confirm
15 the presence of an intact non-mutant allele. In addition, antibodies have been raised that distinguish between p53 proteins with normal versus mutant conformation. These latter p53s have a heightened dependence upon HSP90, and so fall within the scope of the present invention. Specifically, PAb240, from (Oncogene Sciences, Inc.) OSI, is mutant conformation-specific. The corresponding antibody specific for WT is PAb1620, also for OSI (Chene, P, *et al*, 1999, *supra*).

20 In the case of cell proliferative disorders arising due to unwanted proliferation of non-cancer cells, the level of the fusion protein or mutated cellular protein is compared to that level occurring in the general population (*e.g.*, the average level occurring in the general population of people or animals excluding those people or animals suffering from a cell proliferative disorder). If the unwanted cell proliferation disorder is characterized by an abnormal level of a fusion
25 protein than occurs in a normal population, or by the presence of a mutated cellular protein, such as p53, then the disorder is a candidate for treatment using the methods described herein. In a preferred example, the mutated protein is p53 and the proliferative disorder is rheumatoid arthritis. In a particularly preferred example, the p53 mutations may include, but are not limited to, N239S (Asn→Ser), C176R (Cys-Arg) and R213* (Arg→stop) and the mutant forms exert
30 apparent dominant-negative activity over the wild-type protein. (Han, Z *et al*, 1999, *Arthritis Rheum.* 42:1088-1092).

4. Preparation and Administration of Pharmaceutical Compositions

Geldanamycin may be prepared according to U.S. Patent No. 3,595,955 using the subculture of *Streptomyces hygroscopicus* that is on deposit with the U.S. Department of Agriculture, Northern Utilization and Research Division, Agricultural Research, Peoria, Ill., USA, accession number NRRL 3602. It is also available from Sigma/Aldrich Chemical Co., St. Louis, Mo., USA. Numerous derivatives of this compound, including herbimycin A, macbecin, and 17-AAG may be fashioned as specified in U.S. Patent Nos. 4, 261, 989, 5,387,584, and 5,932,566, or according to standard techniques known in the art. Other useful ansamycin derivatives appear in Applicants' co-pending and commonly owned provisional application entitled, "*Ansamycins Having Improved Pharmacological and Biological Properties*," filed February 8, 2002, Serial Number to be determined, and herein incorporated by reference in its entirety.

Those of ordinary skill in the art are familiar with formulation and administration techniques that can be employed in use of the invention, e.g., as discussed in Goodman and Gilman's *The Pharmacological Basis of Therapeutics*, current edition; Pergamon Press; and Remington's *Pharmaceutical Sciences* (current edition.) Mack Publishing Co., Easton, Pa.

The compounds utilized in the methods of the instant invention may be administered either alone or in combination with pharmaceutically acceptable carriers, excipients or diluents, in a pharmaceutical composition, according to standard pharmaceutical practice. The compounds can be administered orally or parenterally, including the intravenous, intramuscular, intraperitoneal, subcutaneous, rectal and topical routes of administration.

The pharmaceutical compositions used in the methods of the instant invention can contain the active ingredient in a form suitable for oral use, for example, as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsions, hard or soft capsules, or syrups or elixirs. Compositions intended for oral use may be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions may contain one or more agents selected from the group consisting of sweetening agents, flavoring agents, coloring agents and preserving agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients which are suitable for the manufacture of tablets. These excipients may be, for example, inert diluents, such as calcium carbonate, sodium carbonate,

lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, such as microcrystalline cellulose, sodium crosscarmellose, corn starch, or alginic acid; binding agents, for example starch, gelatin, polyvinyl-pyrrolidone or acacia, and lubricating agents, for example, magnesium stearate, stearic acid or talc. The tablets may be uncoated or they may be coated by known techniques to mask the unpleasant taste of the drug or delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action over a longer period. For example, a water soluble taste masking material such as hydroxypropylmethyl-cellulose or hydroxypropylcellulose, or a time delay material such as ethyl cellulose, cellulose acetate butyrate may be employed.

Formulations for oral use may also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is mixed with water soluble carrier such as polyethyleneglycol or an oil medium, for example peanut oil, liquid paraffin, or olive oil.

Aqueous suspensions contain the active material in admixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydroxypropylmethyl-cellulose, sodium alginate, polyvinyl-pyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents may be a naturally-occurring phosphatide, for example lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethylene-oxycetanol, or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol such as polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions may also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose, saccharin or aspartame.

Oily suspensions may be formulated by suspending the active ingredient in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in mineral oil such as liquid paraffin. The oily suspensions may contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents such as those set forth above, and flavoring agents

may be added to provide a palatable oral preparation. These compositions may be preserved by the addition of an anti-oxidant such as butylated hydroxyanisol or alpha-tocopherol.

Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents and suspending agents are exemplified by those already mentioned above. Additional excipients, for example sweetening, flavoring and coloring agents, may also be present. These compositions may be preserved by the addition of an anti-oxidant such as ascorbic acid.

The pharmaceutical compositions used in the methods of the instant invention may also be in the form of oil-in-water emulsions. The oily phase may be a vegetable oil, for example olive oil or arachis oil, or a mineral oil, for example liquid paraffin or mixtures of these. Suitable emulsifying agents may be naturally-occurring phosphatides, for example soy bean lecithin, and esters or partial esters derived from fatty acids and hexitol anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions may also contain sweetening, flavoring agents, preservatives and antioxidants.

Syrups and elixirs may be formulated with sweetening agents, for example glycerol, propylene glycol, sorbitol or sucrose. Such formulations may also contain a demulcent, a preservative, flavoring and coloring agents and antioxidant.

The pharmaceutical compositions may be in the form of sterile injectable aqueous solutions. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution and isotonic sodium chloride solution.

The sterile injectable preparation may also be a sterile injectable oil-in-water microemulsion where the active ingredient is dissolved in the oily phase. For example, the active ingredient may be first dissolved in a mixture of soybean oil and lecithin. The oil solution then introduced into a water and glycerol mixture and processed to form a microemulsion.

The injectable solutions or microemulsions may be introduced into a patient's blood-stream by local bolus injection. Alternatively, it may be advantageous to administer the solution or microemulsion in such a way as to maintain a constant circulating concentration of the instant

compound. In order to maintain such a constant concentration, a continuous intravenous delivery device may be utilized. An example of such a device is the Deltec CADD-PLUS™ model 5400 intravenous pump.

5 The pharmaceutical compositions may be in the form of a sterile injectable aqueous or oleagenous suspension for intramuscular and subcutaneous administration. This suspension may be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents which have been mentioned above. The sterile injectable preparation may also be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example as a solution in 1,3-butane diol. In addition, sterile, fixed oils are
10 conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including mono- or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

The HSP90 inhibitors used in the methods of the present invention may also be administered in the form of a suppositories for rectal administration of the drug. These
15 compositions can be prepared by mixing the inhibitors with a suitable non-irritating excipient which is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter, glycerinated gelatin, hydrogenated vegetable oils, mixtures of polyethylene glycols of various molecular weights and fatty acid esters of polyethylene glycol.

20 For topical use, creams, ointments, jellies, solutions or suspensions, etc., containing an HSP90 inhibitor can be used. (As used herein, topical application can include mouth washes and gargles.)

The compounds used in the methods of the present invention can be administered in intranasal form via topical use of suitable intranasal vehicles and delivery devices, or via
25 transdermal routes, using those forms of transdermal skin patches well known to those of ordinary skill in the art. To be administered in the form of a transdermal delivery system, the dosage administration will, of course, be continuous rather than intermittent throughout the dosage regimen.

The HSP90 inhibitors used in the instant invention may also be co-administered with other
30 well known therapeutic agents that are selected for their particular usefulness against the

condition that is being treated. For example, the instant compounds may be useful in combination with known anti-cancer and cytotoxic agents. The instant compounds may also be useful in combination with other inhibitors of parts of the signaling pathway that links cell surface growth factor receptors to nuclear signals initiating cellular proliferation.

5 The methods of the present invention may also be useful with other agents that inhibit angiogenesis and thereby inhibit the growth and invasiveness of tumor cells, including, but not limited to VEGF receptor inhibitors, angiostatin and endostatin.

10 When a HSP90 inhibitor used in the methods of the present invention is administered into a human subject, the daily dosage will normally be determined by the prescribing physician with the dosage generally varying according to the age, weight, and response of the individual patient, as well as the severity of the patient's symptoms.

15 In one exemplary application, a suitable amount of a HSP90 inhibitor is administered to a mammal undergoing treatment for cancer. Administration occurs in an amount of each type of inhibitor of between about 0.1 mg/kg of body weight to about 60 mg/kg of body weight per day, preferably of between 0.5 mg/kg of body weight to about 40 mg/kg of body weight per day. A particular therapeutic dosage that comprises the instant composition includes from about 0.01 mg to about 1000 mg of a HSP90 inhibitor. Preferably, the dosage comprises from about 1 mg to about 1000 mg of a HSP90 inhibitor.

20 Examples of antineoplastic agents which can be used in combination with the methods of the present invention include, in general, alkylating agents, anti-metabolites; epidophyllotoxin; an antineoplastic enzyme; a topoisomerase inhibitor; procarbazine; mitoxantrone; platinum coordination complexes; biological response modifiers and growth inhibitors; hormonal/anti-hormonal therapeutic agents and haematopoietic growth factors.

25 Exemplary classes of antineoplastic agents further include the anthracycline family of drugs, the vinca drugs, the mitomycins, the bleomycins, the cytotoxic nucleosides, the epothilones, discodermolide, the pteridine family of drugs, diylenes and the podophyllotoxins. Particularly useful members of those classes include, for example, carminomycin, daunorubicin, aminopterin, methotrexate, methopterin, dichloromethotrexate, mitomycin C, porfiromycin, 5-fluorouracil, 6-mercaptopurine, gemcitabine, cytosine arabinoside, podophyllotoxin or podophyllotoxin derivatives such as etoposide, etoposide phosphate or teniposide, melphalan,

30

vinblastine, vincristine, leurosidine, vindesine, leurosine, paclitaxel and the like. Other useful antineoplastic agents include estramustine, carboplatin, cyclophosphamide, bleomycin, gemcitabine, ifosamide, melphalan, hexamethyl melamine, thiotepa, cytarabin, idatrexate, trimetrexate, dacarbazine, L-asparaginase, camptothecin, CPT-11, topotecan, ara-C, bicalutamide, flutamide, leuprolide, pyridobenzoindole derivatives, interferons and interleukins.

Preferably, the pharmaceutical preparation is in unit dosage form. In such form, the preparation is subdivided into unit doses containing appropriate quantities of the active component, *e.g.*, an effective amount to achieve the desired purpose.

The quantity of active compound in a unit dose of preparation may be varied or adjusted from about 0.1 mg to 1000 mg, preferably from about 1 mg to 300 mg, more preferably 10 mg to 200 mg, according to the particular application.

The actual dosage employed may be varied depending upon the requirements of the patient and the severity of the condition being treated. Determination of the proper dosage for a particular situation is within the skill of the art. Generally, treatment is initiated with smaller dosages which are less than the optimum dose of the compound. Thereafter, the dosage is increased by small amounts until the optimum effect under the circumstances is reached. For convenience, the total daily dosage may be divided and administered in portions during the day if desired.

The amount and frequency of administration of the HSP90 inhibitors used in the methods of the present invention and, if applicable, other chemotherapeutic agents and/or radiation therapy will be regulated according to the judgment of the attending clinician (physician) considering such factors as age, condition and size of the patient as well as severity of the disease being treated. A dosage regimen of the HSP90 inhibitors can be intravenous administration of from 1 mg to 5gm/day, more preferably 10 mg to 2000 mg/day, more preferably still 10 to 1000 mg/day, and most preferably 50 to 600 mg/day, in one or more (preferably two) doses, to block tumor growth.

The chemotherapeutic agent and/or radiation therapy can be administered according to therapeutic protocols well known in the art. It will be apparent to those skilled in the art that the administration of the chemotherapeutic agent and/or radiation therapy can be varied depending on the disease being treated and the known effects of the chemotherapeutic agent and/or radiation therapy on that disease. Also, in accordance with the knowledge of the skilled clinician, the

therapeutic protocols (*e.g.*, dosage amounts and times of administration) can be varied in view of the observed effects of the administered therapeutic agents (*i.e.*, antineoplastic agent or radiation) on the patient, and in view of the observed responses of the disease to the administered therapeutic agents.

5 Also, in general, the HSP90 inhibitor and the chemotherapeutic agent do not have to be administered in the same pharmaceutical composition, and may, because of different physical and chemical characteristics, have to be administered by different routes. For example, the HSP90 inhibitor may be administered orally to generate and maintain good blood levels, while the chemotherapeutic agent may be administered intravenously. The determination of the mode of
10 administration and the advisability of administration, where possible, in the same pharmaceutical composition, is well within the knowledge of the skilled clinician. The initial administration can be made according to established protocols known in the art, and then, based upon the observed effects, the dosage, modes of administration and times of administration can be modified by the skilled clinician.

15 The particular choice of HSP90 inhibitor, and chemotherapeutic agent and/or radiation will depend upon the diagnosis of the attending physicians and their judgment of the condition of the patient and the appropriate treatment protocol.

 The HSP90 inhibitor, and chemotherapeutic agent and/or radiation may be administered concurrently (*e.g.*, simultaneously, essentially simultaneously or within the same treatment
20 protocol) or sequentially, depending upon the nature of the proliferative disease, the condition of the patient, and the actual choice of chemotherapeutic agent and/or radiation to be administered in conjunction (*i.e.*, within a single treatment protocol) with the HSP90 inhibitor.

 If the HSP90 inhibitor, and the chemotherapeutic agent and/or radiation are not administered simultaneously or essentially simultaneously, then the optimum order of
25 administration of the HSP90 inhibitor, and the chemotherapeutic agent and/or radiation, may be different for different tumors. Thus, in certain situations the HSP90 inhibitor may be administered first followed by the administration of the chemotherapeutic agent and/or radiation; and in other situations the chemotherapeutic agent and/or radiation may be administered first followed by the administration of the HSP90 inhibitor. This alternate administration may be
30 repeated during a single treatment protocol. The determination of the order of administration, and the number of repetitions of administration of each therapeutic agent during a treatment protocol,

is well within the knowledge of the skilled physician after evaluation of the disease being treated and the condition of the patient. For example, the chemotherapeutic agent and/or radiation may be administered first, especially if it is a cytotoxic agent, and then the treatment continued with the administration of the HSP90 inhibitor followed, where determined advantageous, by the administration of the chemotherapeutic agent and/or radiation, and so on until the treatment protocol is complete.

Thus, in accordance with experience and knowledge, the practicing physician can modify each protocol for the administration of a component (therapeutic agent-*i.e.*, HSP90 inhibitor, chemotherapeutic agent or radiation) of the treatment according to the individual patient's needs, as the treatment proceeds.

The attending clinician, in judging whether treatment is effective at the dosage administered, will consider the general well-being of the patient as well as more definite signs such as relief of disease-related symptoms, inhibition of tumor growth, actual shrinkage of the tumor, or inhibition of metastasis. Size of the tumor can be measured by standard methods such as radiological studies, *e.g.*, CAT or MRI scan, and successive measurements can be used to judge whether or not growth of the tumor has been retarded or even reversed. Relief of disease-related symptoms such as pain, and improvement in overall condition can also be used to help judge effectiveness of treatment.

EXAMPLES

The following examples are illustrative only, and are not intended to be limiting of the invention.

Example 1:

Cytotoxic Activity of 17AAG on K562 Versus a Normal Cell Type

Grosveld et al., Mol Cell Biol 6(2):607-16 (1986) showed that the chronic myelocytic cell line K562 produces a chimeric bcr/c-abl transcript, making it a suitable model system to demonstrate the methods of the invention. The cell line is widely available, *e.g.*, from American Type Culture Collection ("ATCC"; Manassas, VA, USA; cat# CCL-243) and can be propagated in a variety of media, *e.g.*, ATCC's Iscove's modified Dulbecco's medium with 4 mM L-glutamine adjusted to contain 1.5 g/L sodium bicarbonate, 90%; fetal bovine serum, 10%; 37C.

Experimental

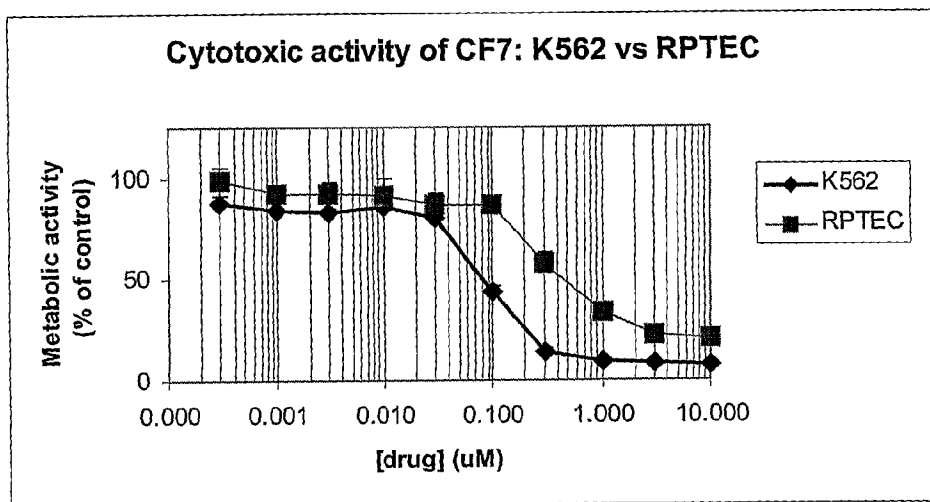
To K562 cells (suspension grown in DMEM media supplemented w/10% Fetal Bovine Serum (FBS) and 1mM HEPES; subcultured biweekly at 100K cells/ml) in a 96 well plate (0.1 ml medium; 2000 cells per well) were added various concentrations of 17-AAG (CF7) and the effects measured over a period of 3-6 days using an MTS assay protocol similar to that offered by Promega Corp (Madison, WI, US; cat# G5421).

The MTS assay is a colorimetric assay for determining the number of viable cells in proliferation, cytotoxicity or chemosensitivity assays. The CellTiter 96® AQueous Assay is composed of solutions of tetrazolium compound (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H- tetrazolium, inner salt; MTS) and an electron coupling reagent (phenazine methosulfate) PMS. MTS is bioreduced by cells into a formazan that is soluble in tissue culture medium. Barltrop et al. (1991) Bioorg. & Med. Chem. Lett. 1, 611. The absorbance of the formazan at 490nm can be measured directly from 96 well assay plates without additional processing. Cory et al. (1991) Cancer Commun. 3, 207; Riss, T.L. and Moravec, R.A. (1992) Mol. Biol. Cell 3 (Suppl.), 184a. The conversion of MTS into the aqueous soluble formazan is accomplished by dehydrogenase enzymes found in metabolically active cells. The quantity of formazan product as measured by the amount of 490nm absorbance is directly proportional to the number of living cells in culture.

Using the MTS assay, cytotoxicity (defined as “growth inhibition” and not necessarily versus renal proximal tubular endothelial cells (normal cells) was determined as shown in the following Tables. “Sem” refers to standard error of the mean, which is calculated as the standard deviation divided by the square root of the sample size; the numbers reflect triplicate replicates. Dilutions of the compounds were prepared in DMSO and straight DMSO was used as a control corresponding to 100% metabolic activity.

Conc (uM)	Metabolic Activity			
	K562	sem1	RPTEC	sem1
10.0000	7.89	0.56	20.10	2.64
3.0000	8.12	1.02	22.01	2.49
1.0000	9.51	0.59	34.01	0.19
0.3000	14.40	1.53	58.03	5.09
0.1000	44.06	2.76	86.46	1.51
0.0300	80.12	2.29	86.40	5.96
0.0100	85.94	0.06	91.81	8.22
0.0030	83.00	2.25	92.73	4.79

0.0010	83.81	0.73	92.26	2.97
0.0003	88.00	0.40	98.69	7.16

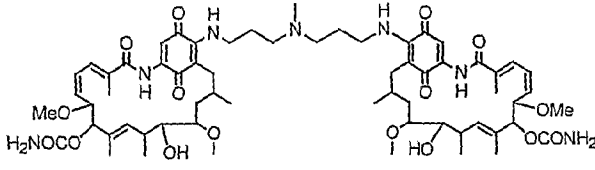
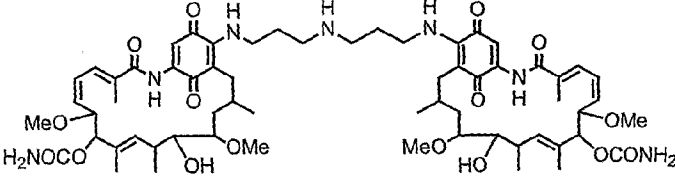
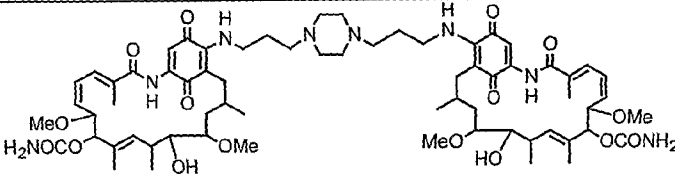
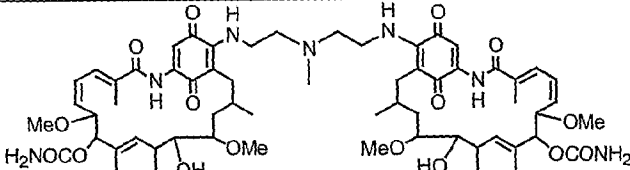
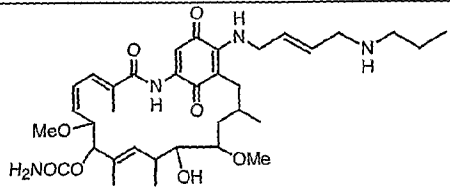


As demonstrated, the fusion protein cancer line K562 is more sensitive to the HSP90 inhibitor than is the normal cell line, RPTEC. It is expected that this will hold true for a variety of tumor cell lines versus a variety of normal cell lines.

In addition to the effects of 17-AAG on K562 versus RPTEC, the effects of a number of other putative HSP90 inhibitors and control compounds were tested side-by-side per the following Table, where "NEC" refers to no effective concentration.

Compound	RPTEC IC ₅₀ (nM)	K562 IC ₅₀ (nM)
CF7	400	70
DMSO	NEC	NEC
208	1000	50
237	4000	100
483	1000	70
481	4000	400

In the table, compound CF7 is the well known 17-AAG and compounds 207, 208, 237, 483, and 481 have the following formulas.

Compound #	Formula
208	 <p>a water soluble dimer</p>
237	 <p>a water soluble dimer</p>
207	 <p>a water soluble dimer</p>
483	 <p>a water soluble dimer</p>
481	 <p>a water soluble prodrug</p>

A separate study using the well known compound, radicicol, yielded results approximating those obtained for compound 237. Preparation of compounds 207, 208, 237, 483, and 481 is described in the following examples.

Example 2:

Preparation of Compound #208

3,3'-diamino-N-methyldipropylamine (1.32g, 9.1mmol) was added dropwise to a solution of Geldanamycin (10g, 17.83mmol) in DMSO (200ml) in a flame-dried flask under N₂ and stirred at room temperature. The reaction mixture was diluted with water after 12 hours. A precipitate was formed and filtered to give the crude product. The crude product was chromatographed by silica chromatography (5% CH₃OH/CH₂Cl₂) to afford the desired dimer as a purple solid (8.92g, 7.2mmol). Yield: 81%; mp 153°C (dec.); ¹H NMR (CDCl₃) δ 0.95 (d, J = 7 Hz, 6H, 2CH₃), 1.0 (d, J = 7 Hz, 6H, 2CH₃), 1.69 (m, 4 H, 2 CH₂), 1.74 (m, 4 H, 2CH₂), 1.76 (s, 6 H, 2 CH₃), 1.83 (m, 2H, 2CH), 2.0 (s, 6H, 2CH₃), 2.3 (s, 3H, N-CH₃), 2.36(dd, J = 14Hz, 2H, 2CH), 2.5 (m, 4H, 2CH₂), 2.63 (d, 2H, 2CH), 2.75(m, 2H, 2CH), 3.25(s, 6H, 2OCH₃), 3.35(s, 6H, 2OCH₃), 3.4 (m, 2H, 2CH), 3.50 (m, 4H, 2CH₂), 3.68(m, 2H, 2CH), 4.2(Bs, 2H, OH), 4.3(d, J = 10 Hz, 2H, 2CH), 4.8(Bs, 4H, 2NH₂), 5.19(s, 2H, 2CH), 5.82(t, J = 15 Hz, 2H, 2CH=), 5.89(d, J = 10 Hz, 2H, 2CH=), 6.59(t, J = 15 Hz, 2H, 2CH=), 6.92 (d, J = 10 Hz, 2H, 2CH=), 7.13 (t, 2H, 2NH), 7.24(s, 2H, 2CH=), 9.21(s, 2H, 2NH); MS (m/z)1203 (M+H).

The corresponding HCl salt was prepared by the following method: an HCl solution in EtOH (5 ml, 0.123N) was added to a solution of compound #208 (1 gm as prepared above) in THF (15 ml) and EtOH (50 ml) at room temperature. The reaction mixture was stirred for 10 min. The salt was precipitated, filtered and washed with large amount of EtOH and dried in vacuo.

Example 3:

Preparation of Compound #207

Compound #207 was prepared by the same method described in example 2 except that 1,4-bis (3-aminopropyl) piperazine was used instead of 3,3'-diamino-N-methyldipropylamine. The pure purple product was obtained after column chromatography (silica gel); yield: 90%; mp 162°C; ¹H NMR (CDCl₃) δ 0.97 (d, J = 6.6 Hz, 6H, 2CH₃), 1.0 (d, J = 6.6 Hz, 6H, 2CH₃), 1.73 (m, 4 H, 2 CH₂), 1.78 (m, 4 H, 2CH₂), 1.80 (s, 6 H, 2 CH₃), 1.85 (m, 2H, 2CH), 2.0 (s, 6H, 2CH₃), 2.4 (dd, J = 11Hz, 2H, 2CH), 2.55 (m, 8H, 4CH₂), 2.67 (d, J = 15 Hz, 2H, 2CH), 2.63 (t, J = 10 HZ, 2H, 2CH), 2.78(t, J = 6.5 Hz, 4H, 2CH₂), 3.26(s, 6H, 2OCH₃), 3.38(s, 6H, 2OCH₃), 3.4 (m, 2H, 2CH), 3.60 (m, 4H, 2CH₂), 3.75(m, 2H, 2CH), 4.6(d, J = 10 Hz, 2H, 2CH), 4.65 (Bs, 2H, 2OH), 4.8(Bs, 4H, 2NH₂), 5.19(s, 2H, CH), 5.83(t, J = 15 Hz, 2H, 2CH=), 5.89(d, J = 10 Hz, 2H, 2CH=), 6.58(t, J = 15 Hz, 2H, 2CH=), 6.94 (d, J = 10 Hz, 2H, 2CH=), 7.24(s, 2H, 2CH=), 7.60 (m, 2H, 2NH), 9.20(s, 2H, 2NH); MS (m/z) 1258 (M+H); The corresponding HCl salt was prepared by the same procedure as described in example 1.

Example 4:**Preparation of Compound #237**

Compound #237 was prepared by the same method described in example 2 except that 3,3'-diamino-dipropylamine was used instead of 3,3'-diamino-N-methyldipropylamine. The pure purple product was obtained after flash chromatography (silica gel); yield: 93%; mp 165°C; ¹H NMR (CDCl₃) □ 0.97 (d, J = 6.6 Hz, 6H, 2CH₃), 1.0 (d, J = 6.6 Hz, 6H, 2CH₃), 1.72 (m, 4 H, 2 CH₂), 1.78 (m, 4 H, 2CH₂), 1.80 (s, 6 H, 2 CH₃), 1.85 (m, 2H, 2CH), 2.0 (s, 6H, 2CH₃), 2.4 (dd, J = 11Hz, 2H, 2CH), 2.67 (d, J = 15 Hz, 2H, 2CH), 2.63 (t, J = 10 HZ, 2H, 2CH), 2.78(t, J = 6.5 Hz, 4H, 2CH₂), 3.26(s, 6H, 2OCH₃), 3.38(s, 6H, 2OCH₃), 3.4 (m, 2H, 2CH), 3.60 (m, 4H, 2CH₂), 3.75(m, 2H, 2CH), 4.6(d, J = 10 Hz, 2H, 2CH), 4.65 (Bs, 2H, 2OH), 4.8(Bs, 4H, 2NH₂), 5.19(s, 2H, 2CH), 5.83(t, J = 15 Hz, 2H, 2CH=), 5.89(d, J = 10 Hz, 2H, 2CH=), 6.58(t, J = 15 Hz, 2H, 2CH=), 6.94 (d, J = 10 Hz, 2H, 2CH=), 7.17 (m, 2H, 2NH), 7.24(s, 2H, 2CH=), 9.20(s, 2H, 2NH); MS (m/z)1189 (M+H); The corresponding HCl salt was prepared by the same procedure as described in example 1.

Example 5:**Preparation of Compound #483**

Compound #483 was prepared by the same method described in example 2 except that 2,2'-diamino-N-methyldiethylamine was used instead of 3,3'-diamino-N-methyldipropylamine. The pure purple product was obtained after flash chromatography; yield: 90%; mp 167-169 °C; ¹H NMR (CDCl₃) □ 0.95 (d, J = 7 Hz, 6H, 2CH₃), 1.00 (d, J = 7 Hz, 6H, 2CH₃), 1.85 (m, 4 H, 2CH₂), 1.75 (s, 6 H, 2 CH₃), 1.80 (m, 2H, 2CH), 2.0 (s, 6H, 2CH₃), 2.30 (s, 3H, N-CH₃), 2.30 (dd, J = 14Hz, 2H, 2CH), 2.5 (m, 4H, 2CH₂), 2.63 (d, 2H, 2CH), 2.75(m, 2H, 2CH), 3.25(s, 6H, 2OCH₃), 3.35(s, 6H, 2OCH₃), 3.4 (m, 2H, 2CH), 3.50 (m, 4H, 2CH₂), 3.68(m, 2H, 2CH), 4.2(Bs, 2H, OH), 4.30 (d, J = 10 Hz, 2H, 2CH), 4.8(Bs, 4H, 2NH₂), 5.19 (s, 2H, 2CH), 5.82 (t, J = 15 Hz, 2H, 2CH=), 5.90 (d, J = 10 Hz, 2H, 2CH=), 6.59(t, J = 15 Hz, 2H, 2CH=), 6.92 (d, J = 10 Hz, 2H, 2CH=), 7.13 (t, 2H, 2NH), 7.24 (s, 2H, 2CH=), 9.20 (s, 2H, 2NH); MS (m/z)1175 (M+H);); The corresponding HCl salt was prepared by the same procedure as described in example 1.

Example 6:**Preparation of Compound #481**

To 200 mg (0.357 mmol) of geldanamycin in 8 ml of dry THF in a flame-dried flask was added 91.6 mg (0.714 mmol) of N-propyl-1,4-diamino-2-butene drop-wise under nitrogen. The reaction mixture was stirred at room temperature for 4 h at which time TLC analysis indicated the reaction was complete. The solvent was removed by rotary evaporation and the crude material was chromatographed (5% CH₃OH/CH₂Cl₂ to 15% CH₃OH/CH₂Cl₂) to afford the desired compound as a purple solid (150 mg, 0.228 mmol); yield: 64%; mp 131 °C; ¹H NMR (CDCl₃) δ 0.97 (m, 9H, 3CH₃), 1.52 (m, 2H, CH₂), 1.72 (m, 3H, CH + CH₂), 1.80 (s, 3H, CH₃), 2.0 (s, 3H, CH₃), 2.38 (dd, J = 11 Hz, 1H, CH), 2.72 (m, 4H, 2CH, CH₂), 3.26 (s, 3H, OCH₃), 3.38 (s, 3H, OCH₃), 3.46 (m, H, CH), 3.6 (m, H, CH), 4.18 (m, 4H, 2CH₂), 4.34 (d, J = 10 Hz, 1H, CH), 4.8 (bs, 2H, NH₂), 5.19 (s, 1H, CH), 5.88 (m, 4H, 4CH=), 6.38 (m, 1H, NH), 6.61 (t, J = 15 Hz, 1H, CH=), 6.94 (d, J = 10 Hz, 1H, CH=), 7.30 (s, H, CH=), 9.16 (s, H, NH); MS (m/z) 658 (M+H). The corresponding HCl salt was prepared by the same procedure as described in example 1.

* * *

Various patents, publications, and formulations are within the levels of ordinary skill in the art to which the invention pertains. All documents including the sequence listing cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually, although none is admitted to be prior art.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, are encompassed within the spirit of the invention, and are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms “comprising,” “consisting essentially of” and “consisting of” may be replaced with either of the other two terms. The terms and expressions
5 which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features,
10 modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is
15 also thereby described in terms of any individual member or subgroup of members of the Markush group or other group, and exclusions of individual members as appropriate.

Claims

We claim:

1. A method of treating a patient having a genetically-defined disease characterized by a chromosomal aberration that yields an oncogenic fusion protein, comprising:
 - 5 providing a cell, tissue, or fluid sample of a patient suspected of having said genetically-defined disease;
 - identifying one or more characteristics indicative of said disease in or on said cell, tissue, or fluid sample; and
 - administering to said patient a pharmaceutically effective amount of an HSP90-
10 inhibiting compound.
2. The method of claim 1, wherein said compound is an ansamycin.
3. The method of claim 2, wherein said ansamycin is selected from the group consisting of geldanamycin, 17-AAG, herbimycin A, and macbecin.
4. The method of claim 2, wherein said ansamycin is 17-AAG.
- 15 5. The method of claim 1, wherein said compound is a compound that binds into the ATP-binding site of a HSP90.
- 6 The method of claim 5 wherein said compound is radicicol or an analog thereof.
7. The method of claim 1 wherein said identifying comprises using PCR or LCR to identify a nucleic acid encoding said oncogenic fusion protein.
- 20 8. The method of claim 1 wherein said identifying comprises using an antibody to identify said fusion protein.
9. The method of claim 1 wherein said identifying comprises using a cytochemical technique.
10. The method of claim 9 wherein said cytochemical technique employs nucleic acid
25 hybridization.

11. The method of claim 10 wherein said cytochemical technique is FISH.
12. The method of claim 1 wherein said disease is a hematopoietic disorder.
13. The method of claim 11 wherein said hematopoietic disorder is selected from the group consisting of a T or B cell lymphoma, CML, APL, ALL, AML, NHL, and CMML.
- 5 14. The method of claim 1 wherein said disease is characterized by a solid tumor.
15. The method of claim 14 wherein said solid tumor is selected from the group consisting of papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma, synovial sarcoma.
- 10 16. The method of claim 1 wherein said fusion protein contains one or more functional domains or portions thereof selected from the group consisting of kinases and DNA binding motifs.
17. The method of claim 12 or 13 wherein said administering employs an *ex vivo* procedure.
- 15 18. The method of claim 14 wherein said administering is intralesional.
19. The method of claim 1 wherein said administering is parenteral.
20. The method of claim 1 wherein said HSP90-inhibiting compound has an IC_{50} at least two-fold higher for cells that do not have characteristics indicative of said genetically-defined proliferative disorder relative to those cells that do have such
20 characteristics.
21. The method of claim 1 wherein said HSP90-inhibiting compound has an IC_{50} at least five-fold higher for cells that do not have characteristics indicative of said genetically-defined proliferative disorder relative to those cells that do have such characteristics.

22. The method of claim 1 wherein said HSP90-inhibiting compound has an IC_{50} at least ten-fold higher for cells that do not have characteristics indicative of said genetically-defined proliferative disorder relative to those cells that do have such characteristics.

23. The method of claim 1 wherein cells of said patient are monitored *in vitro* for sensitivity prior to administration of said compound to said patient.

24. The method of claim 1 wherein said non-random chromosomal aberration is a translocation.

25. The method of claim 1 wherein said non-random chromosomal aberration is a inversion.

26. The method of claim 1 wherein said non-random chromosomal aberration is a deletion.

27. The method of claim 1 wherein said non-random chromosomal aberration is selected from the group consisting of inv14 (q11; q32), t(9; 22)(q34; q11), t(1; 19)(q23; p13.3), t(17; 19)(q22; p13), t(15; 17)(q21-q11-22), t(11; 17)(q23; q21.1), t(4; 11)(q21; q23), t(9; 11)(q21; q23), t(11; 19)(q23; p13), t(X; 11)(q13; q23), t(1; 11)(p32; q23), t(6; 11)(q27; q23), t(11; 17)(q23; q21), t(8; 21)(q22; q22), t(3; 21)(q26; q22), 5(16; 21)(p11; q22), t(6; 9)(p23; q34), t(4; 16)(q26; p13), inv(2; 2)(p13; p11.2-14), inv(16)(p13q22), t(5; 12)(q33; p13), t(2; 5)(2p23; q35), t(9; 12)(q34; p13), del(12p), t(15; 17)(q22; q12), t(11; 17)(q23; q12), t(16; 16)(p13; q22), inv(16)(p13; q22), t(9; 11)(p22; q23), t(1; 22)(p13; q13), t(3; 3)(q21; q26), inv(3)(q21q26), t(3; 5)(q21; q31), t(3; 5)(q25; q34), t(7; 11)(p15; p15), t(8; 16)(p11; p13), t(9; 12)(q34; p13), t(12; 22)(p13; q13), del(5q), del(7q), del(20q), t(11q23), t(12; 21)(p13; q22), t(5; 12)(q31; p13), t(1; 12)(q25; p13), t(12; 15)(p13; q25), t(1; 12)(q21; p13), t(12; 21)(q13; p32), and t(5; 7)(q33; q11.2)).

28. The method of claim 1 wherein said non-random chromosomal aberration is a t(9; 22)(q34; q11) optionally characterized by and comprising a sequence selected from any one of SEQ ID NOs 15-26 or a homolog, isoform, or allelic variation thereof.

29. A method of treating cancerous cells in a heterogeneous population of cells, said heterogeneous population comprising both cancerous and noncancerous, and said

cancerous cells characterized by fusion proteins not found in said noncancerous cells, said method comprising:

administering to said heterogeneous population of cells a pharmaceutically effective amount of an HSP90-inhibiting compound.

- 5 30. The method of claim 29 wherein said compound has an IC_{50} that is at least five-fold lower for said cancerous cells than for said noncancerous cells within said heterogeneous population, and wherein said pharmaceutically effective amount administered is about one half or less of the IC_{50} of said noncancerous cells.
- 10 31. The method of claim 29 wherein said compound has an IC_{50} that is at least ten-fold lower for said cancerous cells than for said noncancerous cells within said heterogeneous population, and wherein said pharmaceutically effective amount administered is about one half or less of the IC_{50} of said noncancerous cells.
32. The method of any of claims 29-31, wherein said compound is an ansamycin.
- 15 33. The method of claim 32, wherein said ansamycin is selected from the group consisting of geldanamycin, 17-AAG, herbimycin A, and macbecin.
34. The method of claim 33, wherein said ansamycin is 17-AAG.
35. The method of any of claims 29-31 wherein said HSP90-inhibiting compound is a compound that binds the ATP-binding site of a HSP90.
- 20 36. The method of any of claims 29-31 wherein said cancerous cells are leukemic cells.
37. The method of claim 36 wherein said leukemic cells are selected from the group consisting of a T or B cell lymphoma, CML, APL, ALL, AML, NHL, and CMML.
- 25 38. The method of any of claims 29-31 wherein said treatment is monitored using one or more techniques selected from the group consisting of PCR, antibody staining, and nucleic acid hybridization, and wherein said techniques are selective for the presence of cancerous cells.

The method of any of claims 29-31 wherein said genetically-defined proliferative disorder is a solid tumor.

40. The method of claim 39 wherein said solid tumor is selected from the group consisting of papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma, and synovial sarcoma.

41. The method of any of claims 29-31 wherein said fusion protein contains one or more functional domains selected from the group consisting of kinases and DNA binding motifs.

42. The method of any of claims 29-31 wherein said administering employs an *ex vivo* procedure.

43. The method of any of claims 29-31 wherein said administering is intralesional.

44. The method of any of claims 29-31 wherein said administering is parenteral.

45. The method of claim 29 wherein said fusion protein arises from a chromosomal translocation.

46. The method of claim 29 wherein said fusion protein arises from a chromosomal inversion.

47. The method of claim 29 wherein said fusion protein arises from a chromosomal deletion.

48. The method of claim 29 wherein said fusion protein is generated from a non-random chromosomal aberration selected from the group consisting of inv14 (q11; q32), t(9; 22)(q34; q11), t(1; 19)(q23; p13.3), t(17; 19)(q22; p13), t(15; 17)(q21-q11-22), t(11; 17)(q23; q21.1), t(4; 11)(q21; q23), t(9; 11)(q21; q23), t(11; 19)(q23; p13), t(X; 11)(q13; q23), t(1; 11)(p32; q23), t(6; 11)(q27; q23), t(11; 17)(q23; q21), t(8; 21)(q22; q22), t(3; 21)(q26; q22), 5(16; 21)(p11; q22), t(6; 9)(p23; q34), t(4; 16)(q26; p13), inv(2; 2)(p13; p11.2-14), inv(16)(p13q22), t(5; 12)(q33; p13), t(2; 5)(2p23; q35), t(9; 12)(q34; p13), del(12p), t(15; 17)(q22; q12), t(11; 17)(q23; q12), t(16; 16)(p13; q22), inv(16)(p13; q22), t(9; 11)(p22; q23), t(1; 22)(p13; q13), t(3; 3)(q21; q26), inv(3)(q21q26), t(3; 5)(q21; q31), t(3; 5)(q25; q34), t(7; 11)(p15; p15), t(8; 16)(p11; p13), t(9; 12)(q34; p13), t(12; 22)(p13; q13),

39. The method of any of claims 29-31 wherein said genetically-defined proliferative disorder is a solid tumor.

40. The method of claim 39 wherein said solid tumor is selected from the group consisting of papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma, and synovial sarcoma.

41. The method of any of claims 29-31 wherein said fusion protein contains one or more functional domains selected from the group consisting of kinases and DNA binding motifs.

42. The method of any of claims 29-31 wherein said administering employs an *ex vivo* procedure.

43. The method of any of claims 29-31 wherein said administering is intralesional.

44. The method of any of claims 29-31 wherein said administering is parenteral.

45. The method of claim 29 wherein said fusion protein arises from a chromosomal translocation.

46. The method of claim 29 wherein said fusion protein arises from a chromosomal inversion.

47. The method of claim 29 wherein said fusion protein arises from a chromosomal deletion.

48. The method of claim 29 wherein said fusion protein is generated from a non-random chromosomal aberration selected from the group consisting of inv14 (q11; q32), t(9; 22)(q34; q11), t(1; 19)(q23; p13.3), t(17; 19)(q22; p13), t(15; 17)(q21-q11-22), t(11; 17)(q23; q21.1), t(4; 11)(q21; q23), t(9; 11)(q21; q23), t(11; 19)(q23; p13), t(X; 11)(q13; q23), t(1; 11)(p32; q23), t(6; 11)(q27; q23), t(11; 17)(q23; q21), t(8; 21)(q22; q22), t(3; 21)(q26; q22), 5(16; 21)(p11; q22), t(6; 9)(p23; q34), t(4; 16)(q26; p13), inv(2; 2)(p13; p11.2-14), inv(16)(p13q22), t(5; 12)(q33; p13), t(2; 5)(2p23; q35), t(9; 12)(q34;p13), del(12p), t(15; 17)(q22; q12), t(11; 17)(q23; q12), t(16; 16)(p13; q22), inv(16)(p13; q22), t(9; 11)(p22; q23), t(1; 22)(p13; q13), t(3; 3)(q21; q26), inv(3)(q21q26), t(3; 5)(q21; q31), t(3; 5)(q25; q34), t(7; 11)(p15; p15), t(8; 16)(p11; p13), t(9; 12)(q34; p13), t(12; 22)(p13; q13),

del(5q), del(7q), del(20q), t(11q23), t(12;21)(p13;q22), t(5;12)(q31;p13), t(1;12)(q25;p13), t(12;15)(p13;q25), t(1;12)(q21;p13), t(12;21)(q13;p32), and t(5;7)(q33;q11.2)).

49. The method of claim 29 wherein said non-random chromosomal aberration is t(9;22)(q34;q11).

50. The method of claim 1 or 29 wherein said fusion protein has a heightened dependence on HSP90.

51. The method of claim 20 or 29 wherein said HSP90-inhibiting compound has an IC₅₀ that is lower for cancerous cells than for noncancerous cells.

52. The method of claim 5 or 35 wherein said inhibitor is a synthetic analog of geldanamycin.

53. A method of treating a patient having a proliferative disease associated with a mutant protein or cellular protein isoform dependent on HSP90, comprising:

providing a cell, tissue, or fluid sample of a patient suspected of having said proliferative disease;

identifying in said cell, tissue, or fluid sample one or more characteristics indicative of said mutant protein or cellular protein isoform; and

administering to said patient a pharmaceutically effective amount of an HSP90-inhibiting compound.

54. The method of claim 53 wherein said mutant protein or cellular protein isoform is selected from the group consisting of src, RET, p53, p51, p63, p73, and homologs and allelic variations thereof.

55. The method of claim 53 wherein said mutant protein or cellular protein isoform is a dominant negative mutant.

56. The method of claim 53 wherein said mutant protein or cellular protein isoform is a human p53 selected from the group consisting of N239S, C176R, and R213*, Y236delta, C176Y, M133T, G245D, E258K, 1-293delta, G245C, R248W, E258K, R282W, R175H,

R280K, V143A, R175H, P177S, H178P, H179R, R181P, 238-9delta, G245S, G245D, M246R, R248Q, R249S, R273H, R273C, R273L, and D281Y.

57. The method of claim 53 wherein said mutant protein or cellular protein isoform is a dominant positive mutant.

5 58. The method of claim 57 wherein said mutant protein or cellular protein isoform is a C176Y mutant.

59. The method of claim 53 wherein said patient is heterozygous for said mutant protein or cellular protein isoform.

60. The method of claim 59 wherein said mutant protein or cellular protein isoform is p53 and wherein said proliferative disease is rheumatoid arthritis.
10

61. The method of claim 53, wherein said compound is an ansamycin.

62. The method of claim 61, wherein said ansamycin is selected from the group consisting of geldanamycin, 17-AAG, herbimycin A, and macbecin.

63. The method of claim 62, wherein said ansamycin is 17-AAG.

15 64. The method of claim 53, wherein said inhibitor is a compound that binds into the ATP-binding site of a HSP90.

65. The method of claim 64 wherein said compound is radicicol or an analog thereof.

66. The method of claim 53 wherein said identifying comprises using at least one technique selected from the group consisting of nucleic acid hybridization, PCR, LCR,
20 antibody staining, and immunoprecipitation to determine the presence of said mutant protein or cellular protein isoform.

67. The method of claim 53 wherein said administering employs an *ex vivo* procedure.

68. The method of claim 53 wherein said administering is intralesional.

69. The method of claim 53 wherein said administering is parenteral.

70. The method of claim 53 wherein said HSP90-inhibiting compound has an IC_{50} at least two-fold higher for cells that do not have characteristics indicative of said mutant protein or cellular protein isoform relative to those cells that do have such characteristics.

71. The method of claim 53 wherein said HSP90-inhibiting compound has an IC_{50} at least ten-fold higher for cells that do not have characteristics indicative of said mutant protein or cellular protein isoform relative to those cells that do have such characteristics.

72. The method of claim 53 wherein cells of said patient are monitored *in vitro* for sensitivity prior to administration of said compound to said patient.

73. A method of selectively treating cells that express a mutant protein or cellular protein isoform that gives rise to a proliferative disorder dependent on HSP90, said method comprising:

providing a population of cells in which at least some of said population express a mutant protein or cellular protein isoform that is differentially dependent on HSP90 for effect and gives rise to a proliferative disorder, and

administering to said population a pharmaceutically effective amount of an HSP90-inhibiting compound.

74. The method of claim 73 wherein said compound has an IC_{50} that is at least five-fold lower for said cells that express said mutant protein or cellular protein isoform than for those cells that do not, and wherein said pharmaceutically effective amount administered is about one half or less of the IC_{50} of cells that do not express said mutant protein or cellular protein isoform.

75. The method of claim 73 wherein said compound has an IC_{50} that is at least ten-fold lower for said cells that express said mutant protein or cellular protein isoform than for those cells that do not, and wherein said pharmaceutically effective amount administered is about one half or less of the IC_{50} of cells that do not express said mutant protein or cellular protein isoform..

76. The method according to any of claims 73-75, wherein said compound is an ansamycin.

77. The method of claim 76, wherein said ansamycin is selected from the group consisting of geldanamycin, 17-AAG, herbimycin A, or macbecin.

78. The method of claim 77, wherein said ansamycin is 17-AAG.

79. The method of any of claims 73-75, wherein said compound is a compound that
5 binds the ATP-binding site of a HSP90.

80. The method of claim 79 wherein said compound is radicicol or an analog thereof.

81. The method of any of claims 73-75 wherein said treatment is monitored using one or more techniques selected from the group consisting of PCR, LCR, nucleic acid hybridization, antibody labeling, and immunoprecipitation, and wherein said techniques
10 are selective for the presence of said mutant protein or cellular protein isoform.

82. The method of any of claims 73-75 wherein said administering employs an *ex vivo* procedure.

83. The method of any of claims 73-75 wherein said administering is intralesional.

84. The method of any of claims 73-75 wherein said administering is parenteral.

85. The method of claim 76 wherein said HSP90-inhibiting compound has an IC₅₀ that
15 is lower for cells expressing the mutant protein or cellular protein isoform than for cells that do not express said mutant protein or cellular protein isoform.

86. The method of claim 64 or 73 wherein said inhibitor is a synthetic analogue of geldanamycin.

87. The method of claim 73 wherein said mutant protein or cellular protein isoform is
20 selected from the group consisting of src, RET, p53, p51, p63, p73, and homologs and allelic variations thereof.

88. The method of claim 73 wherein said mutant protein or cellular protein isoform is a dominant negative mutant.

89. The method of claim 88 wherein said mutant protein or cellular protein isoform is a human p53 selected from the group consisting of N239S, C176R, and R213*, Y236delta, C174Y, M133T, G245D, E258K, 1-293delta, G245C, R248W, E258K, R282W, R175H, R280K, V143A, R175H, P177S, H178P, H179R, R181P, 238-9delta, G245S, G245D,
5 M246R, R248Q, R249S, R273H, R273C, R273L, and D281Y.
90. The method of claim 73 wherein said mutant protein or cellular protein isoform is a dominant positive mutant.
91. The method of claim 90 wherein said mutant protein or cellular protein isoform is C176Y human p53, or a homolog thereof.
- 10 92. The method of claim 73 wherein said cells that express a mutant protein or cellular protein isoform are heterozygous for said mutant protein or cellular protein isoform.
93. The method of claim 92 wherein said mutant protein or cellular protein isoform is p53 and wherein said proliferative disease is rheumatoid arthritis or a cancer.

FIGURE 1

<u>Type of Aberration</u>	<u>Background Literature</u>	<u>Affected Gene(s)</u>	<u>Protein Domain</u>	<u>Fusion Protein</u>	<u>Disease</u>
t(9; 22)(q34; q11)	de Klein, A. et al. Nature 300, 765-767 (1982)	<i>CABL</i> (9q34) <i>BCR</i> (22q11)	tyrosine kinase serine kinase	serine + tyrosine kinase	CML/ALL
inv14 (q11; q32)	Baer, R., Chen, K.-C., Smith, S. D. & Rabbitts, T. H. Cell 43, 705-713 (1985); Denny, C. T. et al. Nature 320, 549-551 (1986)	TCR- α (14q11) VH-(14q32)	TCR-C α Ig VH	VH-TCR-C α	T/B-cell lymphoma
t(1; 19)(q23; p13.3)	Kamps, M. P., Murre, C., Sun, X.-H. & Baltimore, D. Cell 60, 547-555 (1990); Nourse, J. et al. Cell 60, 535-545 (1990)	<i>PBX1</i> (1q23) <i>E2A</i> (19p13.3)	HD AD-b-HLH	AD + HD	pre-B-ALL
t(17; 19)(q22; p13)	Hunger, S. P., Ohyashiki, K., Toyama, K. & Clearly, M. L. Genes Dev. 6, 1608-1620 (1992); Inaba, T. et al. Science 257, 531-534 (1992)	<i>HLF</i> (17q22) <i>E2A</i> (19p13)	bZIP AD-b-HLH	AD + bZIP	pro-B-ALL
t(15; 17)(q21-q11-22)	Gilliard, E. F. & Solomon, E. Sem. Cancer Biol. 4, 359-368 (1993)	<i>PML</i> (15Q21) <i>RARA</i> (17q21)	Zinc-finger Retinoic acid receptor- α	Zinc-finger + RAR DNA and ligand binding	APL
t(11; 17)(q23; q21.1)	Chen, Z. et al. EMBO J. 12, 1161-1167 (1993)	<i>PLZF</i> (11q23) <i>RARA</i> (17q21)	Zinc-finger Retinoic acid receptor α	Zn-finger + RAR DNA and ligand binding	APL
t(4; 11)(q21; q23)	Djabali, M. et al. Nature Genet. 2, 113-118 (1992); Gu, Y. et al. Cell 71, 701-708 (1992)	<i>MLL</i> (11q23) <i>AF4</i> (4q21)	A-T hook/Zn-finger Ser-Pro rich	A-T hook + (Ser-pro)	ALL/preB- ALL/ ANLL
t(9; 11)(q21; q23)	Nakamura, T. et al. Proc. natn. Acad. Sci. U.S.A. 90, 4631-4635 (1993); Lida, S. et al. Oncogene 8, 3085-3092 (1993)	<i>MLL</i> (11q23) <i>AF9/MLLT3</i> (9p22)	A-T hook/Zn-finger Ser-Pro rich	A-T hook + (Ser-Pro)	ALL/preB- ALL/ ANLL
t(11; 19)(q23; p13)	Tkachuk, D. C., Kohler, S. & Cleary, M. L. Cell 71, 691-700 (1992); Yamamoto, K. et al. Oncogene 8, 2617-2625 (1993)	<i>MLL</i> (11q23) <i>ENL</i> (19p13)	A-T hook/Zn-finger Ser-Pro rich	A-T hook + Ser-Pro	pre-B-ALL/ T-ALL/ ANLL

FIGURE 1 (Cont'd)

<u>Type of Aberration</u>	<u>Background Literature</u>	<u>Affected Gene(s)</u>	<u>Protein Domain</u>	<u>Fusion Protein</u>	<u>Disease</u>
t(X; 11)(q13; q23)	Corral, J. et al. Proc. natn. Acad. Sci. U.S.A. 90, 8538-8542 (1993)	<i>MLL</i> (11q23) <i>AFX1</i> (Zq13)	A-T hook/Zn-finger Ser-Pro rich	A-T hook + (Ser-Pro)	T-ALL
t(1; 11)(p32; q23)	Bernard, O. A., Mauchauffe, M., Mecucci, C., Van Den Berghe, H. & Berger, R. Oncogene 9, 1039-1045 (1994)	<i>MLL</i> (11q23) <i>AF1P</i> (1p32)	A-T hook/Zn-finger Eps-15 homologue	A-T hook +	ALL
t(6; 11)(q27; q23)	Prasac, R. et al. Cancer Res. 53, 5624-5628 (1993)	<i>MLL</i> (11q23) <i>AF6</i> (6q27)	A-T hook/Zn-finger myosin homologue	A-T hook +	ALL
t(11; 17)(q23; q21)	Prasac, R. et al. Proc. natn. Acad. Sci. U.S.A. 91, 8107-8111 (1994)	<i>MLL</i> (11q23) <i>AF17</i> (17q21)	A-T hook/Zn-finger Cys-rich/leucine zipper	A-T hook + leucine zipper	AML
t(8; 21)(q22; q22)	Ohki, M. Sem. Cancer Biol. 4, 369-376 (1993)	<i>AML1/CBFα</i> (21q22) <i>ETO/MTG8</i> (8q22)	DNA binding/runts homology Zn-finger	DNA binding + Zn-fingers	AML
t(3; 21)(q26; q22)	Mitani, K. et al. EMBO J. 13, 504-510 (1994)	<i>AML1</i> (21q22) <i>EVI-1</i> (3q26)	DNA binding Zn-finger	DNA binding + Zn-fingers	CML
t(3; 21)(q26; q22)	Nucifora, G., Begy, C. R., Erickson, P., Drackin, H. A. & Rowley, J. D. Proc. natn. Acad. Sci. U.S.A. 90, 7784-7788 (1993)	<i>AML1</i> (21q22) <i>EAP</i> (3q26)	DNA binding Sn protein	DNA binding + out-of-frame EAP	Myelo-dysplasia
5(16; 21)(p11; q22)	Shimizu, K. et al. Proc. natn. Acad. Sci. U.S.A. 90, 10280-10284 (1993)	<i>FUS</i> (16p11) <i>ERG</i> (21q22)	Gin-Ser Tyr/Gly-rich/RNA binding Ets-like DNA binding	Gin-Ser-Tyr + DNA binding	Myeloid
t(6; 9)(p23; q34)	von Lindern, M. et al. Molec. Cell Biol. 12, 1687-1697 (1992)	<i>DEK</i> (6p23) <i>CAN</i> (9q34)	unknown ZIP	ZIP+	AML
9; 9?	von Lindern, M., Breems, D., van Baai, S., Acriansen, H. & Grosveld, G. Genes Chrom. Cancer 5, 227-234 (1992)	<i>SET</i> (9q34) <i>CAN</i> (9p34)	ZIP	ZIP+	AUL
t(4; 16)(q26; p13)	Laabi, Y. et al. EMBO J. 11, 3897-3904 (1992)	<i>IL-2</i> (4q26) <i>BCM</i> (16p13.1)	IL2 TM domain	IL-2/TM	T-lymphoma

FIGURE 1 (Cont'd)

<u>Type of Aberration</u>	<u>Background Literature</u>	<u>Affected Gene(s)</u>	<u>Protein Domain</u>	<u>Fusion Protein</u>	<u>Disease</u>
inv(2; 2)(p13; p11.2-14)	Lu, D. et al. Oncogene 6, 1235-1241 (1991)	<i>REL</i> (2p13) <i>NRG</i> (2p11.2-14)	DNA binding-activator not known	DNA binding +	NHL
inv(16)(p13q22)	Liu, P. et al. Science 261, 1041-1044 (1993)	Myosin MYH11 (16p13) CBF- β (16q22)		DNA binding?	AML
t(5; 12)(q33; p13)	Golub, T. R., Barker, G. F., Lovett, M. & Gilliland, D. G. Cell 77, 307-316 (1994)	PDGF- β (5q33) TEL (12p13)	Receptor kinase Eis-like DNA binding	Kinase + DNA binding	CMMML
t(2; 5)(2p23; q35)	Morris, S. W. et al. Science 263, 1281-1284 (1994)	<i>NPM</i> (5q35) <i>ALK</i> (2p23)	Nuclear phosphoprotein Tyrosine kinase	N terminus NPM + kinase	NHL
t(11; 22)(q24; q12)	Delattre, O. et al. Nature 359, 162-165 (1992)	<i>FLII</i> (11q24) <i>EWS</i> (22q12)	Eis-like DNA binding Gln-Ser-Tyr/Gly- rich/RNA binding	Gln-Ser-Tyr + DNA binding	Ewing's sarcoma
inv10(q11.2; q21)	Pierotti, M. A. et al. Proc. natn. Acad. Sci. U.S.A. 89, 1616-1620 (1992)	<i>RET</i> (10q11.2) <i>D10S170</i> (q21)	tyrosine kinase uncharacterized	Unk + tyrosine kinase	Papillary thyroid carcinoma a melanoma
t(12; 22)(q13; q12)	Zucman, J. et al. Nature Genet. 4, 341-345 (1993)	<i>ATF1</i> (12q13) <i>EWS</i> (22q12)	bZIP Gln-Ser-Tyr/Gly- rich/RNA binding	Gln-Ser-Tyr + bZIP	
t(12; 16)(q13; p11)	Crozat, A., Aman, P., Mandahl, N. & Ron, D. Nature 363, 640-644 (1993); Rabbitts, T. H.; Forster, A., Larson, R. & Nathanael, P. Nature Genet. 4, 175-180 (1993)	<i>CHOP</i> (12q13) <i>FUS</i> (16p11)	(DNA binding?)/ZIP Gln-Ser-Tyr/Gly- rich/RNA binding	Gln-Ser-Tyr +(DNA binding?)/ZIP	Liposarcoma
t(2; 13)(q35; q14)	Ben-David, Y., Giddens, E. B., Letwin, K. & Bernstein, A. Genes Dev. 5, 908-918 (1991)	<i>PAX3</i> (2q35) <i>FKHR</i> (13q14)	Paired box/homeodomain Forkhead domain	PB/HD +DNA binding	Rhabdomyosarcoma
t(X; 18)(p11.2;q11.2)	Clark, J. et al. Nature Genet. 7, 502-5087 (1994)	<i>SYT</i> (18q11.2) <i>SSX</i> (Xp11.2)	None identified None identified		Synovial sarcoma

1/299

SEQUENCE LISTING

<110> CONFORMA THERAPEUTICS CORP.

<120> METHODS FOR TREATING GENETICALLY-DEFINED PROLIFERATIVE
DISORDERS WITH HSP90 INHIBITORS

<130> 031164.0010WO

<140>

<141>

<150> 60/272,751

<151> 2001-03-01

<160> 330

<170> PatentIn Ver. 2.1

<210> 1

<211> 46

<212> PRT

<213> Homo sapiens

<400> 1

Ile Pro Leu Thr Ile Asn Lys Glu Asp Asp Glu Ser Pro Gly Leu Tyr
1 5 10 15Gly Phe Leu Asn Val Ile Val His Ser Ala Thr Gly Phe Lys Gln Ser
20 25 30Ser Ser Glu Lys Leu Arg Val Leu Gly Tyr Asn His Asn Gly
35 40 45

<210> 2

<211> 140

<212> DNA

<213> Homo sapiens

<400> 2

attccgctga ccatcaataa ggaagatgat gagtctccgg ggctctatgg gtttctgaat 60
gtcatctgcc actcagccac tggatttaag cagagttcaa gtgaaaagct ccgggtctta 120
ggctataatc acaatgggga 140

<210> 3

<211> 561

<212> DNA

<213> Homo sapiens

<400> 3

gagcagcaga agaagtgttt cagaagcttc tccctgacat ccgtggagct gcagatgctg 60
accaactcgt gtgtgaaact ccagactgtc cacagcattc cgctgaccat caataaggaa 120
gatgatgagt ctccggggct ctatgggttt ctgaatgtca tcgtccactc agccactgga 180
tttaagcaga gttcaagaag aagccatacg gtgaaccagg tgatgctgag gttatctgga 240
tccaggccat gcagatgaag ccatatttac ctttgtgata ttggggctga tcttggagct 300
gtctggatct gaccagtctc caggttgaaa actcttgcaa ctttcgtttt tggatagtgc 360

2/299

```

tcacctcgta tctgtactcg taactgctat ttctaggcga attgtccctt ttctcctccc 420
tcttccctca tctccctctc tctctgcct ggctgacacc aggaaggagg agttttcttt 480
tatttagata aaaaaaagtt gagaggaggc agctccagaa atgtgggata ctcagcactg 540
gagacatttg ggctggaatt c                                         561

```

<210> 4

<211> 284

<212> PRT

<213> Homo sapiens

<400> 4

```

Thr Asp Leu Leu Leu Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys
  1              5              10              15

Thr Gln Gln Tyr Asp Cys Lys Trp Tyr Ile Pro Val Thr Asp Leu Ser
      20              25              30

Phe Gln Met Val Asp Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val
      35              40              45

Pro Asp Glu Glu Leu Asn Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys
      50              55              60

Ser Asp Ile Gln Arg Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr
      65              70              75              80

Glu Arg Leu Lys Lys Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Leu
      85              90              95

Met Ser Pro Ser Met Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser
      100             105             110

Tyr Thr Phe Leu Ile Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu
      115             120             125

Asn Ile Arg Glu Gln Gln Lys Lys Cys Phe Arg Ser Phe Ser Leu Ala
      130             135             140

Ser Val Glu Leu Gln Met Leu Thr Asn Ser Cys Val Lys Leu Gln Thr
      145             150             155             160

Val His Ser Ile Pro Leu Thr Ile Asn Lys Glu Asp Asp Glu Ser Pro
      165             170             175

Gly Leu Tyr Gly Phe Leu Asn Val Ile Val His Ser Ala Thr Gly Phe
      180             185             190

Lys Gln Ser Ser Lys Leu Gln Arg Pro Val Ala Ser Asp Phe Glu Pro
      195             200             205

Gln Gly Leu Ser Glu Ala Ala Arg Trp Asn Ser Lys Glu Asn Leu Leu
      210             215             220

Ala Gly Pro Ser Glu Asn Asp Pro Asn Leu Phe Val Ala Leu Tyr Asp
      225             230             235             240

Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys Gly Glu Lys

```

3/299

245

250

255

Leu Arg Val Leu Gly Tyr Asn His Asn Gly Glu Trp Cys Glu Ala Gln
 260 265 270

Thr Lys Asn Gly Gln Gly Trp Val Pro Ser Asn Tyr
 275 280

<210> 5

<211> 854

<212> DNA

<213> Homo sapiens

<400> 5

```

accgacctgc ttctctgcac caagctcaag aagcagagcg gaggcaaaac gcagcagtat 60
gactgcaa at ggtacattcc ggtcacggat ctcagcttcc agatgggtgga tgaactggag 120
gcagtgccca acatccccctt ggtgcccgat gaggagctga acgctttgaa gatcaagatc 180
tcccagatca agagtgcacat ccagagagag aagagggcga acaagggcag caaggctacg 240
gagagggctga agaagaagct gtcggagcag gagtcaactgc tgcctgcttat gtctcccagc 300
atggccttca ggggtgcacag ccgcaacggc aagagttaca cgttcctgat ctctctgac 360
tatgagcgtg cagagtggag ggagaacatc cgggagcagc agaagaagtg tttcagaagc 420
ttctccctgg catccgtgga gctgcagatg ctgaccaact cgtgtgtgaa actccagact 480
gtccacagca ttccgctgac catcaataag gaagatgatg agtctccggg gctctatggg 540
tttctgaatg tcatcgtcca ctcagccact ggatttaagc agagttcaaa acttcagcgg 600
ccagtagcat ctgactttga gcctcagggg ctgagtgaag ccgctcgttg gaactccaag 660
gaaaaccttc tcgctggacc cagtgtgaaat gacccaacc ttttcgttgc actgtatgat 720
tttgtggcca gtggagataa cactctaagc ataactaaag gtgaaaagct ccgggtctta 780
ggctataatc acaatgggga atgggtgtgaa gcccaaacca aaaatggcca aggctgggtc 840
ccaagcaact acat

```

<210> 6

<211> 468

<212> DNA

<213> Homo sapiens

<400> 6

```

gtccacagca ttccgctgac catcaataag gaagatgatg agtctccggg gctctatggg 60
tttctgaatg tcatcgtcca ctcagccact ggatttaagc agagttcaaa agccttcag 120
cggccagtag catctgactt tgagcctcag ggtctgagtg aagccgctcg ttggaactcc 180
aaggaaaacc ttctcgtctg acccagtgaa aatgaccca accttttctg tgcactgtat 240
gattttgtgg ccagtggaga taacactcta agcataacta aaggtgaaaa gctccgggtc 300
ttaggctata atcacaatgg ggaatgggtg gaagccaaa ccaaaaatgg ccaaggctgg 360
gtccaagca actacatcac gccagtcaac agtctggaga aacactcctg gtaccatggg 420
cctgtgtccc gcaatgccgc tgagtatctg ctgagcagcg ggatcaat

```

<210> 7

<211> 225

<212> PRT

<213> Homo sapiens

<400> 7

Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg Glu Lys Arg Ala Asn Lys
 1 5 10 15

Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys Lys Leu Ser Glu Gln Glu

20

30

Tyr
225

```
<210> 8
<211> 679
<212> DNA
<213> Homo sapiens
```

<400> 8							
agatctccca	gatcaagagt	gacatccaga	gagagaagag	ggcgaacaag	ggcagcaagg		60
ctacggagag	gctgaagaag	aagctgtcgg	agcaggagtc	actgctgctg	cttatgtctc		120
ccagcatggc	cttcaggggtg	cacagccgca	acggcaagag	ttacacgttc	ctgatctcct		180
ctgactatga	gcgtgcagag	tggagggaga	acatccggga	gcagcagaag	aagtgtttca		240
gaagctttct	cctggcatcc	gtggagctgc	agatgctgac	caactcgtgt	gtgaaactcc		300
agactgtcca	cagcattccg	ctgaccatca	ataagggaaga	tgatgagtct	ccggggctct		360
atggggtttct	gaatgtcatc	gtccactcag	ccactggatt	taagcagagt	tcaaaacttc		420
agcgggccagt	agcatctgac	tttagccctc	agggtctgag	tgaagccgct	cgttggaact		480
ccaaggtaaaa	ccttctcgct	gcaccacgtg	aaaatgacc	caaccttttc	gttgcatctg		540
atqatttttgt	qgccagtqga	gataacactc	taaqcataac	taaaggtgaa	aaqctccqgg		600

5/299

tcttaggcta taatcacaat ggggaatggg gtgaagccca aacccaaatt ggccaaggct 660
 gggttccaag caactacat 679

<210> 9

<211> 332

<212> PRT

<213> Homo sapiens

<400> 9

Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys Lys Leu Ser
 1 5 10 15

Glu Gln Glu Ser Leu Leu Leu Leu Met Ser Pro Ser Met Ala Phe Arg
 20 25 30

Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile Ser Ser Asp
 35 40 45

Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln Gln Lys Lys
 50 55 60

Cys Phe Arg Ser Phe Ser Leu Thr Ser Val Glu Leu Gln Met Leu Thr
 65 70 75 80

Asn Ser Cys Val Lys Leu Gln Thr Val His Ser Ile Pro Leu Thr Ile
 85 90 95

Asn Lys Glu Asp Asp Glu Ser Pro Gly Leu Tyr Gly Phe Leu Asn Val
 100 105 110

Ile Val His Ser Ala Thr Gly Phe Lys Gln Ser Ser Lys Ala Leu Gln
 115 120 125

Arg Pro Val Ala Ser Asp Phe Glu Pro Gln Gly Leu Ser Glu Ala Ala
 130 135 140

Arg Trp Asn Ser Lys Glu Asn Leu Leu Ala Gly Pro Ser Glu Asn Asp
 145 150 155 160

Pro Asn Leu Phe Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn
 165 170 175

Thr Leu Ser Ile Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn
 180 185 190

His Asn Gly Glu Trp Cys Glu Ala Gln Thr Lys Asn Gly Gln Gly Trp
 195 200 205

Val Pro Ser Asn Tyr Ile Thr Pro Val Asn Ser Leu Glu Lys His Ser
 210 215 220

Trp Tyr His Gly Pro Val Ser Arg Asn Ala Ala Glu Tyr Leu Leu Ser
 225 230 235 240

Ser Gly Ile Asn Gly Ser Phe Leu Val Arg Glu Ser Glu Ser Ser Pro
 245 250 255

6/299

Gly Gln Arg Ser Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His Tyr
 260 265 270

Arg Ile Asn Thr Ala Ser Asp Gly Lys Leu Tyr Val Ser Ser Glu Ser
 275 280 285

Arg Phe Asn Thr Leu Ala Glu Leu Val His His His Ser Thr Val Ala
 290 295 300

Asp Gly Leu Ile Thr Thr Leu His Tyr Pro Ala Pro Lys Arg Asn Lys
 305 310 315 320

Pro Thr Val Tyr Gly Val Ser Pro Asn Tyr Asp Lys
 325 330

<210> 10

<211> 997

<212> DNA

<213> Homo sapiens

<400> 10

gcgaacaagg gcagcaaagc tacggagagg ctgaagaaga agctgtcgga gcaggagtca 60
 ctgctgctgc ttatgtctcc cagcatggcc ttcagggtgc acagccgcaa cggcaagagt 120
 tacacgttcc tgatctcctc tgactatgag cgtgcagagt ggagggagaa catccgggag 180
 cagcagaaga agtgttttcag aagcttctcc ctgacatccg tggagctgca gatgctgacc 240
 aactcgtgtg tgaaactcca gactgtccac agcattccgc tgaccatcaa taaggaagat 300
 gatgagtctc cggggctcta tgggtttctg aatgtcatcg tccactcagc cactggattt 360
 aagcagagtt caaaagccct tcagcggcca gtagcatctg actttgagcc tcagggtctg 420
 agtgaagccg ctcggtggaa ctccaaggaa aaccttctcg ctggaccag tgaaaatgac 480
 cccaaccttt tcgttgcaact gtatgatattt gtggccagtg gagataaacac tctaagcata 540
 actaaagggtg aaaagctccg ggtcttaggc tataatcaca atggggaatg gtgtgaagcc 600
 caaaccaaaa atggccaagg ctgggtccca agcaactaca tcacgccagt caacagtctg 660
 gagaaacact cctggtacca tgggcctgtg tcccgcgaatg ccgctgagta tctgctgagc 720
 agcgggatca atggcagctt cttggtgcgt gagagtgaga gcagtcctgg ccagagggtcc 780
 atctcgtga gatacgaagg gaggtgtac cattacagga tcaacactgc ttctgatggc 840
 aagctctacg tctcctccga gagccgcttc aacaccctgg ccgagttggt tcatcatcat 900
 tcaacgggtg ccgacgggct catcaccag ctccattatc cagcccaaaa gcgcaacaag 960
 cccactgtct atggtgtgtc ccctaactac gacaagt 997

<210> 11

<211> 101

<212> PRT

<213> Homo sapiens

<400> 11

Arg Glu Gln Gln Lys Lys Cys Phe Arg Ser Phe Ser Leu Thr Ser Val
 1 5 10 15

Glu Leu Gln Met Leu Thr Asn Ser Cys Val Lys Leu Gln Thr Val His
 20 25 30

Ser Ile Pro Leu Thr Ile Asn Lys Glu His Asp Glu Ser Pro Gly Leu
 35 40 45

Tyr Gly Phe Leu Asn Val Ile Val His Ser Ala Thr Gly Phe Lys Gln
 50 55 60

7/299

Ser Ser Asn Leu Tyr Cys Thr Leu Glu Val Asp Ser Phe Gly Tyr Phe
 65 70 75 80

Val Asn Lys Ala Lys Thr Arg Val Tyr Arg Asp Thr Ala Glu Pro Asn
 85 90 95

Leu Leu Ala Gly Pro
 100

<210> 12

<211> 305

<212> DNA

<213> Homo sapiens

<400> 12

ccgggagcag cagaagaagt gtttcagaag cttctccctg acatccgtgg agctgcagat 60
 gctgaccaac tcgtgtgtga aactccagac tgtccacagc attccgctga ccatcaataa 120
 ggaacatgat gagtctccgg ggctctatgg gtttctgaat gtcacgtcc actcagccac 180
 tggatttaag cagagttcaa atctgtactg caccctggag gtggattcct ttgggtattt 240
 tgtgaataaa gcaaagacgc gcgtctacag ggacacagct gagccaaacc ttctcgctgg 300
 accca 305

<210> 13

<211> 250

<212> DNA

<213> Homo sapiens

<400> 13

tggagctgca gatgctgacc aactcgtgtg tgaaactcca gactgtccac agcattccgc 60
 tgaccatcaa taaggaagat gatgagtctc cggggctcta tgggtttctg aacactcagc 120
 cactggattt aagcagagtt caaatctgta ctgcacctg gaggtggatt cctttgggta 180
 ttttgtgaat aaagcaaaga cgcgcgtcta caggacaca gctgagccaa accttctcgc 240
 tggacccaat 250

<210> 14

<211> 63

<212> DNA

<213> Homo sapiens

<400> 14

gatggcgagg gcgccttcca tggagacgca ggtgagttcc tcacgccacg tgcgtgggca 60
 cac 63

<210> 15

<211> 21

<212> PRT

<213> Homo sapiens

<400> 15

Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
 1 5 10 15

Pro Pro Gly Tyr Gly

8/299

20

<210> 16
<211> 63
<212> DNA
<213> Homo sapiens

<400> 16
gatggcgagg ggcgcttcca tggagacgca gatggctcgt tcggaacacc acctggatac 60
ggc 63

<210> 17
<211> 21
<212> PRT
<213> Homo sapiens

<400> 17
Asp Gly Glu Gly Ala Phe His Gly Asp Ala Glu Ala Leu Gln Arg Pro
1 5 10 15

Val Ala Ser Asp Phe
20

<210> 18
<211> 63
<212> DNA
<213> Homo sapiens

<400> 18
gatggcgagg ggcgcttcca tggagacgca gaagcccttc agcggccagt agcatctgac 60
ttt 63

<210> 19
<211> 140
<212> PRT
<213> Homo sapiens

<400> 19
Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val Leu
1 5 10 15

His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro Leu
20 25 30

Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile Asn
35 40 45

Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly Glu
50 55 60

Gly Glu Asp Arg Met Lys Ala Ser Ser Thr Arg Lys Arg Leu Leu Leu
65 70 75 80

Met Glu Glu Ala Leu Gln Arg Pro Val Ala Ser Asp Phe Glu Pro Gln

9/299

	85		90		95
Gly Leu Ser Glu Ala Ala Arg Trp Asn Ser Lys Glu Asn Leu Leu Ala					
	100		105		110
Gly Pro Ser Glu Asn Asp Pro Asn Leu Phe Val Ala Leu Tyr Asp Phe					
	115		120		125
Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys					
	130		135		140

<210> 20
 <211> 423
 <212> DNA
 <213> Homo sapiens

<400> 20
 ctctgctcta caagcctgtg gaccgtgtga cgaggagcac gctggtcctc catgacttgc 60
 tgaagcacac tccgtgccagc caccctgacc accccttgct gcaggacgcc ctccgcatct 120
 cacagaactt cctgtccagc atcaatgagg agatcacacc ccgacggcag tccatgacgg 180
 tgaagaaggg agagggagaa gacaggatga aagcttcac aacgaggaag agattactcc 240
 ttatggaaga agcccttcag cggccagtag catctgactt tgagcctcag ggtctgagtg 300
 aagccgctcg ttggaactcc aaggaaaacc ttctcgctgg acccagtga aatgacccca 360
 accttttcgt tgcactgtat gattttgtgg ccagtggaga taacactcta agcataacta 420
 aag 423

<210> 21
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 21
 Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys Lys Leu Ser
 1 5 10 15
 Glu Gln Glu Ser Leu Leu Leu Leu Met Ser Pro Ser Met Ala Phe Arg
 20 25 30
 Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile Ser Ser Asp
 35 40 45
 Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln Gln Lys Lys
 50 55 60
 Cys Phe Arg Ser Phe Ser Leu Thr Ser Val Glu Leu Gln Met Leu Thr
 65 70 75 80
 Asn Ser Cys Val Lys Leu Gln Thr Val His Ser Ile Pro Leu Thr Ile
 85 90 95
 Asn Lys Glu Glu Ala Leu Gln Arg Pro Val Ala Ser Asp Phe Glu Pro
 100 105 110
 Gln Gly Leu Ser Glu Ala Ala Arg Trp Asn Ser Lys Glu Asn Leu Leu
 115 120 125

10/299

Ala Gly Pro Ser Glu Asn Asp Pro Asn Leu Phe Val Ala Leu Tyr Asp
 130 135 140

Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys Gly Glu Lys
 145 150 155 160

Leu Arg Val Leu Gly Tyr Asn His Asn Gly Glu Trp Cys Glu Ala Gln
 165 170 175

Thr Lys Asn Gly Gln Gly Trp Val Pro Ser Asn Tyr Ile Thr Pro Val
 180 185 190

Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly Pro Val Ser Arg Asn
 195 200 205

Ala Ala Glu Tyr Leu Leu Ser Ser Gly Ile Asn Gly Ser Phe Leu Val
 210 215 220

Arg Glu Ser Glu Ser Ser Pro Gly Gln Arg Ser Ile Ser Leu Arg Tyr
 225 230 235 240

Glu Gly Arg Val Tyr His Tyr Arg Ile Asn Thr Ala Ser Asp Gly Lys
 245 250 255

Leu Tyr Val Ser Ser Glu Ser Arg Phe Asn Thr Leu Ala Glu Leu Val
 260 265 270

His His His Ser Thr Val Ala Asp Gly Leu Ile Thr Thr Leu His Tyr
 275 280 285

Pro Ala Pro Lys Arg Asn Lys Pro Thr Val Tyr Gly Val Ser Pro Asn
 290 295 300

Tyr Asp Lys
 305

<210> 22
 <211> 922
 <212> DNA
 <213> Homo sapiens

<400> 22
 gcgaacaagg gcagcaaggc tacggagagg ctgaagaaga agctgtcgga gcaggagtca 60
 ctgctgctgc ttatgtctcc cagcatggcc ttcagggtgc acagccgcaa cggcaagagt 120
 tacacgttcc tgatctcctc tgactatgag cgtgcagagt ggagggagaa catccgggag 180
 cagcagaaga agtgtttcag aagcttctcc ctgacatccg tggagctgca gatgctgacc 240
 aactcgtgtg tgaaactcca gactgtccac agcattccgc tgaccatcaa taaggaagaa 300
 gcccttcagc ggccagtagc atctgacttt gagcctcagg gtctgagtga agccgctcgt 360
 tggaactcca aggaaaacct tctcgctgga cccagtgaat atgaccccaa ccttttcggt 420
 gcactgtatg attttgtggc cagtggagat aacactctaa gcataactaa aggtgaaaag 480
 ctccgggtot taggctataa tcacaatggg gaatgggtgtg aagcccaaac caaaaatggc 540
 caaggctggg tccaagcaa ctacatcacg ccagtcaaca gtctggagaa aactcctgg 600
 taccatgggc ctgtgtccc caatgccgct gagtatctgc tgagcagcgg gatcaatggc 660
 agcttcttgg tgcgtgagag tgagagcagt cctggccaga ggtccatctc gctgagatac 720
 gaagggaggg tgtaccatta caggatcaac actgcttctg atggcaagct ctacgtctcc 780
 tccgagagcc gcttcaacac cctggccgag ttggttcac atcattcaac ggtggccgac 840
 gggctcatca ccacgtcca ttatccagcc ccaaagcgca acaagccac tgtctatggt 900

11/299

gtgtccccca actacgacaa gt

922

<210> 23

<211> 359

<212> PRT

<213> Homo sapiens

<400> 23

Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met Glu Gly Glu
 1 5 10 15

Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu Gln Glu Lys
 20 25 30

Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser Phe Glu Asp
 35 40 45

Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu Asn Leu Thr
 50 55 60

Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg Val Ser Pro
 65 70 75 80

Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg Ser Pro Ser
 85 90 95

Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro Thr Pro Gln
 100 105 110

Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser Glu Ala Thr
 115 120 125

Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn Asp Gly Glu
 130 135 140

Gly Ala Phe His Gly Asp Ala Glu Ala Leu Gln Arg Pro Val Ala Ser
 145 150 155 160

Asp Phe Glu Pro Gln Gly Leu Ser Glu Ala Ala Arg Trp Asn Ser Lys
 165 170 175

Glu Asn Leu Leu Ala Gly Pro Ser Glu Asn Asp Pro Asn Leu Phe Val
 180 185 190

Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr
 195 200 205

Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn His Asn Gly Glu Trp
 210 215 220

Cys Glu Ala Gln Thr Lys Asn Gly Gln Gly Trp Val Pro Ser Asn Tyr
 225 230 235 240

Ile Thr Pro Val Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly Pro
 245 250 255

Val Ser Arg Asn Ala Ala Glu Tyr Leu Leu Ser Ser Gly Ile Asn Gly

260

270

Val Ser Pro Asn Tyr Asp Lys
355

```
<210> 24
<211> 1079
<212> DNA
<213> Homo sapiens
```

<400> 24						
gtaccagccc	taccagagca	tctacgtcgg	gggcatgatg	gaaggggagg	gcaagggccc	60
gctcctgcgc	agccagagca	cctctgagca	ggagaagcgc	cttacctggc	ccgcaggtc	120
ctactceccc	cggagttttg	aggattgcgg	aggcggctat	accocggact	gcagctccaa	180
tgagaacctc	acctccagcg	aggaggactt	ctcctctggc	cagtccagcc	gcggtgtccc	240
aagccccacc	acctaccgca	tgttccggga	caaaagccgc	tctccctcgc	agaactcgca	300
acagctcctt	gacagcagca	gtccccccac	gccgcagtgc	cataagcggc	accggcactg	360
ccgggttgtc	gtgtccgagg	ccaccatcgt	gggcgtccgc	aagacccggc	agatctgtgc	420
caacgatggc	gaggcgccct	tccattggaga	cgcagaagcc	cttcagcggc	cagtagcatc	480
tgactttgag	cctcaggggtc	tgagtgaagc	cgctcgttgg	aactccaagg	aaaaccttct	540
cgctggaccc	agtgaaaatg	accccaacct	tttcgttgca	ctgtatgatt	ttgtggccag	600
tggagataac	actctaagca	taactaaagg	tgaaaagctc	cgggtcttag	gctataatca	660
caatggggaa	tggtgtgaag	cccaaaccaa	aaatggccaa	ggctgggtcc	caagcaacta	720
catcacgcca	gtcaacagtc	tggagaaaaca	ctccttggtac	catgggcctg	tgtcccgcaa	780
tgccgctgag	tatctgctga	gcagcgggat	caatggcagc	ttcttggtgc	gtgagagtga	840
gagcagtcct	ggccagaggt	ccatctcgct	gagatacgaa	gggaggggtt	accattacag	900
gatcaacact	gcttctgatg	gcaagctcta	cgtctcctcc	gagagccgct	tcaacacctt	960
ggccgagttg	gttcatacat	attcaacggt	ggccgacggg	ctcatcacca	cgtccatta	1020
tcacgcccga	aagcgcaaca	agcccactgt	ctatggtgtg	tcccccaact	acgacaagt	1079

```
<210> 25
<211> 34
<212> PRT
<213> Homo sapiens
```

<400> 25
Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn Asp Gly Glu Gly
1 5 10 15

Ala Phe His Gly Asp Ala Gly Lys Ser Pro Gly Leu Arg Leu Asn His
20 25 30

13/299

Asn Gly

<210> 26
 <211> 106
 <212> DNA
 <213> Homo sapiens

<400> 26
 tcgtgggcgt ccgcaagacc gggcagatct ggcccaacga tggcgagggc gccttccatg 60
 gagacgcagg taaaagcccg ggtcttaggc taaatcacia tgggga 106

<210> 27
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 27
 Met Ala Glu Cys Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp
 1 5 10 15
 Arg Leu Trp Ala Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His
 20 25 30
 Ala Trp Leu Pro Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg
 35 40 45
 Val Leu Leu Arg Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro
 50 55 60
 Thr Gln Ile Gly Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro
 65 70 75 80
 Asp Gly Arg Tyr Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr
 85 90 95
 His Ile Lys Ile Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro
 100 105 110

Asp Asp

<210> 28
 <211> 1324
 <212> DNA
 <213> Homo sapiens

<400> 28
 cttgagaggg tctggctctt gcttcttagg cggcccaggg acgccatggc cgagtgcccg 60
 acactcgggg aggcagtcac cgaccaccg gaccgcctgt gggcctggga gaagttcgtg 120
 tatttggacg agaagcagca cgcttggtg cccttaacca tcgagataaa ggatagggtta 180
 cagttacggg tgctcttgcg tcgggaagac gtcgtcctgg ggaggcctat gacccccacc 240
 cagataggcc caagcctgct gcctatcatg tggcagctct accctgatgg acgataccga 300
 tcctcagact ccagtttctg gcgcttagtg taccacatca agattgacgg cgtggaggac 360
 atgcttctcg agctgctgcc agatgactga tgtatggtct tggcagcacc tgtctccttt 420

14/299

```

cacccccagg cctgagcctg gccagcctac aatggggatg ttgtgtttct gttcaccttc 480
gtttactatg cctgtgtcct ctccaccacg ctgggggtctg ggaggaatgg acagacagag 540
gatgagctct acccagggcc tgcaggacct gcctgtagcc cactctgctc gccttagcac 600
taccactcct gccaaggagg attccatttg gcagagcttc ttccagggtgc ccagctatac 660
ctgtgcctcg gcttttctca gctggatgat ggtcttcagc ctctttctgt cccttctgtc 720
cctcacagca ctagtatttc atgttgacac cccactcagc tccgtgaact tgtgagaaca 780
cagccgattc acctgagcag gacctctgaa accctggacc agtgggtctca catgggtgcta 840
cgctgcatg taaacacgcc tgcaaacgct gcctgccggt aaacacgcct gcaaacgctg 900
cctgcccgtg aacacgcctg caaacgctgc ctgcccacac aggttcacgt gcagctcaag 960
gaaaggcctg aaaggagccc ttatctgtgc tcaggactca gaagcctctg ggtcagtggg 1020
ccacatcccg ggacgcagca ggaggccagg ccggcgagcc ctgtggatga gccctcagaa 1080
cccttgccct gccacgtgg aaaagggata gaggttgggt tccccccctt tatagatggg 1140
cagcacctg ggtgttacaa agttgtatgt ggcataaata ctttttgtaa tgattgatta 1200
aatgcaagat agtttatcta acttcgtgcg caatcagctt ctatccttga cttagattct 1260
ggtggagaga agtgagaata ggcagccccc aaataaaaaa tattcatgga aaaaaaaaaa 1320
aaaa                                             1324

```

<210> 29
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 29
 Met Ala Glu Cys Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp
 1 5 10 15
 Arg Leu Trp Ala Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His
 20 25 30
 Ala Trp Leu Pro Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg
 35 40 45
 Val Leu Leu Arg Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro
 50 55 60
 Thr Gln Ile Gly Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro
 65 70 75 80
 Asp Gly Arg Tyr Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr
 85 90 95
 His Ile Lys Ile Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro
 100 105 110
 Asp Asp

<210> 30
 <211> 1324
 <212> DNA
 <213> Homo sapiens

<400> 30
 cttgagaggc tctggctcct gcttcttagg cggccccgagg acgccatggc cgagtgtccc 60
 acactcgggg aggcagtcac cgaccacccg gaccgcctgt gggcctggga gaagttcgtg 120
 tatttgacg agaagcagca cgcttggtg cccttaacca tcgagataaa ggatagggtta 180
 cagttacggg tgctcttgcg tcgggaagac gtcgtcctgg ggaggcctat gacccccacc 240

15/299

```

cagataggcc caagcctgct gcctatcatg tggcagctct accctgatgg acgataccga 300
tcctcagact ccagtttctg gcgcttagtg taccacatca agattgacgg cgtggaggac 360
atgcttctcg agctgctgcc agatgactga tgtatggtct tggcagcacc tgtctccttt 420
caccccaggg cctgagcctg gccagcctac aatggggatg ttgtgtttct gttcaccttc 480
gtttactatg cctgtgtctt ctccaccacg ctgggggtctg ggaggaatgg acagacagag 540
gatgagctct acccagggcc tgcaggacct gcctgtagcc cactctgctc gccttagcac 600
taccactcct gccaaaggagg attccatttg gcagagcttc ttccagggtgc ccagctatac 660
ctgtgcctcg gcttttctca gctggatgat ggtcttcagc ctctttctgt cctttctgtc 720
cctcacagca ctagtatctc atgttgacac ccactcagc tccgtgaact tgtgagaaca 780
cagccgattc acctgagcag gacctctgaa accctggacc agtggctcct catggtgcta 840
cgctgcatg taaacacgcc tgcaaagcgt gcctgcgggt aaacacgcct gcaaagcgtg 900
cctgcccgtg aacacgcctg caaacgctgc ctgcccacac aggttcacgt gcagctcaag 960
gaaagggctg aaaggagccc ttatctgtgc tcaggactca gaagcctctg ggtcagtggg 1020
ccacatcccg ggacgcagca ggaggccagg ccggcgagcc ctgtggatga gccctcagaa 1080
cccttggtt gccacgtgg aaaagggata gaggttgggt ttccccctt tatagatggg 1140
cacgcacctg ggtgttacaa agttgtatgt ggcataaata ctttttgtaa tgattgatta 1200
aatgcaagat agtttatcta acttcgtgcg caatcagctt ctatccttga cttagattct 1260
ggtggagaga agtgagaata ggcagcccc aaataaaaaa tattcatgga aaaaaaaaaa 1320
aaaaa 1324

```

<210> 31
 <211> 560
 <212> DNA
 <213> Homo sapiens

```

<400> 31
gtcgactgtg agttcccagc agaggcccag agtcccggtc cggcagccga gggaaagcggg 60
gggggtcttcc agaagaagaa agggccaagg tcaccccggg gcctctccag cagcagcaga 120
gggcggcggg cgggtgctgct gctggccggg gcctcgagga aggcgcgggc cagctggggc 180
cgggtctgctg ttcccaggag ctgccaccgt tccaggagagc aagtcaggcc gggacgttag 240
cgctgcgcg ggacctcac ttgccaccaa ggaccccaca aaccccgccc catccttagc 300
gcctgcgcg gacctcact tgccaccaag acccccacaa accccgcccc atcctgcctt 360
acgccccgcc ccaaggtcgt tctcccgacc cgggggtccc cccaagacc gtcctcccgc 420
cccgccgctt ggtggcggcc gcatgctgcc cggatataaa gggtcggccc cacatcccag 480
ggaccagcga gcggccttga gaggtctctg ctcttgcttc ttaggcggcc cgaggacgcc 540
atggccgagt gcccgacact 560

```

<210> 32
 <211> 125
 <212> PRT
 <213> Homo sapiens

```

<400> 32
Phe Ala Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly
  1               5               10              15
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
      20              25              30
Phe Thr Phe Ser Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly
      35              40              45
Lys Gly Leu Val Trp Val Ser Arg Ile Asn Ser Asp Gly Ser Ser Thr
      50              55              60
Ser Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn

```

16/299

65					70					75					80
Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
				85					90					95	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Pro	Thr	Gly	Gly	Ser	Tyr	Ile
			100					105					110		
Pro	Thr	Phe	Gly	Arg	Gly	Thr	Ser	Leu	Ile	Val	His	Pro			
		115					120					125			

```
<210> 33
<211> 375
<212> DNA
<213> Homo sapiens
```

<400>	33						
tttgcagggtg	tccagtggtga	ggtgcagctg	gtggagtcog	ggggagggctt	agttcagcct	60	
gggggggtccc	tgagactctc	ctgtgcagcc	tctggattca	ccttcagtag	ctactggatg	120	
cactgggtcc	gccaagctcc	aggggaagggg	ctggtgtggg	tctcacgtat	taatagtgat	180	
gggagtagca	caagctacgc	ggactccgtg	aaggggccgat	tcaccatctc	cagagacaac	240	
gccaaagaaca	cgctgtatct	gcaaataaac	agtctgagag	ccgaggacac	ggctgtgtat	300	
tactgtgcaa	gagatccaac	aggaggaagc	tacataccta	catttgggaag	aggaaccagc	360	
cttattgttc	atccg					375	

```
<210> 34
<211> 125
<212> PRT
<213> Homo sapiens
```

```

<400> 34
Thr Gly Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu
  1             5             10             15
Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr
      20             25             30
Ser Ile Ser Ser Gly Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly
      35             40             45
Lys Gly Leu Glu Trp Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr
      50             55             60
Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser
      65             70             75             80
Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr
      85             90             95
Ala Val Tyr Tyr Cys Ala Arg Val Arg Arg Arg Tyr Ser Ser Ala Ser
      100             105             110
Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg
      115             120             125

```

17/299

<210> 35
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 35
 tcacaggggt cctgtcccag gtgcagctgc aggagtcggg cccaggactg gtgaagcctt 60
 cggagaccct gtccctcacc tgcactgtct ctgggttactc catcagcagt gggttactact 120
 ggggctggat ccggcagccc ccagggaagg ggctggagtg gattgggagt atctatcata 180
 gtgggagcac ctactacaac ccgtccctca agagtcgagt caccatatca gtagacacgt 240
 ccaagaacca gttctccctg aagctgagct ctgtgaccgc cgcagacacg gccgtgtatt 300
 actgtgagag agtccgtcgg aggtacagca gtgcttccaa gataatcttt ggatcaggga 360
 ccagactcag catccgg 377

<210> 36
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
 20 25 30
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile
 35 40 45
 Ser Ser Gly Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly
 50 55 60
 Leu Glu Trp Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn
 65 70 75 80
 Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn
 85 90 95
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Val Arg Arg Arg Tyr Ser Ser Ala Ser Lys Ile
 115 120 125
 Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg Pro
 130 135 140

<210> 37
 <211> 675
 <212> DNA
 <213> Homo sapiens

<400> 37
 ccacccacat gcaaatacctc acttaggcgc ccacaggaag ccacaacaca tttccttaaa 60
 ttcaggtcca actcataagg gaaatgcttt ctgagagtca tggacctcct gtgcaagaac 120
 atgaagcacc tgtgggtttt cctcctgctg gtggcagctc ccagatgtga gtgtctcagg 180

18/299

```

gatccagacg tgaagatatg ggaagtgcct ctgatcccag ggctcaccgt ggggtttttct 240
gttcacaggg gtccctgtccc aggtgcagct gcaggagtcg ggcccaggac tgggtgaagcc 300
ttcggagacc ctgtccctca cctgcactgt ctctgggttac tccatcagca gtggttacta 360
ctggggctgg atccggcagc ccccagggaa ggggctggag tggattggga gtatctatca 420
tagtgggagc acctactaca acccgtccct caagagtcga gtcaccatat cagtagacac 480
gtccaagaac cagttctccc tgaagctgag ctctgtgacc gccgcagaca cggccgtgta 540
ttactgtgcg agagtccgtc ggaggtacag cagtgccttc aagataatct ttggatcagg 600
gaccagactc agcatccggc caagtaagta gaatgaagca ggagagcaag ggaggacgga 660
caactatttc ttctt                                     675

```

<210> 38

<211> 158

<212> PRT

<213> Homo sapiens

<400> 38

```

Met Val Thr Gly Gly Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly
  1              5              10              15

```

```

Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val
          20              25              30

```

```

Ser Gly Tyr Ser Ile Ser Ser Gly Tyr Tyr Trp Gly Trp Ile Arg Gln
  35              40              45

```

```

Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Ser Ile Tyr His Ser Gly
  50              55              60

```

```

Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val
  65              70              75              80

```

```

Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala
          85              90              95

```

```

Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Val Arg Arg Arg Tyr Ser
  100              105              110

```

```

Ser Ala Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg Leu Ser Ile Arg
  115              120              125

```

```

Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser
  130              135              140

```

```

Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp
  145              150              155

```

<210> 39

<211> 508

<212> DNA

<213> Homo sapiens

<400> 39

```

tgtcctctga aaactcggga atttgtcact gaaatgggtga caggaggggt cctgtcccag 60
gtgcagctgc aggagtcggg cccaggactg gtgaagcctt cggagaccct gtccctcacc 120
tgcactgtct ctggttactc catcagcagt gggttactact ggggctggat ccggcagccc 180
ccaggggaag ggctggagtg gattgggagt atctatcata gtgggagcac ctactacaac 240

```

19/299

```

ccgtccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 300
aagctgagct ctgtgaccgc cgcagacacg gccgtgtatt actgtgcgag agtccgtcgg 360
aggtacagca gtgcttccaa gataatcttt ggatcaggga ccagactcag catccggcca 420
aatatccaga accctgaccc tgccgtgtac cagctgagag actctaaatc cagtgacaag 480
tctgtctgcc tattcaccga ttttgatt                                508

```

<210> 40

<211> 162

<212> PRT

<213> Homo sapiens

<400> 40

```

Met Ala Glu Ala Leu His Gly Lys Arg Val Leu Ser Gln Val Gln Leu
  1           5           10          15

```

```

Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu
          20          25          30

```

```

Ala Cys Thr Val Ser Gly Tyr Ser Ile Ser Ser Gly Tyr Tyr Trp Gly
          35          40          45

```

```

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Ser Ile
          50          55          60

```

```

Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser Arg Val
          65          70          75          80

```

```

Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser
          85          90          95

```

```

Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Val Arg
          100          105          110

```

```

Arg Arg Tyr Ser Ser Ala Ser Lys Ile Ile Phe Gly Ser Gly Thr Arg
          115          120          125

```

```

Leu Ser Ile Arg Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln
          130          135          140

```

```

Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp
          145          150          155          160

```

Phe Asp

<210> 41

<211> 616

<212> DNA

<213> Homo sapiens

<400> 41

```

tgtcctctga aaactcggga atttgtcact gaaatgggtga caggagccta cagggtggcag 60
atgagaactc tcaacacagt tgtgttagaa gaaggatttc ctagagagac cctgactcaa 120
tgatgataca tggctgaagc attgcatgga aaacgggtcc tgtcccagggt gcagctgcag 180
gagtcggggc caggactggt gaagccttcg gagaccctgt ccctgcctg cactgtctct 240
ggttactcca tcagcagtgg ttactactgg ggctggatcc ggcagccccc aggggaagggg 300
ctggagtggg ttgggagtat ctatcatagt gggagcacct actacaaccg gtccctcaag 360

```

20/299

```

agtcgagtc ccatatcagt agacacgtcc aagaaccagt tctccctgaa gctgagctct 420
gtgaccgccg cagacacggc cgtgtattac tgtgcgagag tccgtcggag gtacagcagt 480
gcttccaaga taatctttgg atcagggacc agactcagca tccggccaaa tatccagaac 540
cctgaccctg ccgtgtacca gctgagagac tctaaatcca gtgacaagtc tgtctgccta 600
ttcaccgatt ttgatt                                     616

```

<210> 42
 <211> 550
 <212> PRT
 <213> Homo sapiens

<400> 42
 Gly Tyr Gln Leu His Gly Ala Glu Val Asn Gly Gly Leu Pro Ser Ala
 1 5 10 15
 Ser Ser Phe Ser Ser Ala Pro Gly Ala Thr Tyr Gly Val Ser Ser His
 20 25 30
 Thr Pro Pro Val Ser Gly Ala Asp Ser Leu Leu Gly Ser Arg Gly Thr
 35 40 45
 Thr Ala Gly Ser Ser Gly Asp Ala Leu Gly Lys Ala Leu Ala Ser Ile
 50 55 60
 Tyr Ser Pro Asp His Ser Ser Asn Asn Phe Ser Ser Ser Pro Ser Thr
 65 70 75 80
 Pro Val Gly Ser Pro Gln Gly Leu Ala Gly Thr Ser Gln Trp Pro Arg
 85 90 95
 Ala Gly Ala Pro Gly Ala Leu Ser Pro Ser Tyr Asp Gly Gly Leu His
 100 105 110
 Gly Leu Gln Ser Lys Ile Glu Asp His Leu Asp Glu Ala Ile His Val
 115 120 125
 Leu Arg Ser His Ala Val Gly Thr Ala Gly Asp Met His Thr Leu Leu
 130 135 140
 Pro Gly His Gly Ala Leu Ala Ser Gly Phe Thr Gly Pro Met Ser Leu
 145 150 155 160
 Gly Gly Arg His Ala Gly Leu Val Gly Gly Ser His Pro Glu Asp Gly
 165 170 175
 Leu Ala Gly Ser Thr Ser Leu Met His Asn His Ala Ala Leu Pro Ser
 180 185 190
 Gln Pro Gly Thr Leu Pro Asp Leu Ser Arg Pro Pro Asp Ser Tyr Ser
 195 200 205
 Val Leu Ser Ile Arg Gly Ala Gln Glu Glu Glu Pro Thr Asp Pro Gln
 210 215 220
 Leu Met Arg Leu Asp Asn Met Leu Leu Ala Glu Gly Val Ala Gly Pro
 225 230 235 240

21/299

Glu Lys Gly Gly Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala Ser
 245 250 255
 Gly Gly Ala Gly Ser Asp Asn Ser Val Glu His Ser Asp Tyr Arg Ala
 260 265 270
 Lys Leu Ser Gln Ile Arg Gln Ile Tyr His Thr Glu Leu Glu Lys Tyr
 275 280 285
 Glu Gln Ala Cys Asn Glu Phe Thr Thr His Val Met Asn Leu Leu Arg
 290 295 300
 Glu Gln Ser Arg Thr Arg Pro Ile Ser Pro Lys Glu Ile Glu Arg Met
 305 310 315 320
 Val Ser Ile Ile His Arg Lys Phe Ser Ser Ile Gln Met Gln Leu Lys
 325 330 335
 Gln Ser Thr Cys Glu Ala Val Met Ile Leu Arg Ser Arg Phe Leu Asp
 340 345 350
 Ala Arg Arg Lys Arg Arg Asn Phe Asn Lys Gln Ala Thr Glu Ile Leu
 355 360 365
 Asn Glu Tyr Phe Tyr Ser His Leu Ser Asn Pro Tyr Pro Ser Glu Glu
 370 375 380
 Ala Lys Glu Glu Leu Ala Lys Lys Cys Gly Ile Thr Val Ser Gln Val
 385 390 395 400
 Ser Asn Trp Phe Gly Asn Lys Arg Ile Arg Tyr Lys Lys Asn Ile Gly
 405 410 415
 Lys Phe Gln Glu Glu Ala Asn Ile Tyr Ala Ala Lys Thr Ala Val Thr
 420 425 430
 Ala Thr Asn Val Ser Ala His Gly Ser Gln Ala Asn Ser Pro Ser Thr
 435 440 445
 Pro Asn Ser Ala Gly Ser Ser Ser Ser Phe Asn Met Ser Asn Ser Gly
 450 455 460
 Asp Leu Phe Met Ser Val Gln Ser Leu Asn Gly Asp Ser Tyr Gln Gly
 465 470 475 480
 Ala Gln Val Gly Ala Asn Val Gln Ser Gln Val Asp Thr Leu Arg His
 485 490 495
 Val Ile Ser Gln Thr Gly Gly Tyr Ser Asp Gly Leu Ala Ala Ser Gln
 500 505 510
 Met Tyr Ser Pro Gln Gly Ile Ser Ala Asn Gly Gly Trp Gln Asp Ala
 515 520 525
 Thr Thr Pro Ser Ser Val Thr Ser Pro Thr Glu Gly Pro Gly Ser Val
 530 535 540
 His Ser Asp Thr Ser Asn

22/299

545

550

<210> 43
 <211> 2049
 <212> DNA
 <213> Homo sapiens

<400> 43
 ggctaccagc tgcattggagc agaggtgaac ggagggctcc catctgcac ctccttctcc 60
 tcagcccccg gagccacgta cggcgtctcc agccacacgc cgcctgtcag cggggccgac 120
 agcctccttg gctcccgagg gaccacagct ggcagctccg gggatgccct cggcaaagca 180
 ctggcctcga tctactcccc ggatcactca agcaataact tctcgtccag cccttctacc 240
 cccgtgggct cccccaggc cctggcagga acgtcacagt ggccctcgagc aggagcccc 300
 ggtgccttat cggccagcta cgacgggggt ctccacggcc tgcagagtaa gatagaagac 360
 cacctggagc agggcatcca cgtgctccgc agccacggcg tgggcacagc cggcgacatg 420
 cacacgctgc tgcctggcca cggggcgtg gcctcaggtt tcaccggccc catgtcactg 480
 ggcgggcggc acgcaggcct ggttgagggc agccaccccg aggacggcct cgcaggcagc 540
 accagcctca tgcacaacca cgcggccctc cccagccagc caggcacctt ccctgacctg 600
 tctcggcctc ccgactccta cagtgttttg agtatccgag gagcccagga ggaggaaccc 660
 acagaccccc agctgatgag gctggacaac atgctgttag cgggaaggcgt ggcggggcct 720
 gagaagggcg gagggctcggc ggcagcggcg gcagcggcg cggcttcttg aggggcagg 780
 tcagacaact cagtggagca ttcagattac agagccaaac tctcacagat cagacaaatc 840
 taccatacgg agctggagaa atacgagcag gcctgcaacg agttcaccac ccacgtgatg 900
 aatctcctgc gagagcaaa cgggaccagg cccatctccc caaaggagat tgagcggatg 960
 gtcagcatca tccaccgcaa gttcagctcc atccagatgc agctcaagca gagcacgtgc 1020
 gaggcgggta tgatcctgag tttccgattt ctggatgcgc ggcggaagag acggaatttc 1080
 aacaagcaag cgacagaaat cctgaatgaa tatttctatt cccatctcag caacccttac 1140
 cccagtggag aagccaaaga ggagttagcc aagaagtgtg gcatcacagt ctcccaggta 1200
 tcaaactggt ttggaataa gcgaatccgg tacaagaaga acataggtaa atttcaagag 1260
 gaagccaata tttatgctgc caaaacagct gtcactgcta ccaatgtgtc agcccatgga 1320
 agccaagcta actcgccctc aactcccaac tcggctgggt ctccagttc ttttaacatg 1380
 tcaaactctg gagatttggt catgagcgtg cagtcactca atggggattc ttaccaaggg 1440
 gcccagggtg gagccaacgt gcaatcacag gtggataccc ttcgccatgt tatcagccag 1500
 acaggaggat acagtgatgg actcgcagcc agtcagatgt acagtccgca gggcatcagt 1560
 gctaattggag gttggcagga tgctactacc cttcatcag tgacctccc tacagaaggc 1620
 cctggcagtg ttcactctga tacctccaac tgatctccca gcaatogcat cccggctgac 1680
 cctgtgcccc agttggggca ggggcaggag ggagggtttc tctcccaacg ctgaagcgg 1740
 cagactggag gtccaagcaa tcagcaaaaca caataagagt ctcttctctt tctcttcttt 1800
 gggatgctat ttcagccaat ctggacactt ctttatactc tcttcccttt ttttctggg 1860
 tagaagccac cttccctgc ctccagctgt cagcctgggt ttcgtcatct tccctgccc 1920
 tgtgcctctg tcttagactc ccgggtccc cgcctctct catatcactg aaggatattt 1980
 tcaacaattg aaggaattta aagagcaaaa aaattacaaa gaaaataata aaagtgtttg 2040
 tacgttttc 2049

<210> 44
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Asn Gln Pro Gln Arg Met Ala Pro Val Gly Thr Asp Lys Glu Leu
 1 5 10 15
 Ser Asp Leu Leu Asp Phe Ser Met Met Phe Pro Leu Pro Val Thr Asn
 20 25 30

23/299

Gly Lys Gly Arg Pro Ala Ser Leu Ala Gly Ala Gln Phe Gly Gly Ser
 35 40 45
 Gly Leu Glu Asp Arg Pro Ser Ser Gly Ser Trp Gly Ser Gly Asp Gln
 50 55 60
 Ser Ser Ser Ser Phe Asp Pro Ser Arg Thr Phe Ser Glu Gly Thr His
 65 70 75 80
 Phe Thr Glu Ser His Ser Ser Leu Ser Ser Thr Phe Leu Gly Pro
 85 90 95
 Gly Leu Gly Gly Lys Ser Gly Glu Arg Gly Ala Tyr Ala Ser Phe Gly
 100 105 110
 Arg Asp Ala Gly Val Gly Gly Leu Thr Gln Ala Gly Phe Leu Ser Gly
 115 120 125
 Glu Leu Ala Leu Asn Ser Pro Gly Pro Leu Ser Pro Ser Gly Met Lys
 130 135 140
 Gly Thr Ser Gln Tyr Tyr Pro Ser Tyr Ser Gly Ser Ser Arg Arg Arg
 145 150 155 160
 Ala Ala Asp Gly Ser Leu Asp Thr Gln Pro Lys Lys Val Arg Lys Val
 165 170 175
 Pro Pro Gly Leu Pro Ser Ser Val Tyr Pro Pro Ser Ser Gly Glu Asp
 180 185 190
 Tyr Gly Arg Asp Ala Thr Ala Tyr Pro Ser Ala Lys Thr Pro Ser Ser
 195 200 205
 Thr Tyr Pro Ala Pro Phe Tyr Val Ala Asp Gly Ser Leu His Pro Ser
 210 215 220
 Ala Glu Leu Trp Ser Pro Pro Gly Gln Ala Gly Phe Gly Pro Met Leu
 225 230 235 240
 Gly Gly Gly Ser Ser Pro Leu Pro Leu Pro Pro Gly Ser Gly Pro Val
 245 250 255
 Gly Ser Ser Gly Ser Ser Ser Thr Phe Gly Gly Leu His Gln His Glu
 260 265 270
 Arg Met Gly Tyr Gln Leu His Gly Ala Glu Val Asn Gly Gly Leu Pro
 275 280 285
 Ser Ala Ser Ser Phe Ser Ser Ala Pro Gly Ala Thr Tyr Gly Gly Val
 290 295 300
 Ser Ser His Thr Pro Pro Val Ser Gly Ala Asp Ser Leu Leu Gly Ser
 305 310 315 320
 Arg Gly Thr Thr Ala Gly Ser Ser Gly Asp Ala Leu Gly Lys Ala Leu
 325 330 335
 Ala Ser Ile Tyr Ser Pro Asp His Ser Ser Asn Asn Phe Ser Ser Ser

24/299

340	345	350
Pro Ser Thr Pro Val Gly Ser Pro Gln Gly Leu Ala Gly Thr Ser Gln		
355	360	365
Trp Pro Arg Ala Gly Ala Pro Gly Ala Leu Ser Pro Ser Tyr Asp Gly		
370	375	380
Gly Leu His Gly Leu Gln Ser Lys Ile Glu Asp His Leu Asp Glu Ala		
385	390	395
Ile His Val Leu Arg Ser His Ala Val Gly Thr Ala Gly Asp Met His		
405	410	415
Thr Leu Leu Pro Gly His Gly Ala Leu Ala Ser Gly Phe Thr Ser Pro		
420	425	430
Met Ser Leu Gly Gly Arg His Ala Gly Leu Val Gly Gly Ser His Pro		
435	440	445
Glu Asp Gly Leu Ala Gly Ser Thr Ser Leu Met His Asn His Ala Ala		
450	455	460
Leu Pro Ser Gln Pro Gly Thr Leu Pro Asp Leu Ser Arg Pro Pro Asp		
465	470	475
Ser Tyr Ser Gly Gln Gly Ile Ser Pro Gln Leu Gly Pro Leu Ser Thr		
485	490	495
Ser Ile Tyr Leu Leu Thr Gln Asp Asp Lys Tyr Trp Ala Arg Arg Arg		
500	505	510
Lys Asn Asn Met Ala Ala Lys Arg Ser Arg Asp Ala Arg Arg Leu Lys		
515	520	525
Glu Asn Gln Ile Ala Ile Arg Ala Ser Phe Leu Glu Lys Glu Asn Ser		
530	535	540
Ala Leu Arg Gln Glu Val Ala Asp Leu Arg Lys Glu Leu Gly Lys Cys		
545	550	555
Lys Asn Ile Leu Ala Lys Tyr Glu Ala Arg His Gly Pro Leu		
565	570	

<210> 45
 <211> 4410
 <212> DNA
 <213> Homo sapiens

<400> 45
 gcctgagggtg cccgcccttg ccccaggaga atgaaccagc cgcagaggat ggcgcctgtg 60
 ggcacagaca aggagctcag tgacctcctg gacttcagca tgatgttccc gctgcctgtc 120
 accaacggga agggccggcc cgcctccctg gccggggcgc agttcggagg ttcaggtctt 180
 gaggaccggc ccagctcagg ctccctggggc agcggcgacc agagcagctc ctcccttgac 240
 cccagccgga ccttcagcga gggcaccac ttactgagt cgcacagcag cctctcttca 300
 tccacattcc tgggaccggg actcggaggc aagagcgggtg agcggggcgc ctatgcctcc 360
 ttcgggagag acgcaggcgt gggcggcctg actcaggctg gcttcctgtc aggcgagctg 420

```

gccctcaaca gccccggggc cctgtccccc tggggcatga aggggacctc ccagtactac 480
ccctcctact ccggcagctc ccggcgggaga ggggcagacg gcagccctaga cacgcagccc 540
aagaaggtcc ggaaggtccc gccgggtctt ccctcctcgg tgtaccacc cagctcaggt 600
gaggactacg gcagggatgc caccgcctac ccgtccgcca agacccccag cagcacctat 660
ccgccccctt tctacgtggc agatggcagc ctgcacccct cagccgagct ctggagtccc 720
ccggggccagg cgggcttcgg gcccatgctg ggtgggggct catccccgt gccctccc 780
ccgggtagcg gccgggtggg cagcagtggg agcagcagca cgtttggtgg cctgcaccag 840
cacgagcgta tgggctacca gctgcatgga gcagaggtga acgggtgggt cccatctgca 900
tcctccttct cctcagcccc cggagccacg tacggcggcg tctccagcca cagcgcct 960
gtcagcgggg ccgacagcct cctgggctcc cgagggacca cagctggcag ctccggggat 1020
gccctcggca aagcactggc ctcgatctac tccccggatc actcaagcaa taactttctc 1080
tcagccctt ctacccccgt gggtccccc cagggcctgg caggaacgtc acagtggcct 1140
cgagcaggag cccccggtgc cttatcgccc agctacgacg ggggtctcca cggcctgcag 1200
agtaagatag aagaccacct ggacgagggc atccacgtgc tccgcagcca cggctgggg 1260
acagccggcg acatgcacac gctgctgctt ggccacgggg cgtggcctc aggtttcacc 1320
agtcccatgt cgtgggtgg gcggcacgca ggctggttg gaggcagcca ccccgaggac 1380
ggcctcgcag gcagcaccag cctcatgcac aaccacggcg cctccccag ccagccaggc 1440
accctcctcg acctgtctcg gcctcccgac tcctacagtg gccagggcat ctaccgcag 1500
cttggctccc tctccacctc gatctacttg ctacccagg atgacaagta ctgggcaagg 1560
cgcagaaaaga acaacatggc agccaagcgc tccgcgacg ccggagggt gaaagagaac 1620
cagatcgcca tccgggcctc gttcctggag aaggagaact cggccctccg ccaggagggtg 1680
gctgacttga ggaaggagct gggcaaatgc aagaacatac ttgccaagta tgaggccagg 1740
cacgggcccc tttaggatgg catttttgca ggctggcttt ggaatagatg gacagtttgt 1800
ttcctgtctg atagaccac acgcaaaaca acccttctga catcagcact ttaccagagg 1860
cataaacaca actgactccc attttgggtg gcactctgtg gtgtgtgcgt gtatatgtgc 1920
ttgtgctcat gtgtgtggtc agcggtatgt gcgtgtgcgt gttcctttgc tcttgccatt 1980
ttaaggtagc cctctcatcg tcttttagtt ccaacaaaga aaggtgccat gtctttacta 2040
gactgaggag ccctctcgcg ggtctcccat cccctccctc cttcactcct gcctcctcag 2100
ctttgcttca tgttcgagct tacctaactt tccaggactc tctgcttggg ttactaaaa 2160
agggccctgg taaaatagtg gatctcagtt ttaagagta caagctcttg tttctgttta 2220
gtccgtaagt taccatgcta atgagggtga cacaataact tagcactact ccgcagctct 2280
agtcttttat aagttgcttt cctcttactt tcagtttttg tgataatcgt ctcaaaatta 2340
aagtgtgttt tagatttatt agatcccata tttacttact gctatctact aagtttctct 2400
ttaattctac caaccccaga taagtaagag tactattaat agaacacaga gtgtgttttt 2460
gcactgtctg tacctaagc aataatccta ttgtacgcta gagcatgctg cctgagtatt 2520
actagtggac gtaggatatt ttccctacct aagaatttca ctgtctttta aaaaacaaaa 2580
agtaaaagta tgcatttgag catggccaga ctattcccta ggacaaggaa gcagagggaa 2640
atgggagggtc taaggatgag gggtaatttt atcagtacat gagccaaaaa ctgctgtctg 2700
gattagcctt tgacattgat gtgttcgggt ttgtgttcc ccttccctca caccctgct 2760
cgccccact tttctagtta actttttcca tatccctctt gacattcaaa acagttaact 2820
aagctttcag tttccactt tttggtaata tataattttt tgtgaattat actttgttgt 2880
ttttaaaaag aaaatcagtt gattaagtta ataagttgat gttttctaag gccctttttc 2940
ctagtgggtg catttttgaa tgcccataa attaatgatt ctgaagctta tgtttcttat 3000
tctctgtttg cttttgaacg tatgtgctct tataaagtgg acttctgaaa aatgaatgta 3060
aaagacactg gtgtatctca gaaggggatg gtgtgtgcac aaactgtggt taatccaatc 3120
aattttaaag tttactatag accaaaagga gagattatta aatcgtttaa tgtttataca 3180
gagtaattat aggaagttct tttttgtaca gtatttttca gatataaata ctgacaatgt 3240
attttggag acatatatta tatatagaaa agaggagagg aaaactattc catgttttaa 3300
aattatatag caaagatata tattcaccaa tgtgtacag agaagaagt cttgggggtt 3360
tttgaaagtct ttaatatttt aagccctatc actgacacat cagcatgttt tctgctttaa 3420
attaaaaatt tatgacagta tcgaggcttg tgatgacgaa tctgctcta aaatacaca 3480
ggagctttct tgtttcttat taggcctcag aaagaagtca gttaacgtca cccaaaagca 3540
caaaatggat tttagtcaaa tatttatagg atgatacagt gttttttagg aaaagcatct 3600
gccacaaaaa tgttcacttc gaaattctga gttcctggaa tggcacgttg ctgccagtgc 3660
cccagacagt tctttctac cctgcgggccc cgcacgtttt atgaggttga tatcgggtgc 3720
atgtgttttg tttataattt gatagatgtt tgactttaaa gatgattgtt cttttgtttc 3780
attaagttgt aaaatgtcaa gaaattctgc tgttacgaca aagaaacatt ttacgctaga 3840
ttaaaatata ctttcatcaa tgggattttc tagtttctg ctttcagagt atctaactct 3900

```


26/299

```

ttaatgatct ggtgggtctcc tcgtcaatcc atcagcaatg cttctctcat agtgtcatag 3960
acttgggaaa cccaaccagt aggatatttc tacaagggtg tcattttgtc acaagctgta 4020
gataacagca agagatgggg gtgtattgga attgcaatac attgttcagg tgaataataa 4080
aatcaaaaac ttttgcaatc ttaagcagag ataaataaaa gatagcaata tgagacacag 4140
gtggacgtag agttggcctt ttacaggca aagaggcgaa ttgtagaatt gttagatggc 4200
aatagtcatt aaaaacatag aaaaatgatg tctttaagtg gagaattgtg gaaggattgt 4260
aacatggacc atccaaattt atggccgtat caaatggtag ctgaaaaaac tatatttgag 4320
cactgggtctc tcttggaatt agatgtttat atcaaatgag catctcaaat gttttctgca 4380
gaaaaaaata aaaagattct aataaaaaaa 4410

```

<210> 46
 <211> 416
 <212> PRT
 <213> Homo sapiens

<400> 46
 Pro Asn Ser Asn His Val Ala Ser Gly Ala Gly Glu Ala Ala Ile Glu
 1 5 10 15
 Thr Gln Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro
 20 25 30
 Pro Pro Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys
 35 40 45
 Ser Ser Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly
 50 55 60
 Phe Phe Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg
 65 70 75 80
 Asp Lys Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr
 85 90 95
 Cys Arg Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val
 100 105 110
 Arg Asn Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys Pro Glu Cys
 115 120 125
 Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys
 130 135 140
 Val Arg Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly
 145 150 155 160
 Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile
 165 170 175
 Asp Leu Trp Asp Lys Phe Ser Glu Leu Ser Thr Lys Cys Ile Ile Lys
 180 185 190
 Thr Val Glu Phe Ala Lys Gln Leu Pro Gly Phe Thr Thr Leu Thr Ile
 195 200 205
 Ala Asp Gln Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Ile
 210 215 220

27/299

Leu Arg Ile Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe
 225 230 235 240
 Ser Asp Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe
 245 250 255
 Gly Pro Leu Thr Asp Leu Val Phe Ala Phe Ala Asn Gln Leu Leu Pro
 260 265 270
 Leu Glu Met Asp Asp Ala Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu
 275 280 285
 Ile Cys Gly Asp Arg Gln Asp Leu Glu Gln Pro Asp Arg Val Asp Met
 290 295 300
 Leu Gln Glu Pro Leu Leu Glu Ala Leu Lys Val Tyr Val Arg Lys Arg
 305 310 315 320
 Arg Pro Ser Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr
 325 330 335
 Asp Leu Arg Ser Ile Ser Ala Lys Gly Ala Glu Arg Val Ile Thr Leu
 340 345 350
 Lys Met Glu Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu
 355 360 365
 Glu Asn Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly
 370 375 380
 Gly Arg Asp Gly Gly Gly Leu Ala Pro Pro Pro Gly Ser Cys Ser Pro
 385 390 395 400
 Ser Leu Ser Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro
 405 410 415

<210> 47

<211> 1284

<212> DNA

<213> Homo sapiens

<400> 47

cccaacagca accacgtggc cagtggcgcc ggggaggcag ccattgagac ccagagcagc 60
 agttctgaag agatagtgcc cagccctccc tcgccacccc ctctaccccg catctacaag 120
 ccttgctttg tctgtcagga caagtcctca ggctaccact atgggggtcag cgcctgtgag 180
 ggctgcaagg gcttcttccg ccgcagcatc cagaagaaca tgggtgtacac gtgtcaccgg 240
 gacaagaact gcatacatcaa caaggtgacc cggaaccgct gccagtactg ccgactgcag 300
 aagtgccttg aagtgggcat gtccaaggag tctgtgagaa acgaccgaaa caagaagaag 360
 aaggaggtgc ccaagcccga gtgctctgag agctacacgc tgacgcgga ggtgggggag 420
 ctattgaga aggtgcgcaa agcgaccag gaaaccttcc ctgccctctg ccagctgggc 480
 aaatacacta cgaacaacag ctcaagaaca cgtgtctctc tggacattga cctctgggac 540
 aagttcagtg aactctccac caagtgcac attagactg tggagttcgc caagcagctg 600
 cccggcttca ccacctcac catcgccgac cagatcacc tcctcaaggc tgcctgcctg 660
 gacatcctga tctgcggtat ctgcacgcgg tacacgcccg agcaggacac catgaccttc 720
 tcggacgggc tgacctgaa ccggaccag atgcacaacg ctggcttcgg cccctcacc 780
 gacctggtct ttgccttcgc caaccagctg ctgccctgg agatggatga tgcggagacg 840

28/299

```

gggctgctca gcgccatctg cctcatctgc ggagaccgcc aggacctgga gcagccggac 900
cgggtggaca tgctgcagga gccgtgctg gaggcgctaa aggtctacgt gcggaagcgg 960
aggcccagcc gccccacat gttccccaag atgctaata gaattactga cctgcgaagc 1020
atcagcgcca agggggctga gcgggtgatc acgctgaaga tggagatccc gggctccatg 1080
ccgcctctca tccaggaaat gttggagaac tcagagggcc tggacactct gagcggacag 1140
ccgggggggtg gggggcgga cgggggtggc ctggccccc cgccaggcag ctgtagcccc 1200
agcctcagcc ccagctccaa cagaagcagc ccggccacc actccccgtg accgcccacg 1260
ccacatggac acagccctcg ccct                                     1284

```

<210> 48

<211> 797

<212> PRT

<213> Homo sapiens

<400> 48

```

Met Glu Pro Ala Pro Ala Arg Ser Pro Arg Pro Gln Gln Asp Pro Ala
  1              5              10              15

Arg Pro Gln Glu Pro Thr Met Pro Pro Pro Glu Thr Pro Ser Glu Gly
          20              25              30

Arg Gln Pro Ser Pro Ser Pro Ser Pro Thr Glu Arg Ala Pro Ala Ser
          35              40              45

Glu Glu Glu Phe Gln Phe Leu Arg Cys Gln Gln Cys Gln Ala Glu Ala
          50              55              60

Lys Cys Pro Lys Leu Leu Pro Cys Leu His Thr Leu Cys Ser Gly Cys
          65              70              75              80

Leu Glu Ala Ser Gly Met Gln Cys Pro Ile Cys Gln Ala Pro Trp Pro
          85              90              95

Leu Gly Ala Asp Thr Pro Ala Leu Asp Asn Val Phe Phe Glu Ser Leu
          100             105             110

Gln Arg Arg Leu Ser Val Tyr Arg Gln Ile Val Asp Ala Gln Ala Val
          115             120             125

Cys Thr Arg Cys Lys Glu Ser Ala Asp Phe Trp Cys Phe Glu Cys Glu
          130             135             140

Gln Leu Leu Cys Ala Lys Cys Phe Glu Ala His Gln Trp Phe Leu Lys
          145             150             155             160

His Glu Ala Arg Pro Leu Ala Glu Leu Arg Asn Gln Ser Val Arg Glu
          165             170             175

Phe Leu Asp Gly Thr Arg Lys Thr Asn Asn Ile Phe Cys Ser Asn Pro
          180             185             190

Asn His Arg Thr Pro Thr Leu Thr Ser Ile Tyr Cys Arg Gly Cys Ser
          195             200             205

Lys Pro Leu Cys Cys Ser Cys Ala Leu Leu Asp Ser Ser His Ser Glu
          210             215             220

```

29/299

Leu Lys Cys Asp Ile Ser Ala Glu Ile Gln Gln Arg Gln Glu Glu Leu
 225 230 235 240
 Asp Ala Met Thr Gln Ala Leu Gln Glu Gln Asp Ser Ala Phe Gly Ala
 245 250 255
 Val His Ala Gln Met His Ala Ala Val Gly Gln Leu Gly Arg Ala Arg
 260 265 270
 Ala Glu Thr Glu Glu Leu Ile Arg Glu Arg Val Arg Gln Val Val Ala
 275 280 285
 His Val Arg Ala Gln Glu Arg Glu Leu Leu Glu Ala Val Asp Ala Arg
 290 295 300
 Tyr Gln Arg Asp Tyr Glu Glu Met Ala Ser Arg Leu Gly Arg Leu Asp
 305 310 315 320
 Ala Val Leu Gln Arg Ile Arg Thr Gly Ser Ala Leu Val Gln Arg Met
 325 330 335
 Lys Cys Tyr Ala Ser Asp Gln Glu Val Leu Asp Met His Gly Phe Leu
 340 345 350
 Arg Gln Ala Leu Cys Arg Leu Arg Gln Glu Glu Pro Gln Ser Leu Gln
 355 360 365
 Ala Ala Val Arg Thr Asp Gly Phe Asp Glu Phe Lys Val Arg Leu Gln
 370 375 380
 Asp Leu Ser Ser Cys Ile Thr Gln Gly Lys Ala Ile Glu Thr Gln Ser
 385 390 395 400
 Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro Pro Pro Leu
 405 410 415
 Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser Gly
 420 425 430
 Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg
 435 440 445
 Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg Asp Lys Asn
 450 455 460
 Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr Cys Arg Leu
 465 470 475 480
 Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val Arg Asn Asp
 485 490 495
 Arg Asn Lys Lys Lys Lys Glu Val Pro Lys Pro Glu Cys Ser Glu Ser
 500 505 510
 Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys Val Arg Lys
 515 520 525
 Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly Lys Tyr Thr

530					535					540					
Thr 545	Asn	Asn	Ser	Ser	Glu 550	Gln	Arg	Val	Ser	Leu 555	Asp	Ile	Asp	Leu	Trp 560
Asp	Lys	Phe	Ser	Glu 565	Leu	Ser	Thr	Lys	Cys 570	Ile	Ile	Lys	Thr	Val	Glu 575
Phe	Ala	Lys	Gln 580	Leu	Pro	Gly	Phe	Thr 585	Thr	Leu	Thr	Ile	Ala	Asp	Gln 590
Ile	Thr	Leu 595	Leu	Lys	Ala	Ala	Cys 600	Leu	Asp	Ile	Leu	Ile 605	Leu	Arg	Ile
Cys 610	Thr	Arg	Tyr	Thr	Pro	Glu 615	Gln	Asp*	Thr	Met	Thr 620	Phe	Ser	Asp	Gly
Leu 625	Thr	Leu	Asn	Arg	Thr 630	Gln	Met	His	Asn	Ala 635	Gly	Phe	Gly	Pro	Leu 640
Thr	Asp	Leu	Val	Phe 645	Ala	Phe	Ala	Asn	Gln 650	Leu	Leu	Pro	Leu	Glu 655	Met
Asp	Asp	Ala	Glu 660	Thr	Gly	Leu	Leu	Ser 665	Ala	Ile	Cys	Leu	Ile 670	Cys	Gly
Asp	Arg	Gln 675	Asp	Leu	Glu	Gln	Pro 680	Asp	Arg	Val	Asp	Met 685	Leu	Gln	Glu
Pro 690	Leu	Leu	Glu	Ala	Leu	Lys 695	Val	Tyr	Val	Arg 700	Lys	Arg	Arg	Pro	Ser
Arg 705	Pro	His	Met	Phe 710	Pro	Lys	Met	Leu	Met	Lys 715	Ile	Thr	Asp	Leu	Arg 720
Ser	Ile	Ser	Ala	Lys 725	Gly	Ala	Glu	Arg	Val 730	Ile	Thr	Leu	Lys	Met 735	Glu
Ile	Pro	Gly 740	Ser	Met	Pro	Pro	Leu	Ile 745	Gln	Glu	Met	Leu	Glu 750	Asn	Ser
Glu	Gly 755	Leu	Asp	Thr	Leu	Ser	Gly 760	Gln	Pro	Gly	Gly	Gly 765	Gly	Arg	Asp
Gly 770	Gly	Gly	Leu	Ala	Pro	Pro 775	Pro	Gly	Ser	Cys	Ser 780	Pro	Ser	Leu	Ser
Pro 785	Ser	Ser	Asn	Arg	Ser 790	Ser	Pro	Ala	Thr	His 795	Ser	Pro			

```
<210> 49
<211> 3036
<212> DNA
<213> Homo sapiens
```

<400> 49
ctccaccttca gcttctcttc acgcactcca agatctaaac cgagaatcga aactaagctg 60

31/299

```

gggtccatgg agcctgcacc cgcccgatct cggaggcccc agcaggaccc cgcccgcccc 120
caggagccca ccctgcctcc ccccgagacc ccctctgaag gccgcccagcc cagccccagc 180
cccagcccta cagagcgagc ccccgcttog gaggaggagt tccagtttct gcgctgccag 240
caatgccagg cggaagccaa gtgcccgaag ctgctgcctt gtctgcacac gctgtgctca 300
ggatgcctgg aggcgtcggg catgcagtgc cccatctgcc aggcgccttg gcccttaggt 360
gcagacacac ccgccctgga taacgtcttt ttcgagagtc tgcagcggcg cctgtcggtg 420
taccggcaga ttgtggatgc gcaggctgtg tgcacccgct gcaaagagtc ggccgacttc 480
tggtgctttg agtgcgagca gctcctctgc gccaaagtgt tccaggccaca ccagtgggtc 540
ctcaagcacg aggcgccggc cctagcagag ctgcgcaacc agtcgggtgc tgagttcctg 600
gacggcaccc gcaagaccaa caacatcttc tgctccaacc ccaaccaccg caccctacg 660
ctgaccagca tctactgccg aggatgttcc aagccgctgt gctgctcgtg cgcgctcctt 720
gacagcagcc acagtgcagc caagtgcgac atcagcgcag agatccagca gcgacaggag 780
gagctggacg ccatgacgca ggcgctgcag gaggaggata gtgcctttgg cgcggttcac 840
gcgcagatgc acgcggccgt cggccagctg ggcgcgcgcg gtgcgcgagc cgaggagctg 900
atccgcgagc gcgtgcgcca ggtggtagct cacgtgcggg ctccaggagc cgagctgctg 960
gaggctgtgg acgcgcggta ccagcgcgac tacgaggaga tggccagtcg gctgggcccg 1020
ctggatgctg tgctgcagcg catccgcacg ggcagcgcgc tgggtgcagag gatgaagtgc 1080
tacgcctcgg accaggaggt gctggacatg cacggtttcc tgcgccaggc gctctgcgcg 1140
ctgcgccagg aggagcccca gagcctgcaa gctgcctgct gcaccgatgg cttcgacgag 1200
ttcaaggtgc gcctgcagga cctcagctct tgcatcacc aggggaaagc cattgagac 1260
cagagcagca gttctgaaga gatagtgcgc agccctccct cgcaccccc tctaccgcg 1320
atctacaagc cttgctttgt ctgtcaggac aagtcctcag gctaccacta tggggtcagc 1380
gcctgtgagg gctgcaaggg cttcttccgc cgcagcatcc agaagaacat ggtgtacacg 1440
tgtcaccggg acaagaactg catcatcaac aaggtgaccc ggaaccgctg ccagtactgc 1500
cgactgcaga agtgctttga agtgggcatg tccaaggagt ctgtgagaaa cgaccgaaac 1560
aagaagaaga aggaggtgcc caagcccagag tgctctgaga gctacacgct gacgcgggag 1620
gtgggggagc tcattgagaa ggtgcgcaaa gcgcaccagg aaaccttccc tgccctctgc 1680
cagctgggca aatacactac gaacaacagc tcagaacaac gtgtctctct ggacattgac 1740
ctctgggaca agttcagtga actctccacc aagtgcacaa ttaagactgt ggagttcgcc 1800
aagcagctgc ccggtctcac caccctcacc atcgccgacc agatcacct cctcaaggct 1860
gcctgcctgc acatcctgat cctgcggatc tgcacgcggt acacgcccga gcaggacacc 1920
atgaccttct cggacgggct gacctgaac cggaccaga tgcacaacgc tggcttcggc 1980
cccctcaccg acctggtctt tgccctcgcc aaccagctgc tgccctgga gatggatgat 2040
gcggagacgg ggctgctcag cgccatctgc ctcatctgcg gagaccgcca ggacctggag 2100
cagccggacc ggggtggacat gctgcaggag ccgctgctgg aggcgctaaa ggtctacgtg 2160
cggaagcgga ggcccagccg cccccacatg ttcccgaaga tgctaataga gattactgac 2220
ctgcgaagca tcagcgccaa gggggctgag cgggtgatca cgctgaagat ggagatcccg 2280
ggctccatgc cgctctcat ccaggaaatg ttggagaact cagagggcct ggacactctg 2340
agcgacagc cggggggtgg ggggcgggac ggggggtggc tggccccccc gccaggcagc 2400
tgtagcccca gcctcagccc cagctccaac agaagcagcc cggccaccca ctccccgtga 2460
ccgccacgc cacatggaca cagccctcgc cctccgcccc ggcttttctc tgcccttcta 2520
ccgaccatgt gaccccgcac cagccctgcc ccacctgcc ctcccgggca gtactgggga 2580
ccttccttgg gggacgggga gggaggaggc agcgactcct tggacagagg cctgggccct 2640
cagtggactg cctgctccca cagcctgggc tgacgtcaga ggccgaggcc aggaactgag 2700
tgaggccctt ggtcctgggt ctccagatgg gtccctgggg cctcgtgttc atcaagacac 2760
ccctctgccc agctcaccac atcttcatca ccagcaaacg ccaggacttg gctcccccat 2820
cctcagaact cacaagccat tgctccccag ctggggaacc tcaacctccc ccctgcctcg 2880
gttggtgaca gaggggggtg gacaggggag ggggggtccc cctgtacata ccctgccata 2940
ccaaccccag gtattaattc tcgctggttt tgtttttatt ttaatttttt tgttttgatt 3000
tttttaataa gaattttcat ttttaagcaaa aaaaaa 3036

```

<210> 50

<211> 99

<212> PRT

<213> Homo sapiens

<400> 50

32/299

Asp Val Ser Asn Thr Thr Thr Ala Gln Lys Arg Lys Cys Ser Gln Thr
 1 5 10 15
 Gln Cys Pro Arg Lys Val Ile Lys Met Glu Ser Glu Glu Gly Lys Glu
 20 25 30
 Ala Arg Leu Ala Leu Pro Ala Pro Gly Pro Tyr Ser Thr Pro Leu Arg
 35 40 45
 Thr Pro Leu Trp Asn Gly Ser Asn His Ser Ile Glu Thr Gln Ser Ser
 50 55 60
 Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro Pro Pro Leu Pro
 65 70 75 80
 Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser Gly Tyr
 85 90 95
 His Tyr Gly

<210> 51
 <211> 296
 <212> DNA
 <213> Homo sapiens

<400> 51
 gatgtctcca atacaacgac agcccagaag aggaagtgca gccagaccca gtgccccagg 60
 aaggatcatca agatggagtc tgaggagggg aaggaggcaa gggtgggtct ccccgccccg 120
 gggtccgtact ccaccccgct ccggactccg ctttggaatg gctcaaacca ctccattgag 180
 acccagagca gcagttctga agagatagtg cccagccctc cctcgccacc cctcttacct 240
 cgcatctaca agccttgctt tgtctgtcag gacaagtctc caggctacca ctatgg 296

<210> 52
 <211> 858
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Asp Leu Thr Lys Met Gly Met Ile Gln Leu Gln Asn Pro Ser His
 1 5 10 15
 Pro Thr Gly Leu Leu Cys Lys Ala Asn Gln Met Arg Leu Ala Gly Thr
 20 25 30
 Leu Cys Asp Val Val Ile Met Val Asp Ser Gln Glu Phe His Ala His
 35 40 45
 Arg Thr Val Leu Ala Cys Thr Ser Lys Met Phe Glu Ile Leu Phe His
 50 55 60
 Arg Asn Ser Gln His Tyr Thr Leu Asp Phe Leu Ser Pro Lys Thr Phe
 65 70 75 80
 Gln Gln Ile Leu Glu Tyr Ala Tyr Thr Ala Thr Leu Gln Ala Lys Ala
 85 90 95

33/299

Glu Asp Leu Asp Asp Leu Leu Tyr Ala Ala Glu Ile Leu Glu Ile Glu
 100 105 110
 Tyr Leu Glu Glu Gln Cys Leu Lys Met Leu Glu Thr Ile Gln Ala Ser
 115 120 125
 Asp Asp Asn Asp Thr Glu Ala Thr Met Ala Asp Gly Gly Ala Glu Glu
 130 135 140
 Glu Glu Asp Arg Lys Ala Arg Tyr Leu Lys Asn Ile Phe Ile Ser Lys
 145 150 155 160
 His Ser Ser Glu Glu Ser Gly Tyr Ala Ser Val Ala Gly Gln Ser Leu
 165 170 175
 Pro Gly Pro Met Val Asp Gln Ser Pro Ser Val Ser Thr Ser Phe Gly
 180 185 190
 Leu Ser Ala Met Ser Pro Thr Lys Ala Ala Val Asp Ser Leu Met Thr
 195 200 205
 Ile Gly Gln Ser Leu Leu Gln Gly Thr Leu Gln Pro Pro Ala Gly Pro
 210 215 220
 Glu Glu Pro Thr Leu Ala Gly Gly Gly Arg His Pro Gly Val Ala Glu
 225 230 235 240
 Val Lys Thr Glu Met Met Gln Val Asp Glu Val Pro Ser Gln Asp Ser
 245 250 255
 Pro Gly Ala Ala Glu Ser Ser Ile Ser Gly Gly Met Gly Asp Lys Val
 260 265 270
 Glu Glu Arg Gly Lys Glu Gly Pro Gly Thr Pro Thr Arg Ser Ser Val
 275 280 285
 Ile Thr Ser Ala Arg Glu Leu His Tyr Gly Arg Glu Glu Ser Ala Glu
 290 295 300
 Gln Val Pro Pro Pro Ala Glu Ala Gly Gln Ala Pro Thr Gly Arg Pro
 305 310 315 320
 Glu His Pro Ala Pro Pro Pro Glu Lys His Leu Gly Ile Tyr Ser Val
 325 330 335
 Leu Pro Asn His Lys Ala Asp Ala Val Leu Ser Met Pro Ser Ser Val
 340 345 350
 Thr Ser Gly Leu His Val Gln Pro Ala Leu Ala Val Ser Met Asp Phe
 355 360 365
 Ser Thr Tyr Gly Gly Leu Leu Pro Gln Gly Phe Ile Gln Arg Glu Leu
 370 375 380
 Phe Ser Lys Leu Gly Glu Leu Ala Val Gly Met Lys Ser Glu Ser Arg
 385 390 395 400
 Thr Ile Gly Glu Gln Cys Ser Val Cys Gly Val Glu Leu Pro Asp Asn

34/299

405					410					415					
Glu	Ala	Val	Glu	Gln	His	Arg	Lys	Leu	His	Ser	Gly	Met	Lys	Thr	Tyr
			420					425					430		
Gly	Cys	Glu	Leu	Cys	Gly	Lys	Arg	Phe	Leu	Asp	Ser	Leu	Arg	Leu	Arg
		435					440					445			
Met	His	Leu	Leu	Ala	His	Ser	Ala	Ile	Glu	Thr	Gln	Ser	Ser	Ser	Ser
		450					455					460			
Glu	Glu	Ile	Val	Pro	Ser	Pro	Pro	Ser	Pro	Pro	Pro	Leu	Pro	Arg	Ile
465							470					475			480
Tyr	Lys	Pro	Cys	Phe	Val	Cys	Gln	Asp	Lys	Ser	Ser	Gly	Tyr	His	Tyr
				485					490					495	
Gly	Val	Ser	Ala	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Ile
			500					505					510		
Gln	Lys	Asn	Met	Val	Tyr	Thr	Cys	His	Arg	Asp	Lys	Asn	Cys	Ile	Ile
			515					520					525		
Asn	Lys	Val	Thr	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Leu	Gln	Lys	Cys
		530					535					540			
Phe	Glu	Val	Gly	Met	Ser	Lys	Glu	Ser	Val	Arg	Asn	Asp	Arg	Asn	Lys
545							550					555			560
Lys	Lys	Lys	Glu	Val	Pro	Lys	Pro	Glu	Cys	Ser	Glu	Ser	Tyr	Thr	Leu
				565					570					575	
Thr	Pro	Glu	Val	Gly	Glu	Leu	Ile	Glu	Lys	Val	Arg	Lys	Ala	His	Gln
			580					585					590		
Glu	Thr	Phe	Pro	Ala	Leu	Cys	Gln	Leu	Gly	Lys	Tyr	Thr	Thr	Asn	Asn
		595					600					605			
Ser	Ser	Glu	Gln	Arg	Val	Ser	Leu	Asp	Ile	Asp	Leu	Trp	Asp	Lys	Phe
		610					615					620			
Ser	Glu	Leu	Ser	Thr	Lys	Cys	Ile	Ile	Lys	Thr	Val	Glu	Phe	Ala	Lys
625							630					635			640
Gln	Leu	Pro	Gly	Phe	Thr	Thr	Leu	Thr	Ile	Ala	Asp	Gln	Ile	Thr	Leu
				645					650					655	
Leu	Lys	Ala	Ala	Cys	Leu	Asp	Ile	Leu	Ile	Leu	Arg	Ile	Cys	Thr	Arg
			660					665					670		
Tyr	Thr	Pro	Glu	Gln	Asp	Thr	Met	Thr	Phe	Ser	Asp	Gly	Leu	Thr	Leu
		675					680					685			
Asn	Arg	Thr	Gln	Met	His	Met	Ala	Gly	Phe	Gly	Pro	Leu	Thr	Asp	Leu
		690					695					700			
Val	Phe	Ala	Phe	Ala	Asn	Gln	Leu	Leu	Pro	Leu	Glu	Met	Asp	Asp	Ala
705							710					715			720

35/299

Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu Ile Cys Gly Asp Arg Gln
 725 730 735
 Asp Leu Glu Gln Pro Asp Arg Val Asp Met Leu Gln Glu Pro Leu Leu
 740 745 750
 Glu Ala Leu Lys Val Tyr Val Arg Lys Arg Arg Pro Ser Arg Pro His
 755 760 765
 Met Phe Pro Lys Met Leu Met Lys Ile Thr Asp Leu Arg Ser Ile Ser
 770 775 780
 Ala Lys Gly Ala Glu Arg Val Ile Thr Leu Lys Met Glu Ile Pro Gly
 785 790 795 800
 Ser Met Pro Pro Leu Ile Gln Glu Met Leu Glu Asn Ser Glu Gly Leu
 805 810 815
 Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly Gly Arg Asp Gly Gly Gly
 820 825 830
 Leu Ala Pro Pro Pro Gly Ser Cys Ser Pro Ser Leu Ser Pro Ser Ser
 835 840 845
 Asn Arg Ser Ser Pro Ala Thr His Ser Pro
 850 855

<210> 53
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 53
 Met Ala Ser Asn Ser Ser Ser Cys Pro Thr Pro Gly Gly Gly His Leu
 1 5 10 15
 Asn Gly Tyr Pro Val Pro Pro Tyr Ala Phe Phe Phe Pro Pro Met Leu
 20 25 30
 Gly Gly Leu Ser Pro Pro Gly Ala Leu Thr Thr Leu Gln His Gln Leu
 35 40 45
 Pro Val Ser Gly Tyr Ser Thr Pro Ser Pro Ala Thr Gly Ala Lys Ala
 50 55 60
 Phe Val Cys Asp Gln Cys Gly Ala Gln Phe Ser Lys Glu Asp Ala Leu
 65 70 75 80
 Glu Thr His Arg Gln Thr His Thr Gly Thr Asp Met Ala Val Phe Cys
 85 90 95
 Leu Leu Cys Gly Lys Arg Phe Gln Ala Gln Ser Ala Leu Gln Gln His
 100 105 110
 Met Glu Val His Ala Gly Val Arg Ser Tyr Ile Cys Ser Glu Cys Asn
 115 120 125

36/299

Arg Thr Phe Pro Ser His Thr Ala Leu Lys Arg His Leu Arg Ser His
 130 135 140
 Thr Gly Asp His Pro Tyr Glu Cys Glu Phe Cys Gly Ser Cys Phe Arg
 145 150 155 160
 Asp Glu Ser Thr Leu Lys Ser His Lys Arg Ile His Thr Gly Glu Lys
 165 170 175
 Pro Tyr Glu Cys Asn Gly Cys Asp Lys Lys Phe Ser Leu Lys His Gln
 180 185 190
 Leu Glu Thr His Tyr Arg Val His Thr Gly Glu Lys Pro Phe Glu Cys
 195 200 205
 Lys Leu Cys His Gln Arg Ser Arg Asp Tyr Ser Ala Met Ile Lys His
 210 215 220
 Leu Arg Thr His Asn Gly Ala Ser Pro Tyr Gln Cys Thr Ile Cys Thr
 225 230 235 240
 Glu Tyr Cys Pro Ser Leu Ser Ser Met Gln Lys His Met Lys Gly His
 245 250 255
 Lys Pro Glu Glu Ile Pro Pro Asp Trp Arg Ile Glu Lys Thr Tyr Leu
 260 265 270
 Tyr Leu Cys Tyr Val
 275

<210> 54
 <211> 2311
 <212> PRT
 <213> Homo sapiens

<400> 54
 Met Ala His Ser Cys Arg Trp Arg Phe Pro Ala Arg Pro Gly Thr Thr
 1 5 10 15
 Gly Gly Gly Gly Gly Gly Gly Arg Arg Gly Leu Gly Gly Gly Pro Arg
 20 25 30
 Gln Arg Val Pro Ala Leu Leu Leu Pro Pro Gly Pro Pro Val Gly Gly
 35 40 45
 Gly Gly Pro Gly Ala Pro Pro Ser Pro Pro Ala Val Ala Ala Ala Ala
 50 55 60
 Ala Ala Ala Gly Ser Ser Gly Ala Gly Val Pro Gly Gly Ala Ala Ala
 65 70 75 80
 Ala Ser Ala Ala Ser Ser Ser Ser Ala Ser Ser Ser Ser Ser Ser
 85 90 95
 Ser Ser Ala Ser Ser Gly Pro Ala Leu Leu Arg Val Gly Pro Gly Phe
 100 105 110

37/299

Asp Ala Ala Leu Gln Val Ser Ala Ala Ile Gly Thr Asn Leu Arg Arg
 115 120 125
 Phe Arg Ala Val Phe Gly Glu Ser Gly Gly Gly Gly Gly Ser Gly Glu
 130 135 140
 Leu Thr Thr Gln Ile Pro Cys Ser Trp Arg Thr Lys Gly His Ile His
 145 150 155 160
 Asp Lys Lys Thr Glu Pro Phe Arg Leu Leu Ala Trp Ser Trp Cys Leu
 165 170 175
 Asn Asp Glu Gln Phe Leu Gly Phe Gly Ser Asp Glu Glu Val Arg Val
 180 185 190
 Arg Ser Pro Thr Arg Ser Pro Ser Val Lys Thr Ser Pro Arg Lys Pro
 195 200 205
 Arg Gly Arg Pro Arg Ser Gly Ser Asp Arg Asn Ser Ala Ile Leu Ser
 210 215 220
 Asp Pro Ser Val Phe Ser Pro Leu Asn Lys Ser Glu Thr Lys Ser Gly
 225 230 235 240
 Asp Lys Ile Lys Lys Lys Asp Ser Lys Ser Ile Glu Lys Lys Arg Gly
 245 250 255
 Arg Pro Pro Thr Phe Pro Gly Val Lys Ile Lys Ile Thr His Gly Lys
 260 265 270
 Asp Ile Ser Glu Leu Pro Lys Gly Asn Lys Glu Asp Ser Leu Lys Lys
 275 280 285
 Ile Lys Arg Thr Pro Ser Ala Thr Phe Gln Gln Ala Thr Lys Ile Lys
 290 295 300
 Lys Leu Arg Ala Gly Lys Leu Ser Pro Leu Lys Ser Lys Phe Lys Thr
 305 310 315 320
 Gly Lys Leu Gln Ile Gly Arg Lys Gly Val Gln Ile Val Arg Arg Arg
 325 330 335
 Gly Arg Pro Pro Ser Thr Glu Arg Ile Lys Thr Pro Ser Gly Leu Leu
 340 345 350
 Ile Asn Ser Glu Leu Glu Lys Pro Gln Lys Val Arg Lys Asp Lys Glu
 355 360 365
 Gly Thr Pro Pro Leu Thr Lys Glu Asp Lys Thr Val Val Arg Gln Ser
 370 375 380
 Pro Arg Arg Ile Lys Pro Val Arg Ile Ile Pro Ser Ser Lys Arg Thr
 385 390 395 400
 Asp Ala Thr Ile Ala Lys Gln Leu Leu Gln Arg Ala Lys Lys Gly Ala
 405 410 415

38/299

Gln Lys Lys Ile Glu Lys Glu Ala Ala Gln Leu Gln Gly Arg Lys Val
 420 425 430
 Lys Thr Gln Val Lys Asn Ile Arg Gln Phe Ile Met Pro Val Val Ser
 435 440 445
 Ala Ile Ser Ser Arg Ile Ile Lys Thr Pro Arg Arg Phe Ile Glu Asp
 450 455 460
 Glu Asp Tyr Asp Pro Pro Ile Lys Ile Ala Arg Leu Glu Ser Thr Pro
 465 470 475 480
 Asn Ser Arg Phe Ser Ala Pro Ser Cys Gly Ser Ser Glu Lys Ser Ser
 485 490 495
 Ala Ala Ser Gln His Ser Ser Gln Met Ser Ser Asp Ser Ser Arg Ser
 500 505 510
 Ser Ser Pro Ser Val Asp Thr Ser Thr Asp Ser Gln Ala Ser Glu Glu
 515 520 525
 Ile Gln Val Leu Pro Glu Glu Arg Ser Asp Thr Pro Glu Val His Pro
 530 535 540
 Pro Leu Pro Ile Ser Gln Ser Pro Glu Asn Glu Ser Asn Asp Arg Arg
 545 550 555 560
 Ser Arg Arg Tyr Ser Val Ser Glu Arg Ser Phe Gly Ser Arg Thr Thr
 565 570 575
 Lys Lys Leu Ser Thr Leu Gln Ser Ala Pro Gln Gln Gln Thr Ser Ser
 580 585 590
 Ser Pro Pro Pro Pro Leu Leu Thr Pro Pro Pro Pro Leu Gln Pro Ala
 595 600 605
 Ser Ser Ile Ser Asp His Thr Pro Trp Leu Met Pro Pro Thr Ile Pro
 610 615 620
 Phe Gly Leu Cys Ser Asn Asn Pro Leu Thr Ser Pro Phe Leu Pro Ala
 625 630 635 640
 Ser Thr Ala Pro Met Gln Gly Lys Arg Lys Ser Ile Leu Arg Glu Pro
 645 650 655
 Thr Phe Arg Trp Thr Ser Leu Lys His Ser Arg Ser Glu Pro Gln Tyr
 660 665 670
 Phe Ser Ser Ala Lys Tyr Ala Lys Glu Gly Leu Ile Arg Lys Pro Ile
 675 680 685
 Phe Asp Asn Phe Arg Pro Pro Pro Leu Thr Pro Glu Asp Val Gly Phe
 690 695 700
 Ala Ser Gly Phe Ser Ala Ser Gly Thr Ala Ala Ser Ala Arg Leu Phe
 705 710 715 720
 Ser Pro Leu His Ser Gly Thr Arg Phe Asp Met His Lys Arg Ser Pro

39/299

725										730				735			
Leu	Leu	Arg	Ala	Pro	Arg	Phe	Thr	Pro	Ser	Glu	Ala	His	Ser	Arg	Ile		
740								745				750					
Phe	Glu	Ser	Val	Thr	Leu	Pro	Ser	Asn	Arg	Thr	Ser	Ala	Gly	Thr	Ser		
755								760				765					
Ser	Ser	Gly	Val	Ser	Asn	Arg	Lys	Arg	Lys	Arg	Lys	Val	Phe	Ser	Pro		
770								775				780					
Ile	Arg	Ser	Glu	Pro	Arg	Ser	Pro	Ser	His	Ser	Met	Arg	Thr	Arg	Ser		
785												795					
Gly	Arg	Leu	Ser	Ser	Ser	Glu	Leu	Ser	Pro	Leu	Thr	Pro	Pro	Ser	Ser		
				805								810					
Val	Ser	Ser	Ser	Leu	Ser	Ile	Ser	Val	Ser	Pro	Leu	Ala	Thr	Ser	Ala		
				820								825					
Leu	Asn	Pro	Thr	Phe	Thr	Phe	Pro	Ser	His	Ser	Leu	Thr	Gln	Ser	Gly		
835								840				845					
Glu	Ser	Ala	Glu	Lys	Asn	Gln	Arg	Pro	Arg	Lys	Gln	Thr	Ser	Ala	Pro		
850								855				860					
Ala	Glu	Pro	Phe	Ser	Ser	Ser	Ser	Pro	Thr	Pro	Leu	Phe	Pro	Trp	Phe		
865												875					
Thr	Pro	Gly	Ser	Gln	Thr	Glu	Arg	Gly	Arg	Asn	Lys	Asp	Lys	Ala	Pro		
				885								890					
Glu	Glu	Leu	Ser	Lys	Asp	Arg	Asp	Ala	Asp	Lys	Ser	Val	Glu	Lys	Asp		
				900				905				910					
Lys	Ser	Arg	Glu	Arg	Asp	Arg	Glu	Arg	Glu	Lys	Glu	Asn	Lys	Arg	Glu		
915								920				925					
Ser	Arg	Lys	Glu	Lys	Arg	Lys	Lys	Gly	Ser	Glu	Ile	Gln	Ser	Ser	Ser		
930								935				940					
Ala	Leu	Tyr	Pro	Val	Gly	Arg	Val	Ser	Lys	Glu	Lys	Val	Val	Gly	Glu		
945								950				955					
Asp	Val	Ala	Thr	Ser	Ser	Ser	Ala	Lys	Lys	Ala	Thr	Gly	Arg	Lys	Lys		
				965								970					
Ser	Ser	Ser	His	Asp	Ser	Gly	Thr	Asp	Ile	Thr	Ser	Val	Thr	Leu	Gly		
				980								985					
Asp	Thr	Thr	Ala	Val	Lys	Thr	Lys	Ile	Leu	Ile	Lys	Lys	Gly	Arg	Gly		
995								1000				1005					
Asn	Leu	Glu	Lys	Thr	Asn	Leu	Asp	Leu	Gly	Pro	Thr	Ala	Pro	Ser	Leu		
1010								1015				1020					
Glu	Lys	Glu	Lys	Thr	Leu	Cys	Leu	Ser	Thr	Pro	Ser	Ser	Ser	Thr	Val		
1025								1030				1035					
1040																	

40/299

Lys His Ser Thr Ser Ser Ile Gly Ser Met Leu Ala Gln Ala Asp Lys
 1045 1050 1055
 Leu Pro Met Thr Asp Lys Arg Val Ala Ser Leu Leu Lys Lys Ala Lys
 1060 1065 1070
 Ala Gln Leu Cys Lys Ile Glu Lys Ser Lys Ser Leu Lys Gln Thr Asp
 1075 1080 1085
 Gln Pro Lys Ala Gln Gly Gln Glu Ser Asp Ser Ser Glu Thr Ser Val
 1090 1095 1100
 Arg Gly Pro Arg Ile Lys His Val Cys Arg Arg Ala Ala Val Ala Leu
 1105 1110 1115 1120
 Gly Arg Lys Arg Ala Val Phe Pro Asp Asp Met Pro Thr Leu Ser Ala
 1125 1130 1135
 Leu Pro Trp Glu Glu Arg Glu Lys Ile Leu Phe Ser Met Gly Asn Asp
 1140 1145 1150
 Asp Lys Ser Ser Ile Ala Gly Ser Glu Asp Ala Glu Pro Leu Ala Pro
 1155 1160 1165
 Pro Ile Lys Pro Ile Lys Pro Val Thr Arg Asn Lys Ala Pro Gln Glu
 1170 1175 1180
 Pro Pro Val Lys Lys Gly Arg Arg Ser Arg Arg Cys Gly Gln Cys Pro
 1185 1190 1195 1200
 Gly Cys Gln Val Pro Glu Asp Cys Gly Val Cys Thr Asn Cys Leu Asp
 1205 1210 1215
 Lys Pro Lys Phe Gly Gly Arg Asn Ile Lys Lys Gln Cys Cys Lys Met
 1220 1225 1230
 Arg Lys Cys Gln Asn Leu Gln Trp Met Pro Ser Lys Ala Tyr Leu Gln
 1235 1240 1245
 Lys Gln Ala Lys Ala Val Lys Lys Lys Glu Lys Lys Ser Lys Thr Ser
 1250 1255 1260
 Glu Lys Lys Asp Ser Lys Glu Ser Ser Val Val Lys Asn Val Val Asp
 1265 1270 1275 1280
 Ser Ser Gln Lys Pro Thr Pro Ser Ala Arg Glu Asp Pro Ala Pro Lys
 1285 1290 1295
 Lys Ser Ser Ser Glu Pro Pro Pro Arg Lys Pro Val Glu Glu Lys Ser
 1300 1305 1310
 Glu Glu Gly Asn Val Ser Ala Pro Gly Pro Glu Ser Lys Gln Ala Thr
 1315 1320 1325
 Thr Pro Ala Ser Arg Lys Ser Ser Lys Gln Val Ser Gln Pro Ala Leu
 1330 1335 1340

41/299

Val Ile Pro Pro Gln Pro Pro Thr Thr Gly Pro Pro Arg Lys Glu Val
 1345 1350 1355 1360
 Pro Lys Thr Thr Pro Ser Glu Pro Lys Lys Lys Gln Pro Pro Pro Pro
 1365 1370 1375
 Glu Ser Gly Pro Glu Gln Ser Lys Gln Lys Lys Val Ala Pro Arg Pro
 1380 1385 1390
 Ser Ile Pro Val Lys Gln Lys Pro Lys Glu Lys Glu Lys Pro Pro Pro
 1395 1400 1405
 Val Asn Lys Gln Glu Asn Ala Gly Thr Leu Asn Ile Phe Ser Thr Leu
 1410 1415 1420
 Ser Asn Gly Asn Ser Ser Lys Gln Lys Ile Pro Ala Asp Gly Val His
 1425 1430 1435 1440
 Arg Ile Arg Val Asp Phe Lys Gln Thr Tyr Ser Asn Glu Val His Cys
 1445 1450 1455
 Val Glu Glu Ile Leu Lys Glu Met Thr His Ser Trp Pro Pro Pro Leu
 1460 1465 1470
 Thr Ala Ile His Thr Pro Ser Thr Ala Glu Pro Ser Lys Phe Pro Phe
 1475 1480 1485
 Pro Thr Lys Asp Ser Gln His Val Ser Ser Val Thr Gln Asn Gln Lys
 1490 1495 1500
 Gln Tyr Asp Thr Ser Ser Lys Thr His Ser Asn Ser Gln Gln Gly Thr
 1505 1510 1515 1520
 Ser Ser Met Leu Glu Asp Asp Leu Gln Leu Ser Asp Ser Glu Asp Ser
 1525 1530 1535
 Asp Ser Glu Gln Thr Pro Glu Lys Pro Pro Ser Ser Ser Ala Pro Pro
 1540 1545 1550
 Ser Ala Pro Gln Ser Leu Pro Glu Pro Val Ala Ser Ala His Ser Ser
 1555 1560 1565
 Ser Ala Glu Ser Glu Ser Thr Ser Asp Ser Asp Ser Ser Ser Asp Ser
 1570 1575 1580
 Glu Ser Glu Ser Ser Ser Ser Asp Ser Glu Glu Asn Glu Pro Leu Glu
 1585 1590 1595 1600
 Thr Pro Ala Pro Glu Pro Glu Pro Pro Thr Thr Asn Lys Trp Gln Leu
 1605 1610 1615
 Asp Asn Trp Leu Thr Lys Val Ser Ser Gln Leu Arg His Gln Arg Ala
 1620 1625 1630
 Pro Gly Ala Gln Ser Pro His Gly Gly Thr Gln Arg Val Arg Ala Ala
 1635 1640 1645
 Ala Thr Val Pro Arg Val Arg Ser Ile Leu Asn Pro Lys Ile Leu Pro

42/299

1650	1655	1660
Leu Lys Ala Pro Ala Lys Pro Pro Arg Pro Pro Glu Ala Pro His Pro		
1665	1670	1675 1680
Gly Lys Arg Ser Cys Gln Lys Ser Pro Ala Gln Gln Glu Pro Pro Gln		
1685	1690	1695
Arg Gln Thr Val Gly Thr Lys Gln Pro Lys Lys Pro Val Lys Ala Ser		
1700	1705	1710
Ala Arg Ala Gly Ser Arg Thr Ser Leu Gln Gly Glu Arg Glu Pro Gly		
1715	1720	1725
Leu Leu Pro Tyr Gly Ser Arg Asp Gln Thr Ser Lys Asp Lys Pro Lys		
1730	1735	1740
Val Lys Thr Lys Gly Arg Pro Arg Ala Ala Ala Ser Asn Glu Pro Lys		
1745	1750	1755 1760
Pro Ala Val Pro Pro Ser Ser Glu Lys Lys Lys His Lys Ser Ser Leu		
1765	1770	1775
Pro Ala Pro Ser Lys Ala Leu Ser Gly Pro Glu Pro Ala Lys Asp Asn		
1780	1785	1790
Val Glu Asp Arg Thr Pro Glu His Phe Ala Leu Val Pro Leu Thr Glu		
1795	1800	1805
Ser Gln Gly Pro Pro His Ser Gly Ser Ser Ser Arg Thr Ser Gly Cys		
1810	1815	1820
Arg Gln Ala Val Val Val Gln Glu Asp Ser Arg Lys Asp Arg Leu Pro		
1825	1830	1835 1840
Leu Pro Leu Arg Asp Thr Lys Leu Leu Ser Pro Leu Arg Asp Thr Pro		
1845	1850	1855
Pro Pro Gln Ser Leu Met Val Lys Ile Thr Leu Asp Leu Leu Ser Arg		
1860	1865	1870
Ile Pro Gln Pro Pro Gly Lys Gly Ser Arg Gln Arg Lys Ala Glu Asp		
1875	1880	1885
Lys Gln Pro Pro Ala Gly Lys Lys His Ser Ser Glu Lys Arg Ser Ser		
1890	1895	1900
Asp Ser Ser Ser Lys Leu Ala Lys Lys Arg Lys Gly Glu Ala Glu Arg		
1905	1910	1915 1920
Asp Cys Asp Asn Lys Lys Ile Arg Leu Glu Lys Glu Ile Lys Ser Gln		
1925	1930	1935
Ser Ser Ser Ser Ser Ser Ser His Lys Glu Ser Ser Lys Thr Lys Pro		
1940	1945	1950
Ser Arg Pro Ser Ser Gln Ser Ser Lys Lys Glu Met Leu Pro Pro Pro		
1955	1960	1965

43/299

Pro Val Ser Ser Ser Ser Gln Lys Pro Ala Lys Pro Ala Leu Lys Arg
 1970 1975 1980
 Ser Arg Arg Glu Ala Asp Thr Cys Gly Gln Asp Pro Pro Lys Ser Ala
 1985 1990 1995 2000
 Ser Ser Thr Lys Ser Asn His Lys Asp Ser Ser Ile Pro Lys Gln Arg
 2005 2010 2015
 Arg Val Glu Gly Lys Gly Ser Arg Ser Ser Ser Glu His Lys Gly Ser
 2020 2025 2030
 Ser Gly Asp Thr Ala Asn Pro Phe Pro Val Pro Ser Leu Pro Asn Gly
 2035 2040 2045
 Asn Ser Lys Pro Gly Lys Pro Gln Val Lys Phe Asp Lys Gln Gln Ala
 2050 2055 2060
 Asp Leu His Met Arg Glu Glu Lys Lys Met Lys Gln Lys Ala Glu Leu
 2065 2070 2075 2080
 Met Thr Asp Arg Val Gly Lys Ala Phe Lys Tyr Leu Glu Ala Val Leu
 2085 2090 2095
 Ser Phe Ile Glu Cys Gly Ile Ala Thr Glu Ser Glu Ser Gln Ser Ser
 2100 2105 2110
 Lys Ser Ala Tyr Ser Val Tyr Ser Glu Thr Val Asp Leu Ile Lys Phe
 2115 2120 2125
 Ile Met Ser Leu Lys Ser Phe Ser Asp Ala Thr Ala Pro Thr Gln Glu
 2130 2135 2140
 Lys Ile Phe Ala Val Leu Cys Met Arg Cys Gln Ser Ile Leu Asn Met
 2145 2150 2155 2160
 Ala Met Phe Arg Cys Lys Lys Asp Ile Ala Ile Lys Tyr Ser Arg Thr
 2165 2170 2175
 Leu Asn Lys His Phe Glu Ser Ser Ser Lys Val Ala Gln Ala Pro Ser
 2180 2185 2190
 Pro Cys Ile Ala Arg Ser Thr Gly Thr Pro Ser Pro Leu Ser Pro Met
 2195 2200 2205
 Pro Ser Pro Ala Ser Ser Val Gly Ser Gln Ser Ser Ala Gly Ser Val
 2210 2215 2220
 Gly Ser Ser Gly Val Ala Ala Thr Ile Ser Thr Pro Val Thr Ile Gln
 2225 2230 2235 2240
 Asn Met Thr Ser Ser Tyr Val Thr Ile Thr Ser His Val Leu Thr Ala
 2245 2250 2255
 Phe Asp Leu Trp Glu Gln Ala Glu Ala Leu Thr Arg Lys Asn Lys Glu
 2260 2265 2270

44/299

Phe Phe Ala Arg Leu Ser Thr Asn Val Cys Thr Leu Ala Leu Asn Ser
 2275 2280 2285

Ser Leu Val Asp Leu Val His Tyr Thr Arg Gln Gly Phe Gln Gln Leu
 2290 2295 2300

Gln Glu Leu Thr Lys Thr Pro
 2305 2310

<210> 55
 <211> 6940
 <212> DNA
 <213> Homo sapiens

<400> 55
 taacatggcg cacagctgtc ggtggcgctt ccccgccga cccgggacca cggggggcgg 60
 cggcggcggg gggcgccggg gcctaggggg cggcccgcg caacgcgtcc cggccctgct 120
 gtttcccccc gggcccccg tccggcggtg cggccccgg gcgccccct cccccccggc 180
 tgtggcggcc gcggcgccgg cggcggggaag cagcgggggt ggggttccag ggggagcggc 240
 cgccgcctca gcagcctcct cgtcgtccgc ctcgctctcg tcttcgtcat cgtcctcagc 300
 ctcttcaggg ccggccctgc tccgggtggg cccgggcttc gacgcggcgc tgcaggtctc 360
 ggccgccatc ggcaccaacc tgcgcgggtt ccgggccgtg tttggggaga gcggcggggg 420
 aggcggcagc ggagagctaa caacacagat cccatgtagt tggagaacca aaggccacat 480
 acatgacaaa aagactgaac cgttcagggtt acttgcatgg agttgggtgct taaatgatga 540
 gcaattctta ggttttggct cagatgaaga agtcagagtg cgaagtccca caaggtctcc 600
 ttcagttaaa actagtcctc gaaaacctcg tgggagacct agaagtggct ctgaccgaaa 660
 ttcagctatc ctctcagatc catctgtgtt tccccctota aataaatcag agaccaaatc 720
 tggagataag atcaagaaga aagattctaa aagtatagaa aagaagagag gaagacctcc 780
 caccttccct ggagtaaaaa tcaaaataac acatggaaaag gacatttcag agttacaaaa 840
 gggaaacaaa gaagatagcc tgaaaaaat taaaaggaca cttctgtcta cgtttcagca 900
 agccacaaaag attaaaaaat taagagcagg taaactctct cctctcaagt ctaagtttaa 960
 gacagggaag cttcaaatag gaaggaaggg ggtacaaatt gtacgacgga gaggaaggcc 1020
 tccatcaaca gaaaggataa agaccccttc ggggtctctc attaatcttg aactggaaaa 1080
 gccccagaaa gtccggaaa acaaggaagg aacacctcca cttacaaaag aagataagac 1140
 agttgtcaga caaagccctc gaaggattaa gccagttagg attattcctt cttcaaaaag 1200
 gacagatgca accattgcta agcaactctt acagagggca aaaaaggggg ctcaaaaaga 1260
 aattgaaaaa gaagcagctc agctgcaggg aagaaagggt aagacacagg tcaaaaatat 1320
 tcgacagttc atcatgcctg ttgtcagtg cgtctctctg cggatcatta agacccctcg 1380
 gcggtttata gaggatgagg attatgacct tccaattaaa attgcccgat tagagtctac 1440
 accgaatagt agattcagtg ccccgctctg cctgactctt gaaaaatcaa gtgcagcttc 1500
 tcagcaactc tctcaaatgt cttcagactc ctctcgatct agtagcccca gtgttgatac 1560
 ctccacagac tctcaggctt ctgaggagat tcaggtaact cctgaggagc ggagcgatac 1620
 ccctgaagtt catcctccac tgcccatttc ccagtcccca gaaaatgaga gtaatgatag 1680
 gagaagcaga aggtattcag tgtcggagag aagttttgga tctagaacga cgaaaaaatt 1740
 atcaactcta caaagtgcc cccagcagca gacctctctg tctccacctc cacctctgct 1800
 gactccaccg ccaccactgc agccagcctc cagtatctct gaccacacac cttggcttat 1860
 gcctccaaca atcccccttg gcttatgtc caacaatccc cttacttcac cctttttgcc 1920
 tgcttccact gctcctatgc aagggaagcg aaaatctatt ttgcgagaac cgacatttag 1980
 gtggacttct ttaaagcatt ctaggtcaga gccacaatac ttttcctcag caaagtatgc 2040
 caaagaaggt cttattcgca aaccaatatt tgataatttc cgacccctc cactaactcc 2100
 cgaggacgtt ggctttgcat ctggtttttc tgcattctgg accgctgctt cagcccgatt 2160
 gttttcgcca ctccattctg gaacaaggtt tgatatgcac aaaaggagcc ctcttctgag 2220
 agtccaaga tttactccaa gtgaggctca ctctagaata tttgagctct taaccttgcc 2280
 tagtaatcga acttctgctg gaacatcttc ttcaggagta tccaatagaa aaaggaaaag 2340
 aaaagtgttt agtctattc gatctgaacc aagatctctt tctcactcca tgaggacaag 2400
 aagtgaagg cttagtagtt ctgagctctc acctctcacc ccccgctctt ctgtctcttc 2460
 ctcgtaagc atttctgtta gtctctctgc cctagtgcc ttaaacccaa cttttacttt 2520

tccttctcat	tccctgactc	agtctgggga	atctgcagag	aaaaatcaga	gaccaaggaa	2580
gcagactagt	gctccggcag	agccattttc	atcaagtagt	cctaactcctc	tcttcccttg	2640
gtttacccca	ggctctcaga	ctgaaagagg	gagaaataaa	gacaaggccc	ccgaggagct	2700
gtccaaagat	cgagatgctg	acaagagcgt	ggagaaggac	aagagtagag	agagagaccg	2760
ggagagagaa	aaggagaata	agcgggagtc	aaggaaaagag	aaaaggaaaa	agggatcaga	2820
aattcagagt	agttctgctt	tgtatcctgt	gggtagggtt	tccaaagaga	aggttgttg	2880
tgaagatggt	gccacttcat	cttctgccaa	aaaagcaaca	gggcggaaga	agtcttcatc	2940
acatgattct	gggactgata	ttactttctgt	gactcttggg	gatacaacag	ctgtcaaaac	3000
caaaatactt	ataaagaaag	ggagaggaaa	tctggaaaaa	accaacttgg	acctcggccc	3060
aactgcccga	tccctggaga	aggagaaaaa	cctctgcctt	tccactcctt	catctagcac	3120
tgttaaacat	tccacttctt	ccataggctc	catgttggct	caggcagaca	agcttccaat	3180
gactgacaag	agggttgcca	gcctcctaaa	aaaggccaaa	gctcagctct	gcaagattga	3240
gaagagtaag	agtcttaaac	aaaccgacca	gccccaaagca	cagggtcaag	aaagtgactc	3300
atcagagacc	tctgtgcgag	gaccccggat	taaacatgtc	tgacagaagag	cagctgttgc	3360
ccttgccga	aaacgagctg	tgtttcctga	tgacatgccc	accctgagtg	ccttaccatg	3420
ggaagaacga	gaaaagattt	tgttttccat	ggggaatgat	gacaagtcat	caattgctgg	3480
ctcagaagat	gctgaacctc	ttgctccacc	catcaaacca	attaaacctg	tcactagaaa	3540
caaggctccc	caggaacctc	cagtaaagaa	aggacgtcga	tcgaggcggt	gtgggcagtg	3600
tcccggctgc	caggtgcctg	aggactgtgg	tgtttgtact	aattgcttag	ataagcccaa	3660
gtttgggtgt	cgcaatataa	agaagcagtg	ctgcaagatg	agaaaatgtc	agaatctaca	3720
atggatgctt	tccaaagcct	acctgcagaa	gcaagctaaa	gctgtgaaaa	agaaagagaa	3780
aaagtctaag	accagtgaag	agaaaagacag	caaagagagc	agtgttgtga	agaacgtggt	3840
ggactctagt	cagaaacctc	ccccatcagc	aagagaggat	cctgccccaa	agaaaagcag	3900
tagtgagcct	cctccacgaa	agcccgctga	ggaaaagagt	gaagaagggg	atgtctcggc	3960
ccttgggctt	gaatccaaac	aggccaccac	tccagcttcc	aggaagtcaa	gcaagcaggt	4020
ctcccagcca	gcaactggtc	tcccgcctca	gccacctact	acaggaccgc	caagaaaaga	4080
agttcccaaa	accactccta	gtgagcccaa	gaaaaagcag	cctccaccac	cagaatcagg	4140
tccagagcag	agcaaacaga	aaaaagtggc	tccccgcccc	agtatccctg	taaaacaaaa	4200
acccaaagaa	aaggaaaaac	cacctccggt	caataagcag	gagaatgcag	gcactttgaa	4260
catcttcagc	actctctcca	atggcaatag	ttctaagcaa	aaaattccag	cagatggagt	4320
ccacagatc	agagtggact	ttaagcagac	ctactccaat	gaagtccatt	gtgttgaaga	4380
gattctgaag	gaaatgacct	attcatggcc	gctccctttg	acagcaatac	atcgccttag	4440
tacagctgag	ccatccaagt	ttcctttccc	tacaaaaggac	tctcagcatg	tcagttctgt	4500
aacccaaaac	caaaaacaat	atgatacatc	ttcaaaaact	cactcaaatt	ctcagcaagg	4560
aacgtcatcc	atgctcgaag	acgaccttca	gctcagtgac	agtgaggaca	gtgacagtga	4620
acaaacccca	gagaagcctc	cctcctcatc	tgcacctcca	agtgtctccac	agtccttctc	4680
agaaccagtg	gcatcagcac	attccagcag	tgacagatca	gaaagcacca	gtgactcaga	4740
cagttcctca	gactcagaga	gcgagagcag	ttcaagtga	agcgaagaaa	atgagccctt	4800
agaaacccca	gctccggagc	ctgagcctcc	aacaacaaac	aatggcgagc	tggaacaactg	4860
gctgcacaaa	gtcagcagcc	agctgcgcca	ccagagggcc	ccaggagcac	agagccccc	4920
cggcgccacc	cagagagtaa	gggcagcagc	gcagagtcca	cgagtacgga	gcattctgaa	4980
tccaaagatc	ctccccctaa	aagctccagc	aaagccccc	cgcccacccg	aagcccccca	5040
ccccggaaag	aggagctgtc	agaagtctcc	ggcacagcag	gagccccac	aaaggcaaac	5100
cgttggaaac	aaacaaccca	aaaaacctgt	caaggcctct	gcccgggcag	gttcacggac	5160
cagcctgcag	ggggaaaggg	agccagggct	tcttccctat	ggctcccag	accagacttc	5220
caaagacaag	cccaaggtga	agacgaaagg	acggccccc	gccgcagcaa	gcaacgaacc	5280
caagccagca	gtgccccctt	ccagtgcagaa	gaagaagcac	aagagctccc	tccctgcccc	5340
ctctaaggct	ctctcaggcc	cagaacccgc	gaaggacaat	gtggaggaca	ggaccctga	5400
gcactttgct	cttgttcccc	tgactgcagc	ccaggggcca	ccccacagt	gcagcagcag	5460
caggactagt	ggctgcccgc	aagccgtggg	ggtccaggag	gacagccgca	aagacagact	5520
cccattgcct	ttgagagaca	ccaagctgct	ctcaccgctc	agggacactc	ctccccaca	5580
aagcttgatg	gtgaagatca	ccctagacct	gctctctcgg	ataccccagc	ctcccgggaa	5640
ggggagccgc	cagaggaaag	cagaagataa	acagccgccc	gcagggaaga	agcacagctc	5700
tgagaagagg	agctcagaca	gctcaagcaa	gttggccaaa	aagagaaagg	gtgaagcaga	5760
aagagactgt	gataacaaga	aaatcagact	ggagaaggaa	atcaaatac	agtcactctt	5820
atcttcatcc	tcccacaaag	aatcttctaa	aacaaagccc	tccaggccct	cctcacagtc	5880
ctcaaagaag	gaaatgctcc	ccccgccacc	cgtgtcctcg	tcctcccaga	agccagccaa	5940
gcctgcactt	aagaggtcaa	ggcggaagc	agacacctgt	ggccaggacc	ctcccaaaag	6000

46/299

```

tgccagcagt accaagagca accacaaaga ctcttccatt cccaagcaga gaagagtaga 6060
ggggaagggc tccagaagct cctcggagca caagggttct tccggagata ctgcaaatac 6120
ttttccagtgc ctttctttgc caaatggtaa ctctaaacca gggaagcctc aagtgaagtt 6180
tgacaaacaa caagcagacc ttcacatgag ggaggaaaaa aagatgaagc agaaagcaga 6240
gttaatgacg gacaggggtg gaaaggcttt taagtacctg gaagccgtct tgtccttcat 6300
tgagtgcgga attgccacag agtctgaaag ccagtcattc aagtcagctt actctgtcta 6360
ctcagaaaact gtagatctca ttaaattcat aatgtcatta aaatccttct cagatgccac 6420
agcgccaaca caagagaaaa tatttctgtg tttatgcatg cgttgccagt ccattttgaa 6480
catggcgatg tttcgttgta aaaaagacat agcaataaag tattctcgtc ctcttaataa 6540
acacttcgag agttctttcca aagtcgccc aagcaccttct ccatgcattg caagaagcac 6600
aggcacacca tccccctctt ccccaatgcc ttctcctgcc agctccgtag ggtcccagtc 6660
aagtgtctggc agtgtgggga gcagtggggt ggctgccact atcagcacc cagtcacccat 6720
ccagaatatg acatcttctt atgtcaccat cacatcccat gttcttaccg cctttgacct 6780
ttgggaacag gcogaggccc tcacgaggaa gaataaagaa ttctttgctc ggctcagcac 6840
aaatgtgtgc accttggccc tcaacagcag tttgggtggac ctggtgcact atacacgaca 6900
gggttttcag cagctacaag aattaaccaa aacaccttaa 6940

```

<210> 56

<211> 277

<212> PRT

<213> Homo sapiens

<400> 56

```

Glu Asp Pro Ala Pro Lys Lys Ser Ser Ser Glu Pro Pro Pro Arg Lys
  1              5              10              15

Pro Val Glu Glu Lys Ser Glu Glu Gly Asn Val Ser Ala Pro Gly Pro
      20              25              30

Glu Ser Lys Gln Ala Thr Thr Pro Ala Ser Arg Lys Ser Ser Lys Gln
      35              40              45

Val Ser Gln Pro Ala Leu Val Ile Pro Pro Gln Pro Pro Thr Thr Gly
      50              55              60

Pro Pro Arg Lys Glu Val Pro Lys Thr Thr Pro Ser Glu Pro Lys Lys
      65              70              75              80

Lys Gln Pro Pro Pro Pro Glu Ser Gly Pro Glu Gln Ser Lys Gln Lys
      85              90              95

Lys Val Ala Pro Arg Pro Ser Ile Pro Val Lys Gln Lys Pro Lys Glu
      100             105             110

Lys Glu Lys Pro Pro Pro Val Asn Lys Gln Glu Asn Ala Gly Thr Leu
      115             120             125

Asn Ile Phe Ser Thr Leu Ser Asn Gly Asn Ser Ser Lys Gln Lys Ile
      130             135             140

Pro Ala Asp Gly Val His Arg Ile Arg Val Asp Phe Lys Glu Asp Cys
      145             150             155             160

Glu Ala Glu Asn Val Trp Glu Met Gly Gly Leu Gly Ile Leu Thr Ser
      165             170             175

Val Pro Ile Thr Pro Arg Val Val Cys Phe Leu Cys Ala Ser Ser Gly

```

47/299

180 185 190
 His Val Glu Thr Tyr Ser Asn Glu Val His Cys Val Glu Glu Ile Leu
 195 200 205
 Lys Glu Met Thr His Ser Trp Pro Pro Pro Leu Thr Ala Ile His Thr
 210 215 220
 Pro Ser Thr Ala Glu Pro Ser Lys Phe Pro Phe Pro Thr Lys Asp Ser
 225 230 235 240
 Gln His Val Ser Ser Val Thr Gln Asn Gln Lys Gln Tyr Asp Thr Ser
 245 250 255
 Ser Lys Thr His Ser Asn Ser Gln Gln Gly Thr Ser Ser Met Leu Glu
 260 265 270
 Asp Gln Leu Gln Leu
 275

<210> 57
 <211> 832
 <212> DNA
 <213> Homo sapiens

<400> 57
 gaggatcctg ccccaaagaa aagcagtagt gagcctcctc cacgaaagcc cgtcgaggaa 60
 aagagtgaag aagggaatgt ctcgggccct gggcctgaat ccaaacaggc caccactcca 120
 gcttccagga agtcaagcaa gcaggctctc cagccagcac tggatcatccc gcctcagcca 180
 cctactacag gaccgccaag aaaagaagtt cccaaaacca ctccctagtga gcccaagaaa 240
 aagcagcctc caccaccaga atcagggtcca gagcagagca aacagaaaaa agtgggtccc 300
 cgcccaagta tccctgtaaa acaaaaacca aaagaaaagg aaaaaccacc tccgggtcaat 360
 aagcaggaga atgcaggcac tttgaacatc ttcagcactc tctccaatgg caatagttct 420
 aagcaaaaaa ttccagcaga tggagtccac aggatcagag tggactttta ggaggattgt 480
 gaagcagaaa atgtgtggga gatgggaggc ttaggaatct tgacttctgt tcctataaca 540
 ccagggttg tttgctttct ctgtgccagt agtgggcatg tagagacctc ctccaatgaa 600
 gtccattgtg ttgaagagat tctgaaggaa atgaccatt catggccgcc tcctttgaca 660
 gcaatacata cgcctagtac agctgagcca tccaagtttc ctttccttac aaaggactct 720
 cagcatgtca gttctgtaac ccaaaaccaa aaacaatatg atacatcttc aaaaactcac 780
 tcaaattctc agcaaggaac gtcattcatg ctgaagacc agcttcagct ca 832

<210> 58
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 58
 Lys Gln Lys Lys Val Ala Pro Arg Pro Ser Ile Pro Val Lys Gln Lys
 1 5 10 15
 Pro Lys Glu Lys Gln Thr Tyr Ser Asn Glu Val His Cys Val Glu Glu
 20 25 30
 Ile Leu Lys Glu Met Thr His Ser Trp Pro Pro Pro Leu Thr Ala Ile
 35 40 45

48/299

His Thr Pro Ser Thr Ala Glu Pro Ser Lys Phe Pro Phe Pro Thr Lys
 50 55 60
 Asp Ser Gln His Val Ser Ser Val Thr Gln Asn Gln Lys Gln Tyr Asp
 65 70 75 80
 Thr Ser Ser Lys Thr His Ser Asn Ser Gln Gln Gly Thr Ser Ser Met
 85 90 95
 Leu Glu Asp Asp Leu Gln Leu Ser Asp Ser Glu Asp Ser Asp Ser Glu
 100 105 110
 Gln Thr Pro Glu Lys Pro Pro Ser Ser Ser Ala Pro Pro Ser Ala Pro
 115 120 125
 Gln Ser Leu Pro Glu Pro Val Ala Ser Ala His Ser Ser Ser Ala Glu
 130 135 140
 Ser Glu Ser Thr Ser Asp Ser Asp Ser Ser Ser Asp Ser Glu Ser Glu
 145 150 155 160
 Ser Ser Ser Ser

<210> 59
 <211> 495
 <212> DNA
 <213> Homo sapiens

<400> 59
 gcaaacacagaa aaaagtggct ccccgcccaa gtatccctgt aaaacaaaaa ccaaaagaaa 60
 agcagaccta ctccaatgaa gtccattgtg ttgaagagat tctgaaggaa atgacccatt 120
 catggccgcc tcctttgaca gcaatacata cgcttagtac agctgagcca tccaagtttc 180
 ctttccttac aaaggactct cagcatgtca gttctgtaac ccaaaaccaa aaacaatatg 240
 atacatcttc aaaaactcac tcaaattctc agcaaggaac gtcattccatg ctggaagacg 300
 accttcagct cagtgacagt gaggacagt acagtgaaca aaccccagag aagcctccct 360
 cctcatctgc acctccaagt gctccacagt cccttcacaga accagtggca tcagcacatt 420
 ccagcagtg agagtcagaa agcaccagt actcagacag ttcctcagac tcagagagcg 480
 agagcagttc aagtg 495

<210> 60
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 60
 Lys Gln Lys Lys Val Ala Pro Arg Pro Ser Ile Pro Val Lys Gln Lys
 1 5 10 15
 Pro Lys Glu Lys Glu Lys Pro Pro Pro Val Asn Lys Gln Glu Asn Ala
 20 25 30
 Gly Thr Leu Asn Ile Leu Ser Thr Leu Ser Asn Gly Asn Ser Ser Lys
 35 40 45
 Gln Lys Ile Pro Ala Asp Gly Val His Arg Ile Arg Val Asp Phe Lys
 50 55 60

49/299

Glu Asp Cys Glu Ala Glu Asn Val Trp Glu Met Gly Gly Leu Gly Ile
 65 70 75 80
 Leu Thr Ser Val Pro Ile Thr Pro Arg Val Val Cys Phe Leu Cys Ala
 85 90 95
 Ser Ser Gly His Val Glu Gln Thr Tyr Ser Asn Glu Val His Cys Val
 100 105 110
 Glu Glu Ile Leu Lys Glu Met Thr His Ser Trp Pro Pro Pro Leu Thr
 115 120 125
 Ala Ile His Thr Pro Ser Thr Ala Glu Pro Ser Lys Phe Pro Phe Pro
 130 135 140
 Thr Lys Asp Ser Gln His Val Ser Ser Val Thr Gln Asn Gln Lys Gln
 145 150 155 160
 Tyr Asp Thr Ser Ser Lys Thr His Ser Asn Ser Gln Gln Gly Thr Ser
 165 170 175
 Ser Met Leu Glu Asp Asp Leu Gln Leu Ser Asp Ser Glu Asp Ser Asp
 180 185 190
 Ser Glu Gln Thr Pro Glu Lys Pro Pro Ser Ser Ser Ala Pro Pro Ser
 195 200 205
 Ala Pro Gln Ser Leu Pro Glu Pro Val Ala Ser Ala His Ser Ser Ser
 210 215 220
 Ala Glu Ser Glu Ser Thr Ser Asp Ser Asp Ser Ser Ser Asp Ser Glu
 225 230 235 240
 Ser Glu Ser Ser Ser Ser
 245

<210> 61
 <211> 741
 <212> DNA
 <213> Homo sapiens

<400> 61
 gcaaacagaa aaaagtggct cccgcgccaa gtatccctgt aaaacaaaaa ccaaagagaa 60
 aggaaaaacc acctccggtc aataagcagg agaatgcagg cactttgaac atcctcagca 120
 ctctctccaa tggcaatagt tctaagcaaa aaattccagc agatggagtc cacaggatca 180
 gagtggactt taaggaggat tgtgaagcag aaaatgtgtg ggagatggga ggcttaggaa 240
 tcttgacttc tgttcctatc acaccagggt tggtttgctt tctctgtgcc agtagtgggc 300
 atgtagagca gacctactcc aatgaagtcc attgtgttga agagattctg aaggaaatga 360
 cccattcatg gccgcctcct ttgacagcaa tacatacgcc tagtacagct gagccatcca 420
 agtttccttt ccctacaaag gactctcagc atgtcagttc tgtaacccaa aacccaaaaac 480
 aatatgatac atcttcaaaa actcactcaa attctcagca aggaacgtca tccatgctcg 540
 aagacgacct tcagctcagt gacagtgagg acagtgcag tgaacaaacc ccagagaagc 600
 ctccctctctc atctgcacct ccaagtgtc cacagtccct tccagaacca gtggcatcag 660
 cacattccag cagtgcagag tcagaaagca ccagtgcact agacagttcc tcagactcag 720
 agagcgagag cagttcaagt g 741

<210> 62

<400> 62
000<210> 63
<211> 14255
<212> DNA
<213> Homo sapiens

<400> 63

gcggcgccg	cgccgggaag	cagcggggct	gggggtccag	ggggagcggc	cgccgcctca	60
gcagcctcct	cgctgtccgc	ctcgtcttcg	tcttcgtcat	cgctctcagc	ctcttcaggg	120
ccggccctgc	tccgggtggg	cccgggcttc	gacgcggcgc	tgcaggtctc	ggccgccatc	180
ggcaccaacc	tgcgccgggt	ccgggcccgtg	tttggggaga	gcggcggggg	aggcggcagc	240
ggagaggatg	agcaattctt	aggttttggc	tcagatgaag	aagtcagagt	gcgaagtccc	300
acaaggctct	cttcagttaa	aactagtcct	cgaaaacctc	gtgggagacc	tagaagtggc	360
tctgaccgaa	attcagctat	cctctcagat	ccatctgtgt	tttccctctc	aaataaatca	420
gagaccaaat	ctggagataa	gatcaagaag	aaagattcta	aaagtataga	aaagaagaga	480
ggaagacctc	ccaccttccc	tggagtaaaa	atcaaaaata	cacatggaaa	ggacatttca	540
gagttacca	agggaaacaa	agaagatagc	ctgaaaaaaa	ttaaaaggac	accttctgct	600
acgtttcagc	aagccacaaa	gattaaaaaa	ttaagagcag	gtaaactctc	tcctctcaag	660
tctaagttta	agacagggaa	gcttcaaata	ggaaggaagg	gggtacaaat	tgtacgacgg	720
agaggaaggc	ctccatcaac	agaaaggata	aagacccttt	cgggtctcct	cattaatctt	780
gaactggaaa	agccccagaa	agtcgggaaa	gacaagggaag	gaacacctcc	acttacaaaa	840
gaagataaga	cagttgtcag	acaaagccct	cgaaggatta	agccagttag	gattattcct	900
tcttcaaaaa	ggacagatgc	aaccattgct	aagcaactct	tacagagggc	aaaaaagggg	960
gctcaaaaga	aaattgaaaa	agaagcagct	cagctgcagg	gaagaaaggt	gaagacacag	1020
gtcaaaaata	ttcgacagtt	catcatgcct	gttgtcagtg	ctatctcctc	gcggatcatt	1080
aagacccttc	ggcgggttat	agaggatgag	gattatgacc	ctccaattaa	aattgcccca	1140
ttagagtcta	caccgaatag	tagattcagt	gccccgtcct	gtggatcttc	tgaaaaatca	1200
agtgcagctt	ctcagcactc	ctctcaaata	tcttcagact	cctctcgatc	tagtagcccc	1260
agtgttgata	cctccacaga	ctctcaggct	tctgaggaga	ttcaggtact	tcctgaggag	1320
cggagcgata	cccctgaagt	tcatcctcca	ctgcccattt	cccagtcccc	agaaaatgag	1380
agtaatgata	ggagaagcag	aaggattatca	gtgtcggaga	gaagtttttg	atctagaacg	1440
acgaaaaaat	tatcaactct	acaaagtgcc	ccccagcagg	agacctcttc	gtctccacct	1500
ccacctctgc	tgactccacc	gccaccactg	cagccagcct	ccagtatctc	tgaccacaca	1560
ccttggtcta	tgcctccaac	aatcccctta	gcataccat	ttttgcctgc	ttccactgct	1620
cctatgcaag	ggaagcgaaa	atctattttg	cgaagaccga	catttaggtg	gacttcttta	1680
aagcatttcta	ggtcagagcc	acaatacttt	tcctcagcaa	agtatgccaa	agaaggctct	1740
attcgcaaac	caatatttga	taatttccga	ccccctccac	taactcccga	ggacgttggc	1800
tttgcatctg	gtttttctgc	atctggtacc	gctgcttcag	cccagttggt	ttcgccactc	1860
cattctggaa	caagggttga	tatgcacaaa	aggagccctc	ttctgagagc	tcgaagattt	1920
actccaagtg	aggctcactc	tagaatattt	gagctgttaa	ccttgccctag	taatcgaaact	1980
tctgctggaa	catcttcttc	aggagtatcc	aatagaaaaa	ggaaaagaaa	agtgtttagt	2040
cctattcgat	ctgaaccaag	atctccttct	cactccatga	ggacaagaag	tggaaaggct	2100
agtagttctg	agctctcacc	tctcaccccc	ccgtcttctg	tctcttcttc	gttaagcatt	2160
tctgttagtc	ctcttgccac	tagtgcccta	aaccacaact	ttacttttcc	ttctcattcc	2220
ctgactcagt	ctggggaatc	tgcagagaaa	aatcagagac	caaggaagca	gactagtgtc	2280
ccggcagagc	catttttcac	aagtagtctc	actcctctct	tcccttggtt	tacccacagg	2340
tctcagactg	aaagagggag	aaataaagac	aaggcccccg	aggagctgtc	caaagatcga	2400
gatgctgaca	agagcgtgga	gaaggacaag	agtagagaga	gagaccggga	gagagaaaag	2460
gagaataaag	gggagtcaag	gaaagagaaa	aggaaaaagg	gatcagaaat	tcagagtagt	2520
tctgctttgt	atcctgtggg	taggggttcc	aaagagaagg	ttgttggtga	agatgttgcc	2580
acttcatctt	ctgccaaaaa	agcaacaggg	cggaaagaag	cttcatcaca	tgattctggg	2640
actgatatta	cttctgtgac	tcttggggat	acaacagctg	tcaaaaccaa	aatacttata	2700

aagaaagggga	gaggaaatct	ggaaaaaacc	aacttggacc	tgggccaac	tgcccatcc	2760
ctggagaagg	agaaaaccct	ctgcctttcc	actccttcat	ctagcactgt	taaacattcc	2820
acttctccca	taggtctccat	gttggctcag	gcagacaagc	ttccaatgac	tgacaagagg	2880
gttgccagcc	tcctaaaaaa	ggccaaagct	cagctctgca	agattgagaa	gagtaagagt	2940
cttaaaaaaa	ccgaccagcc	caaagcacag	ggtcaagaaa	gtgactcatc	agagacctct	3000
gtgcgaggac	cccgatttaa	acatgtctgc	agaagagcag	ctgttgccct	tggccgaaaa	3060
cgagctgtgt	ttctgatga	catgcccacc	ctgagtgcct	taccatggga	agaacgagaa	3120
aagatthttgt	cttccatggg	gaatgatgac	aagtcatcaa	ttgctggctc	agaagatgct	3180
gaacctcttg	ctccacccat	caaaccaatt	aaacctgtca	ctagaaacaa	ggcaccaccag	3240
gaacctccag	taaaagaaag	acgtcgatcg	aggcggtgtg	ggcagtgtcc	cggtcgccag	3300
gtgcctgagg	actgtggtgt	ttgtactaat	tgttagata	agcccaagtt	tgggtggtgc	3360
aatataaaga	agcagtgtcg	caagatgaga	aaatgtcaga	atctacaatg	gatgccttcc	3420
aaagcctacc	tgacagagca	agctaaagct	gtgaaaaaga	aagagaaaaa	gtctaagacc	3480
agtgaagaaga	aagacagcaa	agagagcagt	gttgtgaaga	acgtggtgga	ctctagtcat	3540
aaacctaccc	catcagcaag	agaggatcct	gccccaaaga	aaagcagtag	tgagcctcct	3600
ccacgaaagc	ccgtcgagga	aaagagtga	gaagggaatg	tctcggtccc	tgggcctgaa	3660
tccaaacagg	ccaccactcc	agcttccagg	aagtcaagca	agcaggtctc	ccagccagca	3720
ctgggtcatcc	cgctcagcc	acctactaca	ggaccgcaa	gaaaagaagt	tcccaaaacc	3780
actcctagtgt	agcccaagaa	aaagcagcct	ccaccaccag	aatcaggtcc	agagcagagc	3840
aaacagaaaa	aagtggctcc	ccgcccaggt	atccctgtaa	aacaaaaacc	aaaagaaaag	3900
gaaaaaccac	ctccggtcaa	taagcaggag	aatgcaggca	ctttgaacat	cctcagcact	3960
ctctccaatg	gcaatagtct	taagcaaaaa	attccagcag	atggagtcca	caggatcaga	4020
gtggacttta	aggaggttgg	tgaagcagaa	aatgtgtggg	agatgggagg	cttaggaatc	4080
ttgactttctg	ttctataaac	accagggtgt	gtttgctttc	tctgtgccag	tagtgggcat	4140
gtagagttht	tgtattgcc	agtctgttgt	gagcccttcc	acaagtthttg	tttagaggag	4200
aacgagcgcc	ctctggagga	ccagctggaa	aattgggtgt	gtcgtcgttg	caaattctgt	4260
cacgtthtgt	gaaggcaaca	tcaggctaca	aagcagctgc	tggagtgtaa	taagtgccga	4320
aacagctatc	accctgagtg	cctgggacca	aactacccca	ccaaaccac	aaagaagaag	4380
aaagtctgga	tctgtacca	gtgtgttcgc	tgtaaagact	gtggatccac	aactccaggc	4440
aaaggggtggg	atgcacagtgt	gtctcatgat	ttctcactgt	gtcatgattg	cgccaagctc	4500
tttgctaaag	gaaacttctg	ccctctctgt	gacaaatgtt	atgatgatga	tgactatgac	4560
agtaagatga	tgcaatgtgg	aaagtgtgat	cgctgggtcc	attccaaatg	tgagaatctt	4620
tcagggtacag	aagatgagat	gtatgagatt	ctatctaate	tgccagaaag	tgtggcctac	4680
acttgtgtga	actgtactga	gcggcaccct	gcagagtggc	gactggccct	tgaaaaagag	4740
ctgcagattht	ctctgaagca	agttctgaca	gctttgttga	attctcggac	taccagccat	4800
ttgtctacgt	accggcaggg	tgccaagcct	ccagacttaa	atcccagagc	agaggagagt	4860
ataccttccc	gcagctcccc	cgaaggacct	gatccaccag	ttcttactga	ggtcagcaaa	4920
caggatgatc	agcagccttt	agatctagaa	ggagtcaaga	ggaagatgga	ccaagggaat	4980
tacacatctg	tgttggagtt	cagtgatgat	attgtgaaga	tcattcaagc	agccattaat	5040
tcagatggag	gacagccaga	aattaaaaaa	gccaacagca	tgggtcaagtc	cttcttctatt	5100
cggcaaatgg	aacgtgttht	tccatggttc	agtgtcaaaa	agtccaggtt	ttgggagcca	5160
aataaagtat	caagcaacag	tgggatgtta	ccaaacgcag	tgcttccacc	ttcacttgac	5220
cataattatg	ctcagtggca	ggagcgagag	gaaaacagcc	acactgagca	gcctccttta	5280
atgaagaaaa	tcattccagc	tcccaaacc	aaaggtcctg	gagaaccaga	ctcaccact	5340
cctctgcata	ctcctacacc	accaatthttg	agtactgata	ggagtgcaga	agacagtcca	5400
gagctgaacc	cacccccagg	catagaagac	aatagacagt	gtgcgttatg	tttgacttat	5460
ggtgatgaca	gtgctaata	tgtgtgtcgt	ttactatata	ttggccaaaa	tgagtggaca	5520
catgtaaatt	gtgctthtgt	gtcagcggaa	gtgtttgaag	atgatgacgg	atcactaaag	5580
aatgtgcata	tggctgtgat	caggggcaag	cagctgagat	gtgaattctg	ccaaaagcca	5640
ggagccaccg	tgggttctgt	tctcacatcc	tgccaccagca	actatcactt	catgtgttcc	5700
cgagccaaaga	actgtgtctt	tctggatgat	aaaaaagtat	attgccaacg	acatcgggat	5760
ttgatcaaag	gcgaagtggg	tcttgagaat	ggatttgaag	ttttcagaag	agtgtthtgt	5820
gactthtgaag	gaatcagctt	gagaagggaag	tttctcaatg	gcttggaacc	agaaaatata	5880
catatgatga	ttgggtctat	gacaatcgac	tgcttaggaa	ttctaaatga	tctctccgac	5940
tgtgaagata	agctctthtcc	tattggatat	cagtgttcca	gggtatactg	gagcaccaca	6000
gatgctcgca	agcgtgtgt	atatacatgc	aagatagtgg	agtgcctgcc	tccagtcgta	6060
gagccggata	tcaacagcac	tgttgaacat	gatgaaaaa	ggaccattgc	ccatagtcca	6120
acatctthtta	cagaaagtcc	atcaaaaagag	agtcaaaa	cagctgaaat	tataagtcct	6180

ccatcaccag	accgacctcc	tcattcacaa	acctctgggt	cctgttatta	tcattgtcatc	6240
tcaaagggtcc	ccaggattcg	aacacccagt	tattctccaa	cacagagatc	ccctggctgt	6300
cgaccgttgc	cttctgcagg	aagtcctacc	ccaaccactc	atgaaatagt	cacagttaggt	6360
gatccctttac	tctcctctgg	acttcgaagc	attggctcca	ggcgtcacag	tacctcttcc	6420
ttatcacccc	agcgggtccaa	actccggata	atgtctccaa	tgagaactgg	gaataacttac	6480
tctaggaata	atgtttctct	agtctccacc	accgggaccg	ctactgatct	tgaatcaagt	6540
gccaaagtag	ttgatcatgt	cttagggcca	ctgaattcaa	gtactagttt	agggcaaaaac	6600
acttccacct	cttcaaattt	gcaaaggaca	gtggttactg	taggcaataa	aaacagtcac	6660
ttggatggat	cttcatcttc	agaaatgaag	cagtcagtg	cttcagactt	ggtgtccaag	6720
agctcctctt	taaagggaga	gaagacccaa	gtgctgagtt	ccaagagctc	agagggatct	6780
gcacataatg	tggtctaccc	tggaattcct	aaactggccc	cacaggttca	taacacacaa	6840
tctagagaag	tgaatgtag	taaaatcggc	tcttttctg	aacctcttcc	agtgtcgttt	6900
tcttctaag	aggccctctc	cttcccacac	ctccatttga	gagggcacaag	gaatgatcga	6960
gaccaacaca	cagattctac	ccaatcagca	aactcctctc	cagatgaaga	tactgaagtc	7020
aaaaccttga	agctatctgg	aatgagcaac	agatcatcca	ttatcaacga	acatatggga	7080
tctagttcca	gagataggag	acagaaaggg	aaaaaatcct	gtaaagaaac	tttcaaagaa	7140
aagcattcca	gtaaactctt	tttggaaact	ggtcaggtag	caactggtga	ggaaggaaac	7200
ttgaagccag	agtttatgga	tgagggtttt	actcctgagt	atatgggcca	acgacctagt	7260
aacaatggtt	cttctgataa	gattgggtgat	aaaggccttt	ctatgccagg	agtccccaaa	7320
gctccaccca	tgcaagtaga	aggatctgcc	aaggaattac	aggcaccacg	gaaacgcaca	7380
gtcaaagtga	cactgacacc	tctaaaaaat	gaaaaatgaga	gtcaatccaa	aatgcccctg	7440
aaagaaagta	gtcctgcttc	ccctttgcaa	atagagtcaa	catctcccac	agaaccaatt	7500
tcagcctctg	aaaatccagg	agatgggtcca	gtggcccaac	caagcccca	taatacctca	7560
tgccaggatt	ctcaaagtaa	caactatcag	aatcttccag	tacaggacag	aaacctaatg	7620
cttccagatg	gccccaaacc	tcaggaggat	ggctctttta	aaaggaggta	tccccgtcgc	7680
agtgcccgtag	cacgttctaa	catgtttttt	gggcttacc	cactctatgg	agtaagatcc	7740
tatggtgaag	aagacattcc	attctacagc	agctcaactg	ggaagaagcg	aggcaagaga	7800
tcagctgaag	gacagggtga	tgggggccgat	gacttaagca	cttcagatga	agacgactta	7860
tactattaca	acttcactag	aacagtgtat	tcttcagggtg	gagaggaacg	actggcatcc	7920
cataatttat	ttcgggagga	ggaacagtgt	gatcttccaa	aatcttcaca	gttggatggt	7980
gttgatgatg	ggacagagat	tgatactagt	gtcacagcca	caacaaggaa	aagcagccag	8040
attccaaaaa	gaaatggtta	agaaaaatgga	acagagaact	taaagattga	tagacctgaa	8100
gatgctgggg	agaaagaaca	tgctactaag	agttctgttg	gccacaaaaa	tgagccaaag	8160
atggataact	gccattctgt	aagcagagtt	aaaacacagg	gacaagattc	cttgggaagct	8220
cagctcagct	cattggagtc	aagccgcaga	gtccacacaa	gtacccctc	cgacaaaaat	8280
ttactggaca	cctataatac	tgagctcctg	aaatcagatt	cagacaataa	caacagtgat	8340
gactgtggga	atatcctgcc	ttcagacatt	atggactttg	tactaaagaa	tactccatcc	8400
atgcaggctt	tggtgtgag	cccagagtca	tcttcactag	aactcctgaa	tcttggtgaa	8460
ggattgggtc	ttgacagtaa	tcgtgaaaaa	gacatgggtc	tttttgaagt	attttctcag	8520
cagctgctca	caacagacc	tgtggatagt	agtgtctctt	cctctatctc	agcagaggaa	8580
cagtttgagt	tgctcttaga	gctaccatct	gactgtctctg	tcttgaccac	ccggagtccc	8640
actgtcccca	gccagaatcc	cagtagacta	gctgttatct	cagactcagg	ggagaagaga	8700
gtaaccatca	cagaaaaatc	tgtagcctcc	tctgaaagtg	accagcact	gctgagccca	8760
ggagtagatc	caactcctga	aggccacatg	actcctgatc	attttatcca	aggacacatg	8820
gatgcagacc	acatctctag	ccctccttgt	gggtcagtag	agcaagggtca	tggcaacaat	8880
caggatttaa	ctaggaacag	tagcaccctt	ggccttcagg	tacctgtttc	cccaactgtt	8940
cccatccaga	accagaagta	tgtgcccatt	tctactgata	gtcctggccc	gtctcagatt	9000
tccaatgcag	ctgtccagac	cactccaccc	cacctgaagc	cagccactga	gaaactcata	9060
gttggttaacc	agaacatgca	gccactttat	gttctccaaa	ctcttccaaa	tggagtgacc	9120
caaaaaatcc	aattgacctc	ttctgttagt	tctacaccca	gtgtgatgga	gacaaaatac	9180
tcagtattgg	gacctatggg	agggtgtctc	accttaccca	caggactaaa	tccaagcttg	9240
ccaacttctc	aatcttttgt	cccttctgct	agcaaaaggt	tgctacccat	gtctcatcac	9300
cagcacttac	attccttccc	tgcagctact	caaagtagtt	tcccacaaa	catcagcaat	9360
cctccttcag	gcctgcttat	tgggggttcag	cctcctccgg	atccccaact	tttgggttca	9420
gaatccagcc	agaggacaga	cctcagtacc	acagttagcca	ctccatcctc	tggactcaag	9480
aaaagaccca	tatctcgtct	acagacccga	aagaataaaa	aacttgctcc	ctctagtacc	9540
ccttcaaaaa	ttgccccttc	tgatgtggtt	tctaatatga	cattgattaa	cttcacaccc	9600
tcccagcttc	ctaactcatcc	aagtctgtta	gatttggggt	cacttaatac	ttcatctcac	9660

cgaactgtcc	ccaacatcat	aaaaagatct	aaatctagca	tcatgtattt	tgaaccggca	9720
cccctgttac	cacagagtgt	gggaggaact	gctgccacag	cggcaggcac	atcaacaata	9780
agccaggata	ctagccacct	cacatcaggg	tctgtgtctg	gcttggcatc	cagttcctct	9840
gtcttgaatg	ttgtatccat	gcaaactacc	acaaccccta	caagtagtgc	gtcagttcca	9900
ggacacgtca	ccttaaccaa	cccaagggtg	cttggtatccc	cagatattgg	ctcaataagc	9960
aatcttttaa	tcaaagctag	ccagcagagc	ctggggatcc	aggaccagcc	tgtggcttta	10020
ccgccaagtt	caggaatggt	tccacaactg	gggacatcac	agacccctc	tactgctgca	10080
ataacagcgg	catctagcat	ctgtgtgctc	ccctccactc	agactacggg	cataacagcc	10140
gcttcacctt	ctgggggaagc	agacgaacac	tatcagcttc	agcatgtgaa	ccagctcctt	10200
gccagcaaaa	ctgggattca	ttcttcccag	cgtgatcttg	attctgcttc	agggccccag	10260
gtatccaaat	ttaccagagc	ggtagacgct	cctaatagca	tgggactgga	gcagaacaag	10320
gctttatcct	cagctgtgca	agccagcccc	acctctcctg	ggggttctcc	atcctctcca	10380
tcttctggac	agcggtcagc	aagcccttca	gtgccgggtc	ccactaaacc	caaaccaaaa	10440
accaaaccgt	ttcagctgcc	tctagacaaa	gggaatggca	agaagcacia	tgtttcccat	10500
ttgcggaaca	gttcttctga	agcacacatt	ccagaccaag	aaacgacatc	cctgacctca	10560
ggcacaggga	ctccaggagc	agaggctgag	cagcaggata	cagctagcgt	ggagcagtc	10620
tcccagaagg	agtgtgggca	acctgcaggg	caagtcgctg	ttcttccgga	agttcagggtg	10680
acccaaaatc	cagcaaatga	acaagaaagt	gcagaacctc	aaacagtggc	agaagaggaa	10740
agtaatttca	gctccccact	gatgcttttg	cttcagcaag	aacaaaagcg	gaaggaaagc	10800
attactgaga	aaaaacccaa	gaaaggactt	gtttttgaaa	tttccagtga	tgatggcttt	10860
cagatctgtg	cagaaagtat	tgaagatgcc	tggagtcgat	tgacagataa	agtccaggaa	10920
gctcgatcaa	atgccgcct	aaagcagctc	tcatttgcag	gtgttaacgg	tttgaggatg	10980
ctggggatcc	tccatgatgc	agttgtgttc	ctcattgagc	agctgtctgg	tgccaagcac	11040
tgtcgaaatt	acaaattccg	tttccacaag	ccagaggagg	ccaatgaacc	ccccctgaac	11100
cctcacggct	cagccagggc	tgaagtccac	ctcaggaagt	cagcatttga	catgtttaac	11160
ttcttggtct	ctaaacatcg	tcagcctcct	gaatacaacc	ccaatgatga	agaagaggag	11220
gaggtacagc	tgaagtccagc	tccggaggga	actagcatgg	atctgccaat	gcccattgctc	11280
ttccggcaact	taaaaaagac	ttctaaggag	gcagttgggtg	tctacaggtc	tcccatccat	11340
ggccggggct	ttttctgtaa	gagaaacatt	gatgcagggtg	agatgggtgat	tgagtatgcc	11400
ggcaacgtca	tccgctccat	ccagactgac	aagcgggaaa	agtattacga	cagcaagggc	11460
attggttgct	atatgttccg	aattgatgac	tcagaggtag	tggatgccac	catgcatgga	11520
aatgctgcac	gcttcatcaa	tcactcgtgt	gagcctaact	gctattctcg	ggtcatcaat	11580
attgatgggc	agaagcacat	tgtcatcttt	gccatgcgta	agatctaccg	aggagaggaa	11640
ctcacttacg	actataagtt	ccccattgag	gatgccagca	acaagctgcc	ctgcaactgt	11700
ggcgccaaga	aatgccggaa	gttcctaaac	taaagctgct	cttctcccc	agtgttgag	11760
tgcaggagg	cggggccatc	caaagcaacg	ctgaaggcct	tttccagcag	ctgggagctc	11820
cgggattgct	tggcacagct	gaggggcctc	tgtgatggct	gagctctctt	atgtcctata	11880
ctcacatcag	acatgtgatc	atagtccag	agacagagtt	gaggtctcga	agaaaagatc	11940
catgatcgcc	tttctcctgg	ggccccctca	attgtttact	gttagaaagt	gggaatgggg	12000
tccttagcag	acttgcctgg	aaggagccta	ttatagaggg	ttgggttatgt	tgggagattg	12060
ggcctgaatt	tctccacaga	aataagttgc	catcctcagg	ttggcccttt	cccaagcact	12120
gtaagtgaat	gggtcagcca	aagcccaaaa	tggagggttg	gttagattcc	tgacagtttg	12180
ccagccagcc	gccacctaca	gcgtctgtcg	aacaaacaga	ggtctggtgg	ttttccctac	12240
tgtcctccca	ctcgagagtt	cacttctggt	tgggagacag	gattcctagc	acctccggtg	12300
tcaaaaggct	gtcatggggt	tgtgccaat	aattaccaaa	cattgagcct	gcaggctttg	12360
agtgggagtg	ttgccccag	gagccttata	tcagccaatt	acctttcttg	acagtaggag	12420
cggcttccct	ctccattcc	ctcttcactc	cctttttctc	ctttccccctg	tcttcatgcc	12480
actgctttcc	catgcttctt	tccggttgtag	gggagactga	ctgcctgctc	aaggacactc	12540
cctgctgggc	ataggatgtg	cctgcaaaaa	gttccctgag	cctgtaagca	ctccaggtgg	12600
ggaagtggac	aggagccatt	gggtcataacc	agacagaatt	tggaaacatt	ttcataaagc	12660
tccatggaga	gttttaaaaga	aacatatgta	gcattgattt	gtaggagagg	aaaaagatta	12720
tttaaatagg	atttaaatca	tgcacaacag	agagtatcac	agccaggatg	accttgggtg	12780
ccatttccca	agacatgggt	actttatctt	ccccttggtt	agacatagga	agacttaatt	12840
tttaaacggg	cagtgtccag	ttgaaggcag	aacactaata	agatttcaag	gcccacaact	12900
tggggactag	accaccttat	gttgagggaa	ctctgccacc	tgcgtgcaac	ccacagctaa	12960
agtaaatcca	atgacactac	tgccttgatt	actccttagg	atgtggtcaa	aacagcatca	13020
aatgtttctt	ctcttctctt	ccccaaagaca	gagtcctgaa	cctgttaaat	taagtcattg	13080
gattttactc	tgttctgttt	acagtttact	atttaagggt	ttataaatgt	aaatatattt	13140

54/299

```

tgtatatattt tctatgagaa gcacttcata gggagaagca cttatgacaa ggctatatttt 13200
taaacccggg tattatccta atttaaaaga agatcgggtt ttaataattt tttatatttca 13260
taggatgaag ttagagaaaa tattcagctg tacacacaaa gtctgggttt tcctgccccaa 13320
cttccccctg gaagggtgtac tttttgttgt ttaatgtgta gcttggttgt gcctgttga 13380
cataaatgtt tcctgggttt gctctttgac aataaatgga gaaggaaggt caccctaactc 13440
cattggggcca ctccccctct tccccatttg aagctcctca aaaggctaca gtaatatctt 13500
gatacaacag attctcttct tcccgctctc tctcctttcc ggcgcaactt ccagagtggg 13560
gggagacggc aatcttttaca tttccctcat ctttcttact tcagagttag caaacaacaa 13620
gttgaatggc aacttgacat ttttgcatca ccatctgcct cataggccac tctttccttt 13680
ccctctgccc accaagtcct catatctgca gagaaccat tgatcacctt gtgccctctt 13740
ttggggcagc ctgttgaaac tgaagcacag tctgaccact cagcataaag cagattttct 13800
ctgcctctgc cacaaggttt cagagtagtg tagtccaagt agagggtggg gcaccctttt 13860
ctcgccgcaa gaagccatt cctatggaag tctagcaaag caatacgact cagcccagca 13920
ctctctgccc caggactcat ggctctgctg tgccttccat cctgggctcc cttctctctt 13980
gtgaccttaa gaactttgtc tgggtggcttt gctggaacat tgtcactgtt ttcactgtca 14040
tgcagggagc ccagcactgt ggccaggatg gcagagactt ccttgctcatc atggagaagt 14100
gccagcaggg gactgggaaa agcactctac ccagacctca cctcccttcc tccttttgcc 14160
catgaacaag atgcagtggc cctaggggtt ccactagtgt ctgctttcct ttattattgc 14220
actgtgtgag gttttttgt aaatccttgt attcc 14255

```

<210> 64

<211> 149

<212> PRT

<213> Homo sapiens

<400> 64

```

Lys Gln Lys Lys Val Ala Pro Arg Pro Ser Ile Pro Val Lys Gln Lys
  1              5              10              15

Pro Lys Glu Lys Glu Met Thr His Ser Trp Pro Pro Pro Leu Thr Ala
      20              25              30

Ile His Thr Pro Ser Thr Ala Glu Pro Ser Lys Phe Pro Phe Pro Thr
      35              40              45

Lys Asp Ser Gln His Val Ser Ser Val Thr Gln Asn Gln Lys Gln Tyr
      50              55              60

Asp Thr Ser Ser Lys Thr His Ser Asn Ser Gln Gln Gly Thr Ser Ser
      65              70              75              80

Met Leu Glu Asp Asp Leu Gln Leu Ser Asp Ser Glu Asp Ser Asp Ser
      85              90              95

Glu Gln Thr Pro Glu Lys Pro Pro Ser Ser Ser Ala Pro Pro Ser Ala
      100              105              110

Pro Gln Ser Leu Pro Glu Pro Val Ala Ser Ala His Ser Ser Ser Ala
      115              120              125

Glu Ser Glu Ser Thr Ser Asp Ser Asp Ser Ser Ser Asp Ser Glu Ser
      130              135              140

Glu Ser Ser Ser Ser
145

```

55/299

<210> 65
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 65
 gcaaacagaa aaaagtggct ccccgcccaa gtatccctgt aaaacaaaaa ccaaaagaaa 60
 aggaaatgac ccattcatgg ccgcctcctt tgacagcaat acatacgctt agtacagctg 120
 agccatccaa gtttcctttc cctacaaagg actctcagca tgtcagttct gtaacccaaa 180
 accaaaaaca atatgataca ttttcaaaaa ctactcaaaa ttctcagcaa ggaacgtcat 240
 ccatgctcga agacgacctt cagctcagtg acagtgagga cagtgcagct gaacaaaccc 300
 cagagaagcc tccctcctca tctgcacctc caagtgcctc acagtccctt ccagaaccag 360
 tggcatcagc acattccagc agtgcagagt cagaaagcac cagtgcactca gacagttcct 420
 cagactcaga gagcgagagc agttcaagtg 450

<210> 66
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 66
 Lys Gln Lys Lys Val Ala Pro Arg Pro Ser Ile Pro Val Lys Gln Lys
 1 5 10 15
 Pro Lys Glu Lys Glu Met Thr His Ser Trp Pro Pro Pro Leu Thr Ala
 20 25 30
 Ile His Thr Pro Ser Thr Ala Glu Pro Ser Lys Phe Pro Phe Pro Thr
 35 40 45
 Lys Asp Ser Gln His Val Ser Ser Val Thr Gln Asn Gln Lys Gln Tyr
 50 55 60
 Asp Thr Ser Ser Lys Thr His Ser Asn Ser Gln Gln Gly Thr Ser Ser
 65 70 75 80
 Met Leu Glu Asp Asp Leu Gln Leu Ser Asp Ser Glu Asp Ser Asp Ser
 85 90 95
 Glu Gln Thr Pro Glu Lys Pro Pro Ser Ser Ser Ala Pro Pro Ser Ala
 100 105 110
 Pro Gln Ser Leu Pro Glu Pro Val Ala Ser Ala His Ser Ser Ser Ala
 115 120 125
 Glu Ser Glu Ser Thr Ser Asp Ser Asp Ser Ser Ser Asp Ser Glu Ser
 130 135 140
 Glu Ser Ser Ser Ser
 145

<210> 67
 <211> 450
 <212> DNA
 <213> Homo sapiens

56/299

<400> 67

```

gcaaacagaa aaaagtggct ccccgcccaa gtatccctgt aaaacaaaaa ccaaagaaa 60
aggaaatgac ccattcatgg cggcctcctt tgacagcaat acatacgctt agtacagctg 120
agccatccaa gtttcctttc cctacaaagg actctcagca tgtcagttct gtaacccaaa 180
acaaaaaaca atatgatata ttttcaaaaa ctactcaaa ttctcagcaa ggaacgtcat 240
ccatgctcga agacgacctt cagctcagtg acagtgagga cagtgcagtg gaacaaacc 300
cagagaagcc tccctcctca tctgcacctc caagtgtctc acagtccctt ccagaaccag 360
tggcatcagc acattccagc agtgagagtg cagaaagcac cagtgactca gacagttcct 420
cagactcaga gagcgagagc agttcaagtg

```

<210> 68

<211> 6983

<212> DNA

<213> Homo sapiens

<400> 68

```

tggatcatccc gcctcagcca cctactacag gaccgccaag aaaagaagtt cccaaaacca 60
ctcctagtga gcccaagaaa aagcagcctc caccaccaga atcaggtgag tgaggagggc 120
aagaaggaat tgctgacca caagtactaa caaaaaagca ctgatgtctc aaacagcatt 180
tgaaagcagg aaatgtatga tttgaagtct tcagttcaag aaaatcagct ctctttctaa 240
ctattatggt taataataaa gaaacagaaa caaaaaaac agttaaatgt gaggtattgt 300
tttaatttcc tgttcgaagc ctagagttta aatagttttt tttttttttt tctaattggc 360
ctttcttcac aggtcagtc gtactaaagt agtcgttgcc agcatctgac tgcaatttat 420
tctgaatttt ttaggtccag agcagagcaa acagaaaaaa gtggctcccc gcccaagtat 480
ccctgtaaaa caaaaaccaa aagaaaaggt gagagagat ttgtttctct gccatttctc 540
agggatgtat tctattttgt agggaaaagc cttatccttg acttctatgt agatggcagt 600
ggaatttctt aaaattaaga aacttcaagt ttaggctttt agctgggcac ggtggctcac 660
gctggtaatc ccaacactta gtgaggctga ggtgggagga ttgcttgagg ccagcagttc 720
aagaccagcc tgggcaacat agcaagacc tgtctttatt taaaccaaaa aaaaaaaag 780
aagaagaaga agttagccag gcatgggtggc agttgcgtgt agtcccaggt actcaggagg 840
ctgagataga aggattgtct tgagcccagg aattcaaggc tgtagtgagc tatgattgta 900
ccactgcagt ccagcctggg tgacaaagca aaacactgtc tccaaaaaaa atttaggctt 960
ggcaaggcgc agcggctcac gcctgtgatc ccagcacttt gggaagccga agcaggcaga 1020
tcacttgagg tcaggagttg gagaccagcc tggccaacat ggtgaaacc tgtctctact 1080
gaaaatacaa aaattagccg gttgtggtag tgggtgcttg gtaatcctag ctacttggga 1140
ggctgaggga gggggaattg cctgaaacct gcgaggcgga ggctgcagtg agccgagatt 1200
gcactattgc actctagctt ggacaacaga gctagactcc atcccaaaaa aaaaaaaaaa 1260
aagtagccgg gcacggtggc tcacgcctgt aatcccagca ctttgggagg ccgaggcggg 1320
cggatcatga gggcaggaga tcgagaccat cctggctaac acggtgaaac cctgtctcta 1380
ctaaaaatac aaaaaattag cccggcgagg tggcgggcgc ctgtagtccc agctactcag 1440
gagagtgagc caggagaatg gcgtgaacct ggggggcgga gcctgcagtg agccgagatc 1500
gcgccactgc actccagctt ggggtgacac gagactccgt ctcaaaaaaa aataaaaagt 1560
ttaggcttta gcctgtttct tttttggttt ctctccttgtt gcttttccct tctttgtggc 1620
cccacatgtt ctagcctagg aatctgctta ttctaaaggc catttggcgt aattattttt 1680
tgaccccaac atccttttagc aattatttgt ctgtaaaaa cacccttccc tgtattcact 1740
atttttattt attatggata aagagatagt gtggtggctc acatctataa tcccagcact 1800
ttgggggccc aaggcgggag gatcacttga gggcaggagc tggagaccag cctgggcagc 1860
acagtgcac acagttgcta taaaaaattt aaaacccaac taggcatggt ggcattgcac 1920
tgtagtccca gctactcttg agaagctgag gcaggaggat cacgagccca caaggtctag 1980
gctgcagtga gctgtgactg tgccactgta ttgcagccta ggcaacaaag caagaccag 2040
tctcttttaa aaaaaattc aaagattatt gtttatgttg gaaacatgtt ttttagatct 2100
attaataaaa tttgtcattt gcattattat ctggtgcaaa tgtgaaggca aatagggtgt 2160
gattttgttc tatattcatc ttttgtctcc ttaggaaaaa ccacctccgg tcaataagca 2220
ggagaatgca ggcactttga acatcctcag cactctctcc aatggcaata gttctaagca 2280
aaaaattcca gcagatggag tccacaggat cagagtgga ttaaggtaa aggtgttcag 2340
tgatcataaa gtatattgag tgtcaaagac ttttaataaa gaaaatgcta ctaccaagg 2400
tgttgaaaga ggaaatcagc accaactggg ggaatgaata agaactccca tttagcaggtg 2460

```

ggtttagcgc	tgggagagct	ttggacagtg	ttgttaggtc	actgtttgtg	aactgactgc	2520
agaacataca	taatgaaaca	ttcctatcca	tcctgaggag	tatcagagga	agtaattcct	2580
tcacatggaa	agtatcaaac	catgatgatt	ccttgagtca	gcaaaactgt	aagagaaatt	2640
caatcccagt	gtattttcgc	aatatcttca	ctatgaattg	aacaactagg	tgagcctttt	2700
aatagtcogt	gtctgagatt	aaaacttttt	aaagcagcag	ttatttttgg	actcattgaa	2760
atgaaatact	ctgacattgt	gatgtcacac	taattttatg	cttttcatcc	ttattttcca	2820
tccaaagtgt	tgtaatgtga	aaaactttct	aagtgcctt	tctctctcca	caggaggatt	2880
gtgaagcaga	aaatgtgtgg	gagatgggag	gcttaggaat	cttgacttct	gttctataa	2940
caccaggggt	ggtttgcttt	ctctgtgcc	gtagtgggca	tgtagaggta	aggcatcctg	3000
cttctttgta	ccccaggaag	tacataaatg	attgatctgg	ggatgagatt	actatagtct	3060
gttttgttgg	tatttagcag	gtactattcc	ctgtttaaac	cagctaaaga	aatgttttga	3120
agtatttttag	agatttttag	aaggaatctg	ctattagagt	agcaaagtta	ttgagagtga	3180
aaagataaat	aatcccatct	ctcttaaat	cagcttttat	tagagttctg	atctttctgt	3240
tagatgtcta	aataagagaa	aaaattatac	agtggcttat	taaaagggat	gctatttgat	3300
gttattttat	attgtatata	aaagcctctt	catctataag	gagctcttac	caattaataa	3360
gaaaaaggaa	tgacatccag	aaaaaaaaat	aggcaaaaga	cagaaataga	taattcacaa	3420
aattagaaat	aaatacatgt	tgggtggcag	ggggagggtga	agggagggtg	tctgtttttt	3480
agccctctag	tgaccaaaaa	ctggaaatta	aagcatgata	aaaaagaat	cctgaataaa	3540
tggggacttt	ctgttgggtg	aaagaaatat	agattagtta	caatctttct	ttctgaggga	3600
attattttgga	aatatatata	tctatcttta	aaataggtat	atccgaatat	tatggcttta	3660
agaaaatatg	agtgggaaat	aatgtttcta	atggacagag	ctatggagt	agaatgcatt	3720
ggttcattct	acttcacatt	taaatgggac	agtatttctt	gagctagagg	gctgttgtga	3780
gaattaaatg	ggatatgttt	gctgacatt	tagtatattg	tgagatatac	cacotttctt	3840
tgacatattg	tgttagtaaa	agaaaattta	tgctgttagga	aaattgtata	ttatccatct	3900
tcaagtagtc	tgtatagatg	ttacagctgt	gcctagaagt	cagcagaatc	ccaagaaata	3960
tctttgtgtt	ttaggtttgt	ttgctgggtg	ttcacagttg	ttgtgatgaa	gtaatgaaac	4020
tctgtgtcat	ggattttaatt	ttagtcaagt	ttttaaatgt	tacacttttt	caataagaga	4080
cttgaataga	tatttttatgc	cctaataaag	tactgaatac	ttgctgtagt	ttcaggattc	4140
cagaattgca	ttagttgtga	gaagtatatg	gggcaagggtc	tagtgtgtaa	agggcttttt	4200
gagccccgtc	acattttgagc	attgtgacaa	atagaaaaaa	ttatagtact	gaactgaaca	4260
ctgatgtata	aagtgttaat	tctgtgacct	gggtcacaaa	tttagtaagg	aaagggtgta	4320
gattaaacat	attttcattg	aatctctgaa	ggttcctgaa	tccaatatag	aagataggga	4380
acattttgtat	tgaactgatag	agtaagatgg	ttttacagggt	taggaagctg	gaatgtccca	4440
agatattcat	tcagttttttg	gttcacatag	tattgatgag	tatataaact	tctttaaaaa	4500
agtagggagg	ccaggcacag	tggctcacgc	ctgtaatccc	aacacttttg	gaagccgagg	4560
caggaggatt	cctcgagccc	aggagtttga	gaccaacctg	gacaacatgg	tgagactgtc	4620
tctacaaaaa	attttaaaaa	ttagcggctg	ggcacgggtg	ctcatgtcta	taatctcagc	4680
actttggggag	gctgaggttg	gtggatcatc	tgaggtcagg	aattcgagac	cagcctgggc	4740
aacagggtga	aaccctgtct	ctactaaaaa	tgcaaaaaat	agccaggcat	ggtgggtgggt	4800
gcctgtaaat	ctcaggaggc	tgaggaagga	gaattgcttg	aaccaggaa	gcggagggtg	4860
cagtaaaagt	gagatcgctg	cattgcactc	cagcctgggc	aacaagagtg	aaattccgtc	4920
tcaaaaagaaa	aaaaaaaaaa	agccgggtgt	tgtggcatgc	acctgcggtc	ccagctgtct	4980
aggaggctga	ggtaggagga	tcacttgagc	acaggaagtg	taggctgcag	tgagctgtgt	5040
tcgtgccact	gcactccagc	ctggctgaca	gactctgtca	caagaaaaaa	taatatagtg	5100
tggggacacc	aacctttatt	ttatgtgtct	taatgtgggtg	cattagtctg	ctttcacact	5160
gctgataaag	acatacctga	gactgggcaa	tttacaagg	aaagagggtt	agtggagaac	5220
tcacagttcc	acatggaagc	ctcacagtca	tgcggaaggc	aaggaggagc	aggtcacgtc	5280
tacgtgagtg	gcggcaaaga	gagaggttgt	gcagggaac	tctgtttttt	aaaaccatca	5340
gatctcatga	gactcactgt	tacaagaaca	gcacgggaaa	gacctgcccc	catgatcgaa	5400
ttacctccca	ccagctccct	ccacaacac	atgggaattc	aagatgagat	ttgggtgggg	5460
acacagccaa	atcatgtcat	gtgaattagg	aagaaatata	aaccagcata	tcaaacaaa	5520
ctagggtttc	acaaatattg	cttaggatga	ggtgagggtta	aaaaaaaaaa	agtgggttga	5580
tcataaactg	atctaaaaaa	atagtacaag	tagtattatg	acgcagtgcc	gctatcaaag	5640
tagtatagaa	atgaccgaag	tttgggaaaa	actgttttgg	actgtcctca	tatcatggag	5700
gaaagactgg	ttaaagatgg	ggcagtgtca	gaagaaaaat	aagtttttag	ccggaggtaa	5760
ttttaaacat	tttcttgctt	taccagcgga	tggcttctct	gtgtttaaag	aacttaaaaa	5820
gttgagaatt	aaatttttgc	cattattttt	ccccccctt	tctctgtgca	acctctctgc	5880
cccttaataa	atgttttttg	tactgactac	tgctgtctct	gctaatacca	tcctgtagaa	5940

58/299

```

atgttttcttg agtgaggaat agttttttaga aggccttttat gatgataact tttaaattta 6000
tttttaacta tgccagcagg ttattagata tatagggttca aaggagattg aggctggagt 6060
ctgttcaaac attttcagag gtgaagatga cacagggttc atggagattt cttcatgggt 6120
accagaacag ggcagggttt cactgcatga taatacccat gtttccattg cttgtagacc 6180
taatcatttt tacttattga ttggcactgt gggccaagat cgtgacatcc atcctaataa 6240
gcagggtctca tcaaaagcct tagaatggag aaaattttta taatgcttta ttagttgggt 6300
aagtaagccc tgatgttttg ctttctagt accggtcatt gccctgcaga ctctgtaatg 6360
ggacagtttg gctgggtgta ggggggtcatg ccaggctgag gtgggaggat tactgtaggc 6420
caggagtttt gagactagcc taggcaacat agaccgcccc ccatccctat aaatatttaa 6480
caattagctg agcataatgg tgtgtgtgct tgtagtctta gctgctgagg aggctgaggt 6540
gagaggatca cttcagctca agagcttgag gttacagtga gctatatgat tgcaccagtg 6600
aactccagcc tgggcaacac agtgagacc tgtctcaaaa caaaaacaaa aacaaaaaca 6660
ggtaggggaga gacaaggaga agggtagtac tgacatggcc tgtctttact ttcccccttc 6720
agccctggaa ctctccacag ggaaagggtt tttgttcctt cttcttgtct aataaatggc 6780
ttgacttgag gggatctctg gaggcattct caaccacaacc ctgaagggtt atcagcactt 6840
tcctggtgga cagcacctca gcctctgccc tggctccttt catcctcatc ccctagagcc 6900
aggatcggga agctggagtg gtggcctggt tggattcagg cccaggggccc gagacattcc 6960
cttcttcaact cttttccgga tcc 6983

```

<210> 69

<211> 198

<212> PRT

<213> Homo sapiens

<400> 69

```

Ile Ser Leu Pro Ser Pro Val Pro Pro Leu Ser Pro Ile His Ser Asn
  1              5              10              15

Gln Gln Thr Leu Pro Arg Thr Gln Gly Ser Ser Lys Val His Gly Ser
  20              25              30

Ser Asn Asn Ser Lys Gly Tyr Cys Pro Ala Lys Ser Pro Lys Asp Leu
  35              40              45

Ala Val Lys Val His Asp Lys Glu Thr Pro Gln Asp Ser Leu Val Ala
  50              55              60

Pro Ala Gln Pro Pro Ser Gln Thr Phe Pro Pro Pro Ser Leu Pro Ser
  65              70              75              80

Lys Ser Val Ala Met Gln Gln Lys Pro Thr Ala Tyr Val Arg Pro Met
  85              90              95

Asp Gly Gln Asp Gln Ala Pro Ser Glu Ser Pro Glu Leu Lys Pro Leu
 100              105              110

Pro Glu Asp Tyr Arg Gln Gln Thr Phe Glu Lys Thr Asp Leu Lys Val
 115              120              125

Pro Ala Lys Ala Lys Leu Thr Lys Leu Lys Met Pro Ser Gln Ser Val
 130              135              140

Glu Gln Thr Tyr Ser Asn Glu Val His Cys Val Glu Glu Ile Leu Lys
 145              150              155              160

Glu Lys Pro Pro Pro Val Asn Lys Gln Glu Asn Ala Gly Thr Leu Asn
 165              170              175

```

59/299

Ile Leu Ser Thr Leu Ser Asn Gly Asn Ser Ser Lys Gln Lys Ile Pro
 180 185 190

Ala Asp Gly Val His Arg
 195

<210> 70
 <211> 596
 <212> DNA
 <213> Homo sapiens

<400> 70
 atctctttgc cttccccagt tccccctttg tcacctatac attccaacca gcaaactctt 60
 ccccgagcgc aaggaagcag caaggttcat ggcagcagca ataacagtaa aggctattgc 120
 ccagccaaat ctccaagga cctagcagtg aaagtccatg ataaagagac ccctcaagac 180
 agtttggttg cccctgccc ggcgccttct cagacatttc cacctccctc cctcccctca 240
 aaaagtgttg caatgcagca gaagcccacg gcttatgtcc ggcccatgga tggtaagat 300
 caggccccta gtgaatcccc tgaactgaaa ccactgccgg aggactatcg acagcagacc 360
 ttgaaaaaaa cagacttgaa agtgccctgcc aaagccaagc tcaccaaact gaagatgcct 420
 tctcagtcag ttgagcagac ctactccaat gaagtccatt gtggtgaaga gattctgaag 480
 gaaaaaccac ctccggtcaa taagcaggag aatgcaggca ctttgaacat cctcagcact 540
 ctctccaatg gcaatagttc taagcaaaaa attccagcag atggagtcca caggat 596

<210> 71
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 71
 Ile Ser Leu Pro Ser Pro Val Pro Pro Leu Ser Pro Ile His Ser Asn
 1 5 10 15
 Gln Gln Thr Leu Pro Arg Thr Gln Gly Ser Ser Lys Val His Gly Ser
 20 25 30
 Ser Asn Asn Ser Lys Gly Tyr Cys Pro Ala Lys Ser Pro Lys Asp Leu
 35 40 45
 Ala Val Lys Val His Asp Lys Glu Thr Pro Gln Asp Ser Leu Val Ala
 50 55 60
 Pro Ala Gln Pro Pro Ser Gln Thr Phe Pro Pro Pro Ser Leu Pro Ser
 65 70 75 80
 Lys Ser Val Ala Met Gln Gln Lys Pro Thr Ala Tyr Val Arg Pro Met
 85 90 95
 Asp Gly Gln Asp Gln Ala Pro Ser Glu Ser Pro Glu Leu Lys Pro Leu
 100 105 110
 Pro Glu Asp Tyr Arg Gln Gln Thr Phe Glu Lys Thr Asp Leu Lys Val
 115 120 125
 Pro Ala Lys Ala Lys Leu Thr Lys Leu Lys Met Pro Ser Gln Ser Val
 130 135 140

60/299

Glu Gln Thr Tyr Ser Asn Glu Val His Cys Val Glu Glu Ile Leu Lys
145 150 155 160

Glu Lys Pro Pro Pro Val Asn Lys Gln Glu Asn Ala Gly Thr Leu Asn
165 170 175

Ile Leu Ser Thr Leu Ser Asn Gly Asn Ser Ser Lys Gln Lys Ile Pro
180 185 190

Ala Asp Gly Val His Arg
195

<210> 72
<211> 596
<212> DNA
<213> Homo sapiens

<400> 72
atctctttgc cttccccagt tccccctttg tcacctatac attccaacca gcaaactctt 60
ccccggacgc aaggaagcag caaggttcat ggcagcagca ataacagtaa aggctattgc 120
ccagccaaat ctcccaagga cctagcagtg aaagtccatg ataaagagac ccctcaagac 180
agtttggttg cccctgccca gccgccttct cagacatttc cacctccctc cctccccctca 240
aaaagtgttg caatgcagca gaagcccacg gcttatgtcc ggcccatgga tggcgaagat 300
caggccccct gtgaatcccc tgaactgaaa ccactgccgg aggactatcg acagcagacc 360
tttgaaaaaa cagacttgaa agtgccctgcc aaagccaagc tcaccaaact gaagatgcct 420
tctcagtcag ttgagcagac ctactccaat gaagtccatt gtgttgaaga gattctgaag 480
gaaaaaccac ctccggtcaa taagcaggag aatgcaggca ctttgaacat cctcagcact 540
ctctccaatg gcaatagttc taagcaaaaa attccagcag atggagtcca caggat 596

<210> 73
<211> 747
<212> DNA
<213> Homo sapiens

<400> 73
tccgtaagct cgacctcagt gaggctgggc agacctacat gacctaaatg tgtaggaaa 60
ttgatagcag agtaaagtta tctgtgtgca gaattccctg ctgccatggg tggcgcctgg 120
agcagacgac ttccaaaccg cttgtaagaa agcatgaaga ataagtcacc tgcacttcag 180
aggccaaatt ttaaacctga aaagatctaa atatagaagt tttaaaatag tgacaggcag 240
gtttttttaga gcagaagctg taaaccagca gcctgagggc taggttgggc ctgcagacaa 300
attattttgt ttggcctgta gggcttgttt tctttctttc tccctaccgc cccccacact 360
tttagccagt atttacaac tggagaattt agggaaaaaa tcattattgg ctgagtagag 420
gcaattttctg gaacctggcc actgtattgc agcctaggca acaaagcaag acccagtcctc 480
ttttaaaaaa aaattcaaag attatttgtt tatgttggaa acatgttttt tagatctatt 540
aataaaattt gtcatttgca ttattatctg ttgcaaattg gaaggcaaat aggggtgtgat 600
tttgttctat attcatcttt tgtctcctta ggaaaaacca cctccggtca ataagcagga 660
gaatgcaggc actttgaaca tcctcagcac tctctccaat ggcaatagtt ctaagcaaaa 720
aattccagca gatggagtcc acaggat 747

<210> 74
<211> 2598
<212> DNA
<213> Homo sapiens

61/299

<400> 74

```
ggatccgtgg  tcatcccgcc  tcagccacct  actacaggac  cgccaagaaa  agaagttccc  60
aaaaccactc  ctagtgagcc  caagaaaaag  cagcctccac  caccagaatc  aggtgagtga  120
ggagggcaag  aaggaatcgc  tgaaccacaa  gtactaacia  aaaagcactg  atgtctcaaa  180
cagcatttga  aagcaggaaa  tgtatgattt  gaagtcttca  gttcaagaaa  atcagctctc  240
tttctaacta  ttatgtttaa  taataaagaa  acagaaacia  aaaaaacagt  taaattggag  300
gtattgtttt  aatttcctgt  tcgaagccta  gagtttaaata  agtttttttt  tttttttcta  360
atggcccttt  cttcacaggt  cagtcagtac  taaagtagtc  gttgccagca  tctgactgca  420
atttattctg  aatttttttag  gtccagggca  gagcaaacag  aaaaaagtgg  ctccccgccc  480
aagtatccct  gtaaaacaaa  aacaaaaaga  aaaggtgagg  agagatttgt  ttctctgcca  540
tttctcaggg  atgtattcta  tttttagagg  aaaagcctta  tccttgactt  ctatgtagat  600
ggcagtggaa  tttcttaaaa  ttaagaaact  tcaagtttag  gcttttagct  gggcacgggtg  660
gctcatgctg  gtaatcccaa  cacttattga  ggctgagggtg  ggaggattgc  ttgaggccag  720
cagttcaaga  ccagcctggg  caacatagca  agaccctgtc  tttatttaaa  ccaaaaaaaaa  780
aaaaagaaga  agaagaagaa  gttagccagg  catggtggca  gttgcgtgta  gtcccaggta  840
ctcaggaggc  tgagatagaa  ggattgtctt  gagccaggga  attcaaggct  gtagtgagct  900
atgattgtac  cactgcagtc  cagcctgggt  gacaaagcaa  aacactgtct  ccaaaaaaaaa  960
tttaggcttg  gcaaggcgca  gcggctcacg  cctgtgatcc  cagcactttg  ggaagccgaa  1020
gcaggcagat  cacttgaggt  caggagttgg  agaccagcct  ggccaacatg  gtgaaaccct  1080
gtctctactg  aaaatacaaa  aattagccgg  ttgtggtagt  ggggtgctgt  aatcctagct  1140
acttgggagg  ctgaggcagg  ggaattgcct  gaacctgcga  ggcggaggct  gcagtgagcc  1200
gagattgcat  cattgcactc  tagcctggac  aacagagcta  gactccatcc  caaaaaaaaa  1260
aagtagccgg  gcacgggtgg  tcacgcctgt  aatcccagca  ctttgggagg  ccgaggcggg  1320
cggatcatga  gggcaggaga  tcgagaccat  cctggctaac  acggtgaaac  cctgtctcta  1380
ctaaaaatac  aaaaaattag  cccggcgagg  tggcggcgcg  ctgtagtccc  agctactcag  1440
gagagtgagg  caggagaatg  gcgtgaacct  gggggcgga  gcctgcagtg  agccgagatc  1500
gcgccactgc  actccagctt  ggggtgacac  gagactccgt  ctcaaaaaaa  aataaaaagt  1560
ttaggcttta  gcctgtttct  tttttggtt  cttccttggt  gcttttccct  tctttgtggc  1620
cccacatggt  ctaccctagg  aatctgctta  ttctaaaggc  catttggtgt  aattattttt  1680
tgaccccaac  atccttttag  aattatttgt  ctgtaaaaat  cacccttccc  tgtattcact  1740
atttttattt  attatggata  aagagatagt  gtggtggcto  acatctataa  tcccagcact  1800
ttggggggcc  aaggcgggag  gatcacttga  gggcaggagc  tggagaccag  cctgggcagc  1860
acagtgcac  acagttgcta  taaaaaattt  aaaaatcaac  taggcattgt  ggcatgcacc  1920
tgtagtccca  gctactcttg  agaagctgag  gcaggaggat  cacgagccca  caaggtctag  1980
gctgcagtga  gctgtgactg  tggcaatctt  tagagtctct  ctctctcacc  cgggctggaa  2040
tgcagtagca  cgatcacagc  tcacttcagc  cttgaactcc  tgggtccaag  caatgcccac  2100
ttttccatcc  tgagttagta  ggactgcagg  cacatggcag  catgcttggc  tgatttattt  2160
ttattttttg  tagagacaag  gtcttggggg  gttgcccagg  ctgaacctgg  caatcttatg  2220
aagaaacact  ttaactctg  aaggaaactt  tttaagtaat  atagacacia  tatttttgaa  2280
aagctcttaa  attgctaaaa  attaatgcaa  agaatagaat  tgcttatagt  agcccaagag  2340
gaaagcataa  aattgaaact  ggaagaactt  tttgggtggg  attaattgga  gttgttttta  2400
ctttgtgcat  ttcactttct  attccttctc  ggaaatgcca  gaagtacatt  tggtagcagg  2460
atgagaaatt  cctgttctct  cttgttttca  cacttgagat  gtttgtggat  gggtatttga  2520
tcggaagctg  gagtgggtgg  ctgtttggat  tcaggcccag  gggccgagac  attcccttct  2580
tcactctttt  ccggtacc  2598
```

<210> 75

<211> 60

<212> DNA

<213> Homo sapiens

<400> 75

```
tctctgtgcc  agtagtgggc  atgtagagga  ccctaataagg  agtattcata  ccagcagcag  60
```

<210> 76

<211> 74

```

<400> 78
Met Arg Ile Gln Pro Gln Lys Ala Ala Ala Ile Ile Asp Leu Asp Pro
  1             5             10             15

Asp Phe Glu Pro Gln Ser Arg Pro Arg Ser Cys Thr Trp Pro Leu Pro
      20             25             30

Arg Pro Glu Ile Ala Asn Gln Pro Ser Glu Pro Pro Glu Val Glu Pro
      35             40             45

Asp Leu Gly Glu Lys Val His Thr Glu Gly Arg Ser Glu Pro Ile Leu
      50             55             60

Leu Pro Ser Arg Leu Ser Glu Pro Ala Gly Gly Pro Gln Pro Gly Ile
      65             70             75             80

Leu Gly Ala Val Thr Gly Pro Arg Lys Gly Gly Ser Arg Arg Asn Ala
      85             90             95

Trp Gly Asn Gln Ser Tyr Ala Glu Phe Ile Ser Gln Ala Ile Glu Ser
      100            105            110

Ala Pro Glu Lys Arg Leu Thr Leu Ala Gln Ile Tyr Glu Trp Met Val
      115            120            125

Arg Thr Val Pro Tyr Phe Lys Asp Lys Gly Asp Ser Asn Ser Ser Ala
      130            135            140

Gly Trp Lys Asn Ser Ile Arg His Asn Leu Ser Leu His Ser Lys Phe
      145            150            155            160

Ile Lys Val His Asn Glu Ala Thr Gly Lys Ser Ser Trp Trp Met Leu
      165            170            175

Asn Pro Glu Gly Gly Lys Ser Gly Lys Ala Pro Arg Arg Arg Ala Ala

```

63/299

180					185					190					
Ser	Met	Asp	Ser	Ser	Ser	Lys	Leu	Leu	Arg	Gly	Arg	Ser	Lys	Ala	Pro
	195						200					205			
Lys	Lys	Lys	Pro	Ser	Val	Leu	Pro	Ala	Pro	Pro	Glu	Gly	Ala	Thr	Pro
	210					215					220				
Thr	Ser	Pro	Val	Gly	His	Phe	Ala	Lys	Trp	Ser	Gly	Ser	Pro	Cys	Ser
225					230					235					240
Arg	Asn	Arg	Glu	Glu	Ala	Asp	Met	Trp	Thr	Thr	Phe	Arg	Pro	Arg	Ser
			245						250					255	
Ser	Ser	Asn	Ala	Ser	Ser	Val	Ser	Thr	Arg	Leu	Ser	Pro	Leu	Arg	Pro
			260					265					270		
Glu	Ser	Glu	Val	Leu	Ala	Glu	Glu	Ile	Pro	Ala	Ser	Val	Ser	Ser	Tyr
	275						280					285			
Ala	Gly	Gly	Val	Pro	Pro	Thr	Leu	Asn	Glu	Gly	Leu	Glu	Leu	Leu	Asp
	290					295					300				
Gly	Leu	Asn	Leu	Thr	Ser	Ser	His	Ser	Leu	Leu	Ser	Arg	Ser	Gly	Leu
305					310					315					320
Ser	Gly	Phe	Ser	Leu	Gln	His	Pro	Gly	Val	Thr	Gly	Pro	Leu	His	Thr
				325					330					335	
Tyr	Ser	Ser	Ser	Leu	Phe	Ser	Pro	Ala	Glu	Gly	Pro	Leu	Ser	Ala	Gly
			340					345					350		
Glu	Gly	Cys	Phe	Ser	Ser	Ser	Gln	Ala	Leu	Glu	Ala	Leu	Leu	Thr	Ser
		355					360					365			
Asp	Thr	Pro	Pro	Pro	Pro	Ala	Asp	Val	Leu	Met	Thr	Gln	Val	Asp	Pro
	370					375					380				
Ile	Leu	Ser	Gln	Ala	Pro	Thr	Leu	Leu	Leu	Leu	Gly	Gly	Leu	Pro	Ser
385					390					395					400
Ser	Ser	Lys	Leu	Ala	Thr	Gly	Val	Gly	Leu	Cys	Pro	Lys	Pro	Leu	Glu
				405					410					415	
Ala	Arg	Gly	Pro	Ser	Ser	Leu	Val	Pro	Thr	Leu	Ser	Met	Ile	Ala	Pro
			420					425					430		
Pro	Pro	Val	Met	Ala	Ser	Ala	Pro	Ile	Pro	Lys	Ala	Leu	Gly	Thr	Pro
		435					440					445			
Val	Leu	Thr	Pro	Pro	Thr	Glu	Ala	Ala	Ser	Gln	Asp	Arg	Met	Pro	Gln
	450					455					460				
Asp	Leu	Asp	Leu	Asp	Met	Tyr	Met	Glu	Asn	Leu	Glu	Cys	Asp	Met	Asp
465					470					475					480
Asn	Ile	Ile	Ser	Asp	Leu	Met	Asp	Glu	Gly	Glu	Gly	Leu	Asp	Phe	Asn
				485					490					495	

64/299

Phe Glu Pro Asp Pro
500

<210> 79
<211> 3171
<212> DNA
<213> Homo sapiens

<400> 79
gggacagctt agggactatc gtcctgggac tagggggaag ttcggcactt tctgaagact 60
ggcaggaatg tgcctcctgg ccctcgatgc ttccccctg aggggaggca tcgtgaggga 120
ctgtggcagg cttcactgaa cgctgagccg gggaggtcca actccacgta tggatccggg 180
gaatgagaat tcagccacag aaggccgccc cgatcataga cctagatccc gacttcgaac 240
cccagagccg tccccgctcc tgcacctggc cccttccccg accagagatc gctaaccagc 300
cgtccgagcc gcccagagtg gagccagatc tgggggaaaa ggtacacacg gagggcgct 360
cagagccgat cctgttgccc tctcggctct cagagccggc cgggggcccc cagcccgaa 420
tcttgggggc tgtaacaggt cctcggaagg gaggtccccg ccggaatgcc tggggaaatc 480
agtcatatgc agaattcatc agccaggcca ttgaaagcgc cccggagaag cgaactgacac 540
ttgcccagat ttacgagtgg atgggtccgta ctgtacccta cttcaaggac aagggtgaca 600
gcaacagctc agcaggatgg aagaactcga tccgccacaa cctgtccctg cacagcaagt 660
tcatcaaggt tcacaacgag gccaccggca aaagctcttg gtggatgctg aaccctgagg 720
gaggcaagag cggcaaaagcc ccccgccgcc gggccgcctc catggatagc agcagcaagc 780
tgctccgggg ccgcagtaaa gcccccaaga agaaaccatc tgtgctgcca gctccaccgc 840
aagggtccac tccaacgagc cctgtcggcc actttgccaa gtggtcaggc agcccttgct 900
ctcgaaccgg tgaagaagcc gatatgtgga ccaccttccg tccacgaagc agttcaaagt 960
ccagcagtgt cagcaccggg ctgtccccct tgaggccaga gtctgagggt ctggcggagg 1020
aaataaccagc ttcagtcagc agttatgcag ggggtgtccc tcccaccctc aatgaagggtc 1080
tagagctgtt agatgggtc aatctcacct cttcccatc cctgctatct cggagtgggtc 1140
tctctggctt ctccttgag catcctgggg ttaccggccc cttacacacc tacagcagct 1200
cccttttcag cccagcagag gggccctgt acctctgata cgccaccacc cctgctgac gtctcatga 1320
aggctctgga ggccctgtc tcccaggctc cgactcttct gttgctgggg gggttctct 1380
cccaggtaga tccattctg tccagggctc tgtgtcccaa gcccctagag gctcagggcc 1440
cctccagtaa gctggccacg ggcgtcggcc tttctatga tagcaccacc tccagtcag gcaagtccc 1500
ccagcagctt gggtcccacc ctttctatga actcctgtgc tcacacccc tactgaagct gcaagccaag 1560
acagaatgcc tcaggatcta gatcttgata tgtatatgga gaacctggag tgtgacatgg 1620
ataacatcat cagtgcctc atggatgagg gcgagggact ggacttcaac tttgagccag 1680
atccctgagt catgcctgga agctttgtcc cctgcttcag atgtggagcc aggcgtgttc 1740
atatctactc tttacccttg agccctcccc aggaatttgg gacctgtct tagagctagg 1800
gtggggtctg gtcacacaca ggtgttgaag aaattataaa gataaagctg ccccatctgg 1860
ggacgatatg gggaggggaga tgggagggga aaggggagag ggtttttctc actgtgccaa 1920
ttagggggta agggccccctc tcaggagcca tcctcggett tccccattcc taccactta 1980
ggctttgtag caagatgagc aatgctgttg gaaatgtgaa gtcaccagt gcttacccc 2040
tgcttttggg agcaggattt tttttagtag agtcttatct gagctgagcc aggctagctg 2100
gagcctggga tttctatgca gtggccccctt aggccagtga tgtgcggtgg gtgggctgtt 2160
taggggatct ggaagggccca aggtctgagc actggagtgg ctgccaggc caaatcacc 2220
ttagaaggct gcagataaca gaaaggcttt ttataaactt ttaaagaaat ataaacaca 2280
atatagagat tttttaacca tggcaggggt ctagtgttgg gcagaatgct tttttttctt 2340
tctgaaggct ttgtgatagt gacatgatac aaacactaca gacaataaat attaggagac 2400
acagggaagt ggggagaggt ggggagtaat agtaaacaca ggggaagagc cccctacgga 2460
ccaggatatag agaaaggctc atgcagaaat aggttagagt ttcctaaca aaaaagctaa 2520
ccagggtccc ctcatctctt caacttgtgc ctgggagtgt gtggtgttag ggtgcagcca 2580
cactcttcta tgaccagca tgggttagtg ctatggtggg agagtacatt gaaggcctgg 2640
aattagcttg gggccaggga agggactggg aggggagaga agagaaggag ggaaggattt 2700
aggatggtaa agttaggtac agagacctc ctgttcaagg cccctgacag ctgtccctgc 2760
ccttcttccc cttccctgac tgcaggggtt atgtggaagt gtgtgtggca gcaggcagcg 2820

65/299

```

gggaggggag gaacagggaa gggggagctg gggagcttgg ctgaggggtct gggaaatgag 2880
cagggatggg gggggatgtg gatcaggttt actagcacct gccagggagg ccatctgggg 2940
ctccttctcc accccagccc ccaaagcagc ccttccccca gtgccctttg catcgtcccc 3000
tccccacccc ctgctgtggg ttcccatcat ttctgtgtgc agcgctggc ctaccagat 3060
tgtatcatgt gctagattgg agtggggaag tgtgtcaaat caataaatga ataaattcaa 3120
taaatgccta taaccagcag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 3171

```

<210> 80
 <211> 501
 <212> PRT
 <213> Homo sapiens

<400> 80
 Met Arg Ile Gln Pro Gln Lys Ala Ala Ala Ile Ile Asp Leu Asp Pro
 1 5 10 15
 Asp Phe Glu Pro Gln Ser Arg Pro Arg Ser Cys Thr Trp Pro Leu Pro
 20 25 30
 Arg Pro Glu Ile Ala Asn Gln Pro Ser Glu Pro Pro Glu Val Glu Pro
 35 40 45
 Asp Leu Gly Glu Lys Val His Thr Glu Gly Arg Ser Glu Pro Ile Leu
 50 55 60
 Leu Pro Ser Arg Leu Ser Glu Pro Ala Gly Gly Pro Gln Pro Gly Ile
 65 70 75 80
 Leu Gly Ala Val Thr Gly Pro Arg Lys Gly Gly Ser Arg Arg Asn Ala
 85 90 95
 Trp Gly Asn Gln Ser Tyr Ala Glu Phe Ile Ser Gln Ala Ile Glu Ser
 100 105 110
 Ala Pro Glu Lys Arg Leu Thr Leu Ala Gln Ile Tyr Glu Trp Met Val
 115 120 125
 Arg Thr Val Pro Tyr Phe Lys Asp Lys Gly Asp Ser Asn Ser Ser Ala
 130 135 140
 Gly Trp Lys Asn Ser Ile Arg His Asn Leu Ser Leu His Ser Lys Phe
 145 150 155 160
 Ile Lys Val His Asn Glu Ala Thr Gly Lys Ser Ser Trp Trp Met Leu
 165 170 175
 Asn Pro Glu Gly Gly Lys Ser Gly Lys Ala Pro Arg Arg Arg Ala Ala
 180 185 190
 Ser Met Asp Ser Ser Ser Lys Leu Leu Arg Gly Arg Ser Lys Ala Pro
 195 200 205
 Lys Lys Lys Pro Ser Val Leu Pro Ala Pro Pro Glu Gly Ala Thr Pro
 210 215 220
 Thr Ser Pro Val Gly His Phe Ala Lys Trp Ser Gly Ser Pro Cys Ser
 225 230 235 240

66/299

Arg Asn Arg Glu Glu Ala Asp Met Trp Thr Thr Phe Arg Pro Arg Ser
 245 250 255
 Ser Ser Asn Ala Ser Ser Val Ser Thr Arg Leu Ser Pro Leu Arg Pro
 260 265 270
 Glu Ser Glu Val Leu Ala Glu Glu Ile Pro Ala Ser Val Ser Ser Tyr
 275 280 285
 Ala Gly Gly Val Pro Pro Thr Leu Asn Glu Gly Leu Glu Leu Leu Asp
 290 295 300
 Gly Leu Asn Leu Thr Ser Ser His Ser Leu Leu Ser Arg Ser Gly Leu
 305 310 315 320
 Ser Gly Phe Ser Leu Gln His Pro Gly Val Thr Gly Pro Leu His Thr
 325 330 335
 Tyr Ser Ser Ser Leu Phe Ser Pro Ala Glu Gly Pro Leu Ser Ala Gly
 340 345 350
 Glu Gly Cys Phe Ser Ser Ser Gln Ala Leu Glu Ala Leu Leu Thr Ser
 355 360 365
 Asp Thr Pro Pro Pro Pro Ala Asp Val Leu Met Thr Gln Val Asp Pro
 370 375 380
 Ile Leu Ser Gln Ala Pro Thr Leu Leu Leu Leu Gly Gly Leu Pro Ser
 385 390 395 400
 Ser Ser Lys Leu Ala Thr Gly Val Gly Leu Cys Pro Lys Pro Leu Glu
 405 410 415
 Ala Arg Gly Pro Ser Ser Leu Val Pro Thr Leu Ser Met Ile Ala Pro
 420 425 430
 Pro Pro Val Met Ala Ser Ala Pro Ile Pro Lys Ala Leu Gly Thr Pro
 435 440 445
 Val Leu Thr Pro Pro Thr Glu Ala Ala Ser Gln Asp Arg Met Pro Gln
 450 455 460
 Asp Leu Asp Leu Asp Met Tyr Met Glu Asn Leu Glu Cys Asp Met Asp
 465 470 475 480
 Asn Ile Ile Ser Asp Leu Met Asp Glu Gly Glu Gly Leu Asp Phe Asn
 485 490 495
 Phe Glu Pro Asp Pro
 500

<210> 81
 <211> 3171
 <212> DNA
 <213> Homo sapiens

67/299

<400> 81

```
gggacagctt agggactatc gtccctgggac taggggggaag ttcgcgactt tctgaagact 60
ggcaggaatg tgcctcctgg ccctcgatgc ttccccctg aggggaggca tcgtgaggga 120
ctgtggcagg cttcactgaa cgctgagccg gggaggtcca actccacgta tggatccggg 180
gaatgagaat tcagccacag aaggccgccc cgatcataga cctagatccc gacttcgaac 240
cccagagccg tccccgctcc tgcacctggc cccttccccg accagagatc gctaaccagc 300
cgtccgagcc gcccagagtg gagccagatc tgggggaaaa ggtacacacg gaggggcgct 360
cagagccgat cctgttgccc tctcggtctt cagagccggc cgggggcccc cagcccggaa 420
tcctgggggc tgtaacaggt cctcggaagg gaggtctccg ccggaatgcc tggggaaatc 480
agtcatatgc agaattcatc agccaggcca ttgaaagcgc cccggagaag cgactgacac 540
ttgccagat ttacgagtgg atggctccgta ctgtacccta cttcaaggac aagggtgaca 600
gcaacagctc agcaggatgg aagaactcga tccgccacaa cctgtccctg cacagcaagt 660
tcatcaaggc tcacaacgag gccaccggca aaagctcttg gtggatgctg aaccctgagg 720
gaggcaagag cggcaaaagg ccccgccgccc gggccgcctc catggatagc agcagcaagc 780
tgctccgggg ccgcagtaaa gcccccaaga agaaaccatc tgtgctgcca gctccacccg 840
aagggtgccac tccaacgagc cctgtcggcc actttgccaa gtggtcaggc agcccttgct 900
ctcgaacccg tgaagaagcc gatattgtga ccaccttccg tccacgaagc agttcaaagt 960
ccagcagtgat cagcaccocg ctgtccccct tgaggccaga gtctgagggt ctggcggagg 1020
aaataccagc ttcagtcagc agttatgcag ggggtgtccc tcccaccctc aatgaagggtc 1080
tagagctgtt agatgggctc aatctcacct cttcccatc cctgctatct cggagtgggtc 1140
tctctggctt ctctttgcag catcctgggg ttaccggccc cttacacacc tacagcagct 1200
cccttttcag cccagcagag gggcccctgt cagcaggaga aggggtgctt tccagctccc 1260
aggctctgga gggcctgctc acctctgata cgccaccacc cctgtctgac gtccctcatga 1320
cccaggtaga tcccatctgt tcccaggctc cgactcttct gttgctgggg gggcttccct 1380
cctccagtaa gctggccacg ggcgtcggcc tgtgtcccaa gcccctagag gctcgaggcc 1440
ccagcagctc ggttcccacc ctttctatga tagcaccacc tccagtcagt gcaagtgcc 1500
ccatcccaa ggctctgggg actcctgtgc tcacacccc tactgaagct gcaagccaag 1560
acagaatgcc tcaggatcta gatcttgata tgtatatgga gaacctggag tgtgacatgg 1620
ataacatcat cagtgcctc atggatgagg gcgagggact ggacttcaac tttgagccag 1680
atccctgagt catgcctgga agctttgtcc cctgcttcag atgtggagcc aggcgtgttc 1740
atatctactc tttacccttg agccctcccc aggaatttgg gacctgctt tagagctagg 1800
gtgggtctcg gtcacacaca ggtgttgaag aaattataaa gataaagctg ccccatctgg 1860
ggacgatatg gggagggaga tgggagggga aaggggagag ggtttttctc actgtgccaa 1920
ttagggggta agggccctc tcaggagcca tcctcggtt tccccattcc taccactta 1980
ggctttgtag caagatgagc aatgctgttg gaaatgtgaa gtcaccagtg gccttacc 2040
tgcccttggg agcaggatct tttttagag agtcttatct gagctgagcc aggctagctg 2100
gagcctggga tttctatgca gtggcccccctt aggccagtga tgtgcgggtg gtgggctgtt 2160
taggggatct ggaagggcc aaggtctgagc actggagtgg ctgcgcaggc caaatcacc 2220
ttagaaggct gcagataaca gaaaggcttt ttataaactt ttaaagaaat ataaacaca 2280
atatagagat tttttaacca tggcagggtg ctagtgggtg gcagaatgct ttttttctt 2340
tctgaaggct ttgtgatagt gacatgatac aaacactaca gacaataaat attaggagac 2400
acagggaagt ggggagaggt ggggagtaat agtaaacaca gggaagagct cccctacgga 2460
ccaggatatag agaaaggct atgcagaaat aggttagagt tccctaaca aaaaagctaa 2520
cccaggctcc ctcatctct caacttgtgc ctgggagtgt gtggtgttag ggtgcagcca 2580
cactcttcta tgaccagca tgggttagtg ctatggtggg agagtacatt gaaggcctgg 2640
aattagcttg gggccaggga agggactggg aggggagaga agagaaggag ggaaggattt 2700
aggatggtaa agttaggtag agagacctcc ctggtcaagg cccctgacag ctgtccctgc 2760
ccttcttccc cttccctgac tgcagggggt atgtggaagt gtgtgtggca gcaggcagcg 2820
gggaggggag gaacaggga gggggagctg gggagcttg ctgagggctc gggaaatga 2880
cagggatggg gggggatgtg gatcaggttt actagacct gccagggagg ccatctgggg 2940
ctccttctcc ccccagccc ccaaagcagc ccttcccca gtgcccttg catcgtcccc 3000
tccccacccc ctgctgtggg ttcccatcat ttctgtgtc agcgcctggc ctaccagat 3060
tgtatcatgt gctagattgg agtggggaag tgtgtcaaat caataaatga ataaattcaa 3120
taaatgccta taaccagcag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 3171
```

<210> 82

<211> 74

68/299

<212> DNA

<213> Homo sapiens

<400> 82

ggagtccaca ggatcagagt ggactttaag catgatacca gtagtccttt gctaatcagt 60
ggaacctctg caga 74

<210> 83

<211> 22

<212> PRT

<213> Homo sapiens

<400> 83

Lys Gln Pro Pro Pro Pro Glu Ser Gly Phe Gly Val Pro Trp Ser Asp
1 5 10 15

Glu Ile Leu Phe Ser Arg
20

<210> 84

<211> 69

<212> DNA

<213> Homo sapiens

<400> 84

aagcagcctc caccaccaga atcaggattt ggagttccat ggagtgatga gattttattt 60
tcaagataa 69

<210> 85

<211> 23

<212> PRT

<213> Homo sapiens

<400> 85

Val Lys Gln Lys Pro Lys Glu Lys Asp Leu Glu Phe His Gly Val Met
1 5 10 15

Arg Phe Tyr Phe Gln Asp Lys
20

<210> 86

<211> 69

<212> DNA

<213> Homo sapiens

<400> 86

gtaaaacaaa aaccaaaaga aaaggatttg gagttccatg gagtggatgag attttatttt 60
caagataaa 69

<210> 87

<211> 23

<212> PRT

<213> Homo sapiens

69/299

<400> 87

His Arg Ile Arg Val Asp Phe Lys Asp Leu Glu Phe His Gly Val Met
1 5 10 15

Arg Phe Tyr Phe Gln Asp Lys
20

<210> 88

<211> 69

<212> DNA

<213> Homo sapiens

<400> 88

cacaggatca gagtggactt taaggatttg gagttccatg gagtgatgag attttatttt 60
caagataaa 69

<210> 89

<211> 76

<212> PRT

<213> Homo sapiens

<400> 89

Pro Pro Thr Thr Gly Pro Pro Arg Lys Glu Val Pro Lys Thr Thr Pro
1 5 10 15

Ser Glu Pro Lys Lys Lys Gln Pro Pro Pro Glu Ser Gly Ile Tyr
20 25 30

Thr Ser Asn Lys Asp Pro Ile Ser His Ser Gly Gly Met Leu Arg Ala
35 40 45

Val Cys Ser Thr Pro Leu Ser Ser Ser Leu Leu Gly Pro Pro Gly Thr
50 55 60

Ser Ala Leu Pro Arg Leu Ser Arg Ser Pro Phe Thr
65 70 75

<210> 90

<211> 228

<212> DNA

<213> Homo sapiens

<400> 90

ccacctacta caggaccgcc aagaaaagaa gttcccaaaa ccactcctag tgagcccaag 60
aaaaagcagc ctccaccacc agaatacaggc atctacacca gtaataagga ccccatctcc 120
cacagtggcg ggatgtctgc ggetgtctgc agcaccctc tctcctccag cctcctgggg 180
ccccaggga cctcggcct gcccgctc agccgctccc cggttcacc 228

<210> 91

<211> 1093

<212> PRT

<213> Homo sapiens

70/299

<400> 91

```

Met Lys Glu Met Val Gly Gly Cys Cys Val Cys Ser Asp Glu Arg Gly
 1           5           10           15

Trp Ala Glu Asn Pro Leu Val Tyr Cys Asp Gly His Ala Cys Ser Val
          20           25           30

Ala Val His Gln Ala Cys Tyr Gly Ile Val Gln Val Pro Thr Gly Pro
          35           40           45

Trp Phe Cys Arg Lys Cys Glu Ser Gln Glu Arg Ala Ala Arg Val Arg
          50           55           60

Cys Glu Leu Cys Pro His Lys Asp Gly Ala Leu Lys Arg Thr Asp Asn
          65           70           75           80

Gly Gly Trp Ala His Val Val Cys Ala Leu Tyr Ile Pro Glu Val Gln
          85           90           95

Phe Ala Asn Val Leu Thr Met Glu Pro Ile Val Leu Gln Tyr Val Pro
          100          105          110

His Asp Arg Phe Asn Lys Thr Cys Tyr Ile Cys Glu Glu Thr Gly Arg
          115          120          125

Glu Ser Lys Ala Ala Ser Gly Ala Cys Met Thr Cys Asn Arg His Gly
          130          135          140

Cys Arg Gln Ala Phe His Val Thr Cys Ala Gln Met Ala Gly Leu Leu
          145          150          155          160

Cys Glu Glu Glu Val Leu Glu Val Asp Asn Val Lys Tyr Cys Gly Tyr
          165          170          175

Cys Lys Tyr His Phe Ser Lys Met Lys Thr Ser Arg His Ser Ser Gly
          180          185          190

Gly Gly Gly Gly Gly Ala Gly Gly Gly Gly Gly Ser Met Gly Gly Gly
          195          200          205

Gly Ser Gly Phe Ile Ser Gly Arg Arg Ser Arg Ser Ala Ser Pro Ser
          210          215          220

Thr Gln Gln Glu Lys His Pro Thr His His Glu Arg Gly Gln Lys Lys
          225          230          235          240

Ser Arg Lys Asp Lys Glu Arg Leu Lys Gln Lys His Lys Lys Arg Pro
          245          250          255

Glu Ser Pro Pro Ser Ile Leu Thr Pro Pro Val Val Pro Thr Ala Asp
          260          265          270

Lys Val Ser Ser Ser Ala Ser Ser Ser Ser His His Glu Ala Ser Thr
          275          280          285

Gln Glu Thr Ser Glu Ser Ser Arg Glu Ser Lys Gly Lys Lys Ser Ser
          290          295          300

```

71/299

Ser His Ser Leu Ser His Lys Gly Lys Lys Leu Ser Ser Gly Lys Gly
 305 310 315 320
 Val Ser Ser Phe Thr Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser
 325 330 335
 Ser Ser Gly Gly Pro Phe Gln Pro Ala Val Ser Ser Leu Gln Ser Ser
 340 345 350
 Pro Asp Phe Ser Ala Phe Pro Lys Leu Glu Gln Pro Glu Glu Asp Lys
 355 360 365
 Tyr Ser Lys Pro Thr Ala Pro Ala Pro Ser Ala Pro Pro Ser Pro Ser
 370 375 380
 Ala Pro Glu Pro Pro Lys Ala Asp Leu Phe Glu Gln Lys Val Val Phe
 385 390 395 400
 Ser Gly Phe Gly Pro Ile Met Arg Phe Ser Thr Thr Thr Ser Ser Ser
 405 410 415
 Gly Arg Ala Arg Ala Pro Ser Pro Gly Asp Tyr Lys Ser Pro His Val
 420 425 430
 Thr Gly Ser Gly Ala Ser Ala Gly Thr His Lys Arg Met Pro Ala Leu
 435 440 445
 Ser Ala Thr Pro Val Pro Ala Asp Glu Thr Pro Glu Thr Gly Leu Lys
 450 455 460
 Glu Lys Lys His Lys Ala Ser Lys Arg Ser Arg His Gly Pro Gly Arg
 465 470 475 480
 Pro Lys Gly Ser Arg Asn Lys Glu Gly Thr Gly Gly Pro Ala Ala Pro
 485 490 495
 Ser Leu Pro Ser Ala Gln Leu Ala Gly Phe Thr Ala Thr Ala Ala Ser
 500 505 510
 Pro Phe Ser Gly Gly Ser Leu Val Ser Ser Gly Leu Gly Gly Leu Ser
 515 520 525
 Ser Arg Thr Phe Gly Pro Ser Gly Ser Leu Pro Ser Leu Ser Leu Glu
 530 535 540
 Ser Pro Leu Leu Gly Ala Gly Ile Tyr Thr Ser Asn Lys Asp Pro Ile
 545 550 555 560
 Ser His Ser Gly Gly Met Leu Arg Ala Val Cys Ser Thr Pro Leu Ser
 565 570 575
 Ser Ser Leu Leu Gly Pro Pro Gly Thr Ser Ala Leu Pro Arg Leu Ser
 580 585 590
 Arg Ser Pro Phe Thr Ser Thr Leu Pro Ser Ser Ser Ala Ser Ile Ser
 595 600 605
 Thr Thr Gln Val Phe Ser Leu Ala Gly Ser Thr Phe Ser Leu Pro Ser

72/299

610	615	620
Thr His Ile Phe Gly	Thr Pro Met Gly Ala	Val Asn Pro Leu Leu Ser
625	630	635 640
Gln Ala Glu Ser Ser	His Thr Glu Pro Asp	Leu Glu Asp Cys Ser Phe
	645	650 655
Arg Cys Arg Gly Thr	Ser Pro Gln Glu Ser	Leu Ser Ser Met Ser Pro
	660	665 670
Ile Ser Ser Leu Pro	Ala Leu Phe Asp Gln	Thr Ala Ser Ala Pro Cys
	675	680 685
Gly Gly Gly Gln Leu	Asp Pro Ala Ala Pro	Gly Thr Thr Asn Met Glu
	690	695 700
Gln Leu Leu Glu Lys	Gln Gly Asp Gly Glu	Ala Gly Val Asn Ile Val
	705	710 715 720
Glu Met Leu Lys Ala	Leu His Ala Leu Gln	Lys Glu Asn Gln Arg Leu
	725	730 735
Gln Glu Gln Ile Leu	Ser Leu Thr Ala Lys	Lys Glu Arg Leu Gln Ile
	740	745 750
Leu Asn Val Gln Leu	Ser Val Pro Phe Pro	Ala Leu Pro Ala Ala Leu
	755	760 765
Pro Ala Ala Asn Gly	Pro Val Pro Gly Pro	Tyr Gly Leu Pro Pro Gln
	770	775 780
Ala Gly Ser Ser Asp	Ser Leu Ser Thr Ser	Lys Ser Pro Pro Gly Lys
	785	790 795 800
Ser Ser Leu Gly Leu	Asp Asn Ser Leu Ser	Thr Ser Ser Glu Asp Pro
	805	810 815
His Ser Gly Cys Pro	Ser Arg Ser Ser Ser	Leu Ser Phe His Ser
	820	825 830
Thr Pro Pro Pro Leu	Pro Leu Leu Gln Gln	Ser Pro Ala Thr Leu Pro
	835	840 845
Leu Ala Leu Pro Gly	Ala Pro Ala Pro Leu	Pro Pro Gln Pro Gln Asn
	850	855 860
Gly Leu Gly Arg Ala	Pro Gly Ala Ala Gly	Leu Gly Ala Met Pro Met
	865	870 875 880
Ala Glu Gly Leu Leu	Gly Gly Leu Ala Gly	Ser Gly Gly Leu Pro Leu
	885	890 895
Asn Gly Leu Leu Gly	Gly Gly Leu Asn Gly	Ala Ala Ala Pro Asn Pro Ala
	900	905 910
Ser Leu Ser Gln Ala	Gly Gly Ala Pro Thr	Leu Gln Leu Pro Gly Cys
	915	920 925

73/299

Leu Asn Ser Leu Thr Glu Gln Gln Arg His Leu Leu Gln Gln Gln Glu
 930 935 940
 Gln Gln Leu Gln Gln Leu Gln Gln Leu Leu Ala Ser Pro Gln Leu Thr
 945 950 955 960
 Pro Glu His Gln Thr Val Val Tyr Gln Met Ile Gln Gln Ile Gln Gln
 965 970 975
 Lys Arg Glu Leu Gln Arg Leu Gln Met Ala Gly Gly Ser Gln Leu Pro
 980 985 990
 Met Ala Ser Leu Leu Ala Gly Ser Ser Thr Pro Leu Leu Ser Ala Gly
 995 1000 1005
 Thr Pro Gly Leu Leu Pro Thr Ala Ser Ala Pro Pro Leu Leu Pro Ala
 1010 1015 1020
 Gly Ala Leu Val Ala Pro Ser Leu Gly Asn Asn Thr Ser Leu Met Ala
 1025 1030 1035 1040
 Ala Ala Ala Ala Ala Ala Ala Val Ala Ala Ala Gly Gly Pro Pro Val
 1045 1050 1055
 Leu Thr Ala Gln Thr Asn Pro Phe Leu Ser Leu Ser Gly Ala Glu Gly
 1060 1065 1070
 Ser Gly Gly Gly Pro Lys Gly Gly Thr Ala Asp Lys Gly Ala Ser Ala
 1075 1080 1085
 Asn Gln Glu Lys Gly
 1090

<210> 92
 <211> 3282
 <212> DNA
 <213> Homo sapiens

<400> 92
 atgaaggaga tggtaggagg ctgctgcgta tggtcggacg agaggggctg ggccgagAAC 60
 ccgctgggtct actgcgatgg gcacgcgtgc agcgtggccg tccaccaagc ttgctatggc 120
 atcgttcagg tgccaacggg accctgggtc tgccggaaat gtgaatctca ggagcgagca 180
 gccaggggtga ggtgtgagct gtgcccacac aaagacgggg cattgaagag gactgataat 240
 ggaggctggg cacacgtggg gtgtgccctc tacatccccg aggtgcaatt tgccaacgtg 300
 ctcaccatgg agcccatcgt gctgcagtac gtgcctcatg atcgcttcaa caagacctgt 360
 tacatctgcg aggagacggg cgggagagc aaggcggcct cgggagcctg catgacctgt 420
 aaccgccatg gatgtcgaca agctttccac gtcaacctgt cccaaatggc aggcttgctg 480
 tgtgaggaag aagtgtctga ggtggacaac gtcaagtact gcggctactg caaataccac 540
 ttcagcaaga tgaagacatc ccggcacagc agcgggggag gcggaggagg cgctggagga 600
 ggaggtggca gcatgggggg aggtggcagt ggtttcatct ctgggaggag aagccggtca 660
 gcctcaccat ccacgcagca ggagaagcac cccaccacc acgagagggg ccagaagaag 720
 agtcgaaagg acaaagaacg ccttaagcag aagcacaaga agcggcctga gtcgcccccc 780
 agcatcctca cccgcgccgt ggtccccact gctgacaagg tctctctctc ggcttctctc 840
 tctctccacc ccagggccag cagcgaggag acctctgaga gcagcaggga gtcaaagggg 900
 aaaagtctt ccagccatag cctgagtcac aaaggggaaga aactgagcag tgggaaaggt 960
 gtgagcagtt ttacctccgc ctctctctct tctctctct cttctctctc ctctgggggg 1020

74/299

```

cccttcacgc ctgcagtctc gtccctgcag agctcccctg actttctctgc attcccccaag 1080
ctggagcagc cagaggagga caagtactcc aagcccacag cccccgcccc ttccagcccct 1140
ccttctccct cagctccoga gcccccaag gctgaccttt ttgagcagaa ggtgggtcttc 1200
tctggctttg ggccatcat gcgcttctcc accaccacct ccagctcagg cggggcccg 1260
gcgccctccc ctggggacta taagtctccc cagctcacgg ggtctggggc ctgggcaggc 1320
acccacaaac ggatgcccgc actgagtgcc acccctgtgc ctgctgatga gaccctgag 1380
acaggcctga aggagaagaa gcacaaagcc agcaagagga gccgcatgg gccaggccgt 1440
cccaagggca gccggaacaa ggagggcact ggggggccag ctgccccatc cttgcccagt 1500
gcccagctgg ctggctttac cgccactgct gcctcaccct tctctggagg ttccctggtc 1560
agctccggcc tgggaggtct gtctctccga acctttgggc cttctgggag cttgcccagc 1620
ttgagcctgg agtccccctt actaggggca ggcattctaca ccagtaataa ggacccatc 1680
tcccacagtg gcgggatgct gcgggctgtc tgcagcacc cttctctctc cagcctcctg 1740
gggccccccag ggacctcggc cctgccccgc ctcagccgct ccccgttcac cagcaccctc 1800
ccctcctctt ctgcttctat ctccaccact cagggtgtttt ctctggctgg ctctaccttt 1860
agcctccctt ctaccacat ctttggaacc cccatgggtg ccgttaatcc cctcctctcc 1920
caagctgaga gcagccacac agagccagac ctggaggact gcagcttccg gtgtcggggg 1980
acctccctc aggagagtct gtcttccatg tcccccatca gcagcctccc cgcactcttc 2040
gaccagacag cctctgcacc ctgtgggggc ggccagttag acccgcggcg cccagggacg 2100
actaacatgg agcagcttct ggagaagcag ggcgacgggg aggcggcggt caacatcgtg 2160
gagatgctga agcgctgca cgcgctgcag aaggagaacc agcggtgca agagcagatc 2220
ctgagcctga cggccaaaaa ggagcggctg cagattctca acgtgcagct ctctgtgccc 2280
ttccctgccc tgcctgctgc cctgcctgcc gccaacgggc ctgtccctgg gccctatggc 2340
ctgcctcccc aagccgggag cagcgactcc ttgagcacca gcaagagccc tccgggaaag 2400
agcagcctcg gcctggacaa ctgctgttcc acttctcttg aggaccaca ctcaggctgc 2460
ccgagccgca gcagctcgtc gctgtccttc cacagcacgc cccaccgct gccctcctc 2520
cagcagagcc ctgccactct gccctggcc ctgcctgggg cccctgcccc actccgccc 2580
cagccgcaga acgggttggg ccgggcaccc ggggcagcgg ggctgggggc catgcccag 2640
gctgaggggc tgttgggggg gctggcaggc agtgggggccc tgcccctcaa tgggctcctt 2700
gggggggtga atggggccgc tgccccaac cccgcaagct tgagccaggc tggcggggcc 2760
cccacgctgc agctgccagg ctgtctcaac agccttacag agcagcagag acatctcctt 2820
cagcagcaag agcagcagct ccagcaactc cagcagctcc tggcctcccc gcagctgacc 2880
ccggaacacc agactgttgt ctaccagatg atccagcaga tccagcagaa acgggagctg 2940
cagcgtctgc agatggctgg gggctcccag ctgccatgg ccagcctgct ggcaggaagc 3000
tccaccccg cgtgtctgc gggtaacctt ggctgtctgc ccacagcgtc tgctccaccc 3060
ctgctgcccg ctggagccct agtggctccc tgccttggca acaacacaag tctcatggcc 3120
gcagcagctg cagctgcagc agtagcagca gcaggcggac ctccagtcct cactgcccag 3180
accaacccct tcctcagcct gtcgggagca gagggcagtg gcggtggccc caaaggaggg 3240
accgctgaca aaggagcctc agccaaccag gaaaaaggct aa 3282

```

<210> 93
 <211> 752
 <212> PRT
 <213> Homo sapiens

<400> 93
 Met Arg Ile Pro Val Asp Ala Ser Thr Ser Arg Arg Phe Thr Pro Pro
 1 5 10 15
 Ser Thr Ala Leu Ser Pro Gly Lys Met Ser Glu Ala Leu Pro Leu Gly
 20 25 30
 Ala Pro Asp Ala Gly Ala Ala Leu Ala Gly Lys Leu Arg Ser Gly Asp
 35 40 45
 Arg Ser Met Val Glu Val Leu Ala Asp His Pro Gly Glu Leu Val Arg
 50 55 60

75/299

Thr	Asp	Ser	Pro	Asn	Phe	Leu	Cys	Ser	Val	Leu	Pro	Thr	His	Trp	Arg	
65					70					75					80	
Cys	Asn	Lys	Thr	Leu	Pro	Ile	Ala	Phe	Lys	Val	Val	Ala	Leu	Gly	Asp	
				85					90					95		
Val	Pro	Asp	Gly	Thr	Leu	Val	Thr	Val	Met	Ala	Gly	Asn	Asp	Glu	Asn	
			100					105					110			
Tyr	Ser	Ala	Glu	Leu	Arg	Asn	Ala	Thr	Ala	Ala	Met	Lys	Asn	Gln	Val	
		115					120					125				
Ala	Arg	Phe	Asn	Asp	Leu	Arg	Phe	Val	Gly	Arg	Ser	Gly	Arg	Gly	Lys	
	130					135					140					
Ser	Phe	Thr	Leu	Thr	Ile	Thr	Val	Phe	Thr	Asn	Pro	Pro	Gln	Val	Ala	
145					150					155					160	
Thr	Tyr	His	Arg	Ala	Ile	Lys	Ile	Thr	Val	Asp	Gly	Pro	Arg	Glu	Pro	
				165					170					175		
Arg	Asn	Arg	Thr	Glu	Lys	His	Ser	Thr	Met	Pro	Asp	Ser	Pro	Val	Asp	
			180					185					190			
Val	Lys	Thr	Gln	Ser	Arg	Leu	Thr	Pro	Pro	Thr	Met	Pro	Pro	Pro	Pro	
	195						200					205				
Thr	Thr	Gln	Gly	Ala	Pro	Arg	Thr	Ser	Ser	Phe	Thr	Pro	Thr	Thr	Leu	
	210					215					220					
Thr	Asn	Gly	Thr	Ser	His	Ser	Pro	Thr	Ala	Leu	Asn	Gly	Ala	Pro	Ser	
225					230					235					240	
Pro	Pro	Asn	Gly	Phe	Ser	Asn	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	
				245					250					255		
Leu	Ala	Asn	Gln	Gln	Leu	Pro	Pro	Ala	Cys	Gly	Ala	Arg	Gln	Leu	Ser	
		260						265					270			
Lys	Leu	Lys	Arg	Phe	Leu	Thr	Thr	Leu	Gln	Gln	Phe	Gly	Asn	Asp	Ile	
	275						280					285				
Ser	Pro	Glu	Ile	Gly	Glu	Arg	Val	Arg	Thr	Leu	Val	Leu	Gly	Leu	Val	
	290					295					300					
Asn	Ser	Thr	Leu	Thr	Ile	Glu	Glu	Phe	His	Ser	Lys	Leu	Gln	Glu	Ala	
305					310					315					320	
Thr	Asn	Phe	Pro	Leu	Arg	Pro	Phe	Val	Ile	Pro	Phe	Leu	Lys	Ala	Asn	
				325					330					335		
Leu	Pro	Leu	Leu	Gln	Arg	Glu	Leu	Leu	His	Cys	Ala	Arg	Leu	Ala	Lys	
		340						345					350			
Gln	Asn	Pro	Ala	Gln	Tyr	Leu	Ala	Gln	His	Glu	Gln	Leu	Leu	Leu	Asp	
	355						360					365				
Ala	Ser	Thr	Thr	Ser	Pro	Val	Asp	Ser	Ser	Glu	Leu	Leu	Leu	Asp	Val	

76/299

370	375	380
Asn Glu Asn Gly Lys Arg Arg Thr Pro Asp Arg Thr Lys Glu Asn Gly		
385	390	395 400
Phe Asp Arg Glu Pro Leu His Ser Glu His Pro Ser Lys Arg Pro Cys		
	405 410	415
Thr Ile Ser Pro Gly Gln Arg Tyr Ser Pro Asn Asn Gly Leu Ser Tyr		
	420 425	430
Gln Pro Asn Gly Leu Pro His Pro Thr Pro Pro Pro Gln His Tyr		
	435 440	445
Arg Leu Asp Asp Met Ala Ile Ala His His Tyr Arg Asp Ser Tyr Arg		
	450 455	460
His Pro Ser His Arg Asp Leu Arg Asp Arg Asn Arg Pro Met Gly Leu		
	465 470	480
His Gly Thr Arg Gln Glu Glu Met Ile Asp His Arg Leu Thr Asp Arg		
	485 490	495
Glu Trp Ala Glu Glu Trp Lys His Leu Asp His Leu Leu Asn Cys Ile		
	500 505	510
Met Asp Met Val Glu Lys Thr Arg Arg Ser Leu Thr Val Leu Arg Arg		
	515 520	525
Cys Gln Glu Ala Asp Arg Glu Glu Leu Asn Tyr Trp Ile Arg Arg Tyr		
	530 535	540
Ser Asp Ala Glu Asp Leu Lys Lys Gly Gly Gly Ser Ser Ser Ser His		
	545 550	555 560
Ser Arg Gln Gln Ser Pro Val Asn Pro Asp Pro Val Ala Leu Asp Ala		
	565 570	575
His Arg Glu Phe Leu His Arg Pro Ala Ser Gly Tyr Val Pro Glu Glu		
	580 585	590
Ile Trp Lys Lys Ala Glu Glu Ala Val Asn Glu Val Lys Arg Gln Ala		
	595 600	605
Met Thr Glu Leu Gln Lys Ala Val Ser Glu Ala Glu Arg Lys Ala His		
	610 615	620
Asp Met Ile Thr Thr Glu Arg Ala Lys Met Glu Arg Thr Val Ala Glu		
	625 630	635 640
Ala Lys Arg Gln Ala Ala Glu Asp Ala Leu Ala Val Ile Asn Gln Gln		
	645 650	655
Glu Asp Ser Ser Glu Ser Cys Trp Asn Cys Gly Arg Lys Ala Ser Glu		
	660 665	670
Thr Cys Ser Gly Cys Asn Thr Ala Arg Tyr Cys Gly Ser Phe Cys Gln		
	675 680	685

77/299

His Lys Asp Trp Glu Lys His His His Ile Cys Gly Gln Thr Leu Gln
690 695 700

Ala Gln Gln Gln Gly Asp Thr Pro Ala Val Ser Ser Ser Val Thr Pro
705 710 715 720

Asn Ser Gly Ala Gly Ser Pro Met Asp Thr Pro Pro Ala Ala Thr Pro
725 730 735

Arg Ser Thr Thr Pro Gly Thr Pro Ser Thr Ile Glu Thr Thr Pro Arg
740 745 750

<210> 94
<211> 4272
<212> DNA
<213> Homo sapiens

<400> 94
catagagcca gcggggcgcg gcggggacggg cgccccgcgg ccggaccag ccagggcacc 60
acgctgcccc gccctgcgcc gccagggcact tctttccggg gctcctaggg acgccagaag 120
gaagtcaacc tctgctgctt ctctctggcc tgcgttggac cttccttttt ttgttgtttt 180
tttttgtttt tcccccttct tctttttgaa ttaactggct tcttggctgg atgttttcaa 240
cttcttttct ggctgcgaac ttttcccaa ttgttttctt ttacaacag ggggagaaaag 300
tgctctgtgg tccgaggcga gccgtgaagt tgcgtgtgct tggcagtgtg cgtggcagga 360
tgtgcgtgct tgtgtaacct gagccgccc atctgtttct atctgcgcc cggagccctc 420
cctcaaggcc cgtccacct gctgcgggta cgcggcgctc gtgggtgttc gtgcctcgga 480
gcagctaacc ggcggtgctt gggcgacggg ggaggagtat cgtctcgctg ctgcccagat 540
cagggtgag tcaccagct gatgtagaca gtggctgctt tccgaagat gcgtgtttgc 600
atgtgtgtga ctctgcggct gctcaactcc caacaacca gaggaccagc cacaactta 660
accaacatcc ccaaaccgga gttcacagat gtgggagagc tgtagaacct tgagtgtcat 720
cgactgggct tcttatgat tgttgtttta agattagctg aagatctctg aaacgctgaa 780
ttttctgcac tgagcgtttt gacagaattc attgagagaa cagagaacat gacaagtact 840
tctagctcag cactgctcca actactgaag ctgattttca aggctactta aaaaaatctg 900
cagcgtacat taatggattt ctgttgtgtt taaattctcc acagattgta ttgtaaatat 960
tttatgaagt agagcatatg tatatattta tatatacgtg cacatacatt agtagcacta 1020
cctttggaag tctcagctct tgccttttcgg gactgaagcc agttttgcat gataaaagt 1080
gccttgttac gggagataat tgtgttctgt tgggacttta gacaaaactc acctgcaaaa 1140
aactgacagg cattaactac tggaacttcc aaataatgtg tttgctgacg gttttactct 1200
tcgcataaag atttttaggaa gtgtatgaga attttgcctt cagggaacttt tctaacagcc 1260
aaagacagaa cttaacctct gcaagcaaga ttctgtggaag atagtctcca ctttttaagt 1320
cactaagcaa tcggttgcta ggagcccact ctgggtcaga ggccgatccg cagaaccaga 1380
acgttttccc ctctggact gttagtaact tagtctcctt cctcccctaa ccaccccgcc 1440
cccccccccac ccccgagct aataaaggcc cctgaacgtg tatgttggtc tcccgggagc 1500
tgcttgetga agatccgcgc ccctgtcgcc gtctggtagg agctgtttgc agggtcctaa 1560
ctcaatcgcc ttgttgtgat gcgtatcccc gtatagacca gcacgagccg ccgcttcacg 1620
ccgccttcca ccgcgctgag cccaggcaag atgagcgagg cgttgccgct gggcgccccg 1680
gacgcggcg ctgccctggc cggcaagctg aggagcggcg accgcagcat ggtggaggtg 1740
ctggcgagcc acccgggcga cctgggtgctg accgacagcc ccaacttctt ctgctccgtg 1800
ctgcctacgc actggcgctg caacaagacc ctgcccactg ctttcaaggt ggtggcccta 1860
ggggatgttc cagatggcac tctggtcact gtgatggctg gcaatgatga aaactactcg 1920
gctgagctga gaaatgctac cgcagccatg aagaaccagg ttgcaagatt taatgacctc 1980
aggtttgtcg gtcgaagtgg aagagggaaa agcttccact tgaccatcac tgtcttcaca 2040
aaccacccgc aagtcgccac ctaccacaga gccatcaaaa tcacagtgga tgggccccga 2100
gaacctcgaa atcgtactga gaagcactcc acaatgccag actcacctgt ggatgtgaag 2160
acgcaatcta ggctgactcc tccaacaatg ccacctcccc caactactca aggagctcca 2220
agaaccagtt catttacacc gacaacgtta actaatggca cgagccattc tctacagcc 2280

78/299

```

ttgaatggcg cccctcacc acccaatggc ttcagcaatg ggccttcctc ttcttccctc 2340
tcctctctgg ctaatcaaca gctgccccca gctgtgggtg ccaggcaact cagcaagctg 2400
aaaagggttc ttactaccct gcagcagttt ggcaatgaca ttccaccga gataggagaa 2460
agagttcgca ccctcgttct gggactagtg aactccactt tgacaattga agaatttcat 2520
tccaaactgc aagaagctac taacttccca ctgagacctt ttgtcatccc atttttgaag 2580
gccaaactgc ccctgtgca gcgtagctc ctccactggc caagactggc caaacagaac 2640
cctgcccagt acctcgccca gcatgaacag ctgcttctgg atgccagcac cacctcacct 2700
gttgactcct cagagctgct tctcgatgtg aacgaaaacg ggaagaggcg aactccagac 2760
agaaccaaag aaaatggctt tgacagagag cctttgcact cagaacatcc aagcaagcga 2820
ccatgcacta ttagcccagg ccagcggtag agtccaaata acggcttatc ctaccagccc 2880
aatggcctgc ctcaccctac cccacctcca cctcagcatt accgtttgga tgatatggcc 2940
attgcccacc actacaggga ctctatcgca caccacagcc acagggacct cagggacaga 3000
aacagacctt tggggttgca tggcacacgt caagaagaaa tgattgatca cagactaaca 3060
gacagagaaat gggcagaaga gtggaaacat cttgaccatc tgttaaactg cataatggac 3120
atggtagaaa aaacaaggcg atctctcacc gtactaaggc ggtgtcaaga agcagaccgg 3180
gaagaattga attactggat ccggcggtag agtgacgcgc aggacttaaa aaaagggtggc 3240
ggcagtagca gcagccactc taggcagcag agtcccgta acccagaccc agttgcacta 3300
gacgcgcata gggaattcct tcacaggcct gcgtctggat acgtgccaga ggagatctgg 3360
aagaaagctg aggaggccgt caatgaggtg aagcgccagg cgatgacgga gctgcagaag 3420
gccgtgtctg aggcggagcg gaaagcccac gacatgatca caacagagag ggccaagatg 3480
gagcgcacgg tcgccgaggg caaacggcag gcggcggagg acgcactggc agttatcaat 3540
cagcaggagg attcaagcga gagttgctgg aattgtggcc gtaaagcgag tgaaacctgc 3600
agtggctgta acacagcccg atactgtggc tcattttgcc agcacaaaaga ctggggagaag 3660
caccatcaca tctgtggaca gacctgcag gccagcagc agggagacac acctgcagtc 3720
agtcctctg tcacgcccac cagcggggct gggagccga tggacacacc accagcagcc 3780
actccgaggt caaccacccc gggaaccctt tccaccatag agacaacccc tcgctagacg 3840
tgaactcaga actgtcggag gaaagacaac acaaccaacg cgaaaccaat tcctcatcct 3900
cagatgctca aagttgtttt ttttgtttgt ttgtttatta gatgaattat cctatttcag 3960
tacttcagca agagagaacc taactgtatc ttgaggtggt agtaaaacac agaggggccag 4020
taacgggtcg taatgactta ttgtggataa caaagatata ttttcttttag agaactgaaa 4080
agagagcaga gaatataaca tgaaatgata gatttgacct cctccctgtt attttcaagt 4140
agctgggatt ttaactaga tgacctcatt aaccgatgct ttaccaaaca gcaaaocaa 4200
agattgctaa ttgctgttga aagcaaaaat gctaataata aaagtcacaa tgttctttat 4260
atacaataat gg 4272

```

<210> 95
 <211> 588
 <212> PRT
 <213> Homo sapiens

<400> 95
 Ala Ile Lys Ile Thr Val Asp Gly Pro Arg Glu Pro Arg Asn Arg Thr
 1 5 10 15
 Glu Lys His Ser Thr Met Pro Asp Ser Pro Val Asp Val Lys Thr Gln
 20 25 30
 Ser Arg Leu Thr Pro Pro Thr Met Pro Pro Pro Pro Thr Thr Gln Gly
 35 40 45
 Ala Pro Arg Thr Ser Ser Phe Thr Pro Thr Thr Leu Thr Asn Gly Thr
 50 55 60
 Ser His Ser Pro Thr Ala Leu Asn Gly Ala Pro Ser Pro Pro Asn Gly
 65 70 75 80
 Phe Ser Asn Gly Pro Ser Ser Ser Ser Ser Ser Ser Leu Ala Asn Gln

79/299

85					90					95					
Gln	Leu	Pro	Pro	Ala	Cys	Gly	Ala	Arg	Gln	Leu	Ser	Lys	Leu	Lys	Arg
			100					105							110
Phe	Leu	Thr	Thr	Leu	Gln	Gln	Phe	Gly	Asn	Asp	Ile	Ser	Pro	Glu	Ile
			115					120							125
Gly	Glu	Arg	Val	Arg	Thr	Leu	Val	Leu	Gly	Leu	Val	Asn	Ser	Thr	Leu
			130					135							140
Thr	Ile	Glu	Glu	Phe	His	Ser	Lys	Leu	Gln	Glu	Ala	Thr	Asn	Phe	Pro
								150							160
Leu	Arg	Pro	Phe	Val	Ile	Pro	Phe	Leu	Lys	Ala	Asn	Leu	Pro	Leu	Leu
															175
Gln	Arg	Glu	Leu	Leu	His	Cys	Ala	Arg	Leu	Ala	Lys	Gln	Asn	Pro	Ala
															190
Gln	Tyr	Leu	Ala	Gln	His	Glu	Gln	Leu	Leu	Leu	Asp	Ala	Ser	Thr	Thr
															205
Ser	Pro	Val	Asp	Ser	Ser	Glu	Leu	Leu	Leu	Asp	Val	Asn	Glu	Asn	Gly
															220
Lys	Arg	Arg	Thr	Pro	Asp	Arg	Thr	Lys	Glu	Asn	Gly	Phe	Asp	Arg	Glu
															240
Pro	Leu	His	Ser	Glu	His	Pro	Ser	Lys	Arg	Pro	Cys	Thr	Ile	Ser	Pro
															255
Gly	Gln	Arg	Tyr	Ser	Pro	Asn	Asn	Gly	Leu	Ser	Tyr	Gln	Pro	Asn	Gly
															270
Leu	Pro	His	Pro	Thr	Pro	Pro	Pro	Pro	Gln	His	Tyr	Arg	Leu	Asp	Asp
															285
Met	Ala	Ile	Ala	His	His	Tyr	Arg	Asp	Ser	Tyr	Arg	His	Pro	Ser	His
															300
Arg	Asp	Leu	Arg	Asp	Arg	Asn	Arg	Pro	Met	Gly	Leu	His	Gly	Thr	Arg
															320
Gln	Glu	Glu	Met	Ile	Asp	His	Arg	Leu	Thr	Asp	Arg	Glu	Trp	Ala	Glu
															335
Glu	Trp	Lys	His	Leu	Asp	His	Leu	Leu	Asn	Cys	Ile	Met	Asp	Met	Val
															350
Glu	Lys	Thr	Arg	Arg	Ser	Leu	Thr	Val	Leu	Arg	Arg	Cys	Gln	Glu	Ala
															365
Asp	Arg	Glu	Glu	Leu	Asn	Tyr	Trp	Ile	Arg	Arg	Tyr	Ser	Asp	Ala	Glu
															380
Asp	Leu	Lys	Lys	Gly	Gly	Gly	Ser	Ser	Ser	Ser	His	Ser	Arg	Gln	Gln
															400

Ser	Pro	Val	Asn	Pro	Asp	Pro	Val	Ala	Leu	Asp	Ala	His	Arg	Glu	Phe	
				405					410					415		
Leu	His	Arg	Pro	Ala	Ser	Gly	Tyr	Val	Pro	Glu	Glu	Ile	Trp	Lys	Lys	
				420					425					430		
Ala	Glu	Glu	Ala	Val	Asn	Glu	Val	Lys	Arg	Gln	Ala	Met	Thr	Glu	Leu	
				435					440					445		
Gln	Lys	Ala	Val	Ser	Glu	Ala	Glu	Arg	Lys	Ala	His	Asp	Met	Ile	Thr	
				450					455					460		
Thr	Glu	Arg	Ala	Lys	Met	Glu	Arg	Thr	Val	Ala	Glu	Ala	Lys	Arg	Gln	
				465					470					475		
Ala	Ala	Glu	Asp	Ala	Leu	Ala	Val	Ile	Asn	Gln	Gln	Glu	Asp	Ser	Ser	
				485					490					495		
Glu	Ser	Cys	Trp	Asn	Cys	Gly	Arg	Lys	Ala	Ser	Glu	Thr	Cys	Ser	Gly	
				500					505					510		
Cys	Asn	Thr	Ala	Arg	Tyr	Cys	Gly	Ser	Phe	Cys	Gln	His	Lys	Asp	Trp	
				515					520					525		
Glu	Lys	His	His	His	Ile	Cys	Gly	Gln	Thr	Leu	Gln	Ala	Gln	Gln	Gln	
				530					535					540		
Gly	Asp	Thr	Pro	Ala	Val	Ser	Ser	Ser	Val	Thr	Pro	Asn	Ser	Gly	Ala	
				545					550					555		
Gly	Ser	Pro	Met	Asp	Thr	Pro	Pro	Ala	Ala	Thr	Pro	Arg	Ser	Thr	Thr	
				565					570					575		
Pro	Gly	Thr	Pro	Ser	Thr	Ile	Glu	Thr	Thr	Pro	Arg					
				580					585							

<400> 96							
gccatcaaaa	tcacagtggga	tggggcccccga	gaacctcgaa	atcgtactga	gaagcactcc	60	
acaatgccag	actcacctgt	ggatgtgaag	acgcaatcta	ggctgactcc	tccaacaatg	120	
ccacctcccc	caactactca	aggagctcca	agaaccagtt	catttacacc	gacaacgtta	180	
actaatggca	cgagccattc	tcctacagcc	ttgaatggcg	ccccctcacc	acccaatggc	240	
ttcagtaagt	ggccttcctc	ttcttctctc	tcctctctgg	ctaatacaac	gctgccccca	300	
gcctgtggtg	ccaggcaact	cagcaagctg	aaaaggttcc	ttactacctc	gcagcagttt	360	
ggcaatgaca	tttcacccga	gataggagaa	agagttcgca	ccctcgttct	gggactatgt	420	
aactccactt	tgacaattga	agaatttcat	tccaaactgc	aagaagctac	taacttccca	480	
ctgagacctt	tbgtcatccc	atttttgaag	gccaaactgc	ccctgctgca	gcgtgagctc	540	
ctccactgcg	caagactggc	caaacagaac	cctgccagtt	acctcgccca	gcataaacag	600	
ctgctttctg	atgccagcac	cacctcacct	gttgactcct	cagagctgct	tctcgatgtg	660	
aacgaaaaac	ggaagaggcg	aactccagac	agaaccaaaag	aaaatggcct	tgacagagag	720	
cccttgctact	cagaaactcc	aagcaagcga	ccatgcacta	ttagcccagg	ccagcgggtac	780	
agtccaaaata	caggccttatc	ctaccagccc	aatggcctgc	ctcacctcac	cccacctcca	840	

81/299

```

cctcagcatt accgtttggga tgatatggcc attgcccacc actacagggga ctccatatcga 900
caccccagcc acagggacct cagggacaga aacagaccta tgggggttgca tggcacacgt 960
caagaagaaa tgattgatca cagactaaca gacagagaat gggcagaaga gtggaaacat 1020
cttgaccatc tgttaaactg cataatggac atggtagaaa aaacaaggcg atctctcacc 1080
gtactaaggc ggtgtcaaga agcagaccgg gaagaattga attactggat cggcggttac 1140
agtgacgcgg aggacttaaa aaaagggtggc ggcagtagca gcagccactc taggcagcag 1200
agtcccgctc acccagaccc agttgcaact gacgcgcacg gggaattcct tcacaggcct 1260
gcgtctggat acgtgccaga ggagatctgg aagaaagctg aggaggccgt caatgagggtg 1320
aagcgccagg cgatgacgga gctgcagaag gccgtgtctg aggcggagcg gaaagcccac 1380
gacatgatca caacagagag ggccaagatg gagcgcacgg tcgccgaggc caaacggcag 1440
gcggcggagg acgcactggc agttatcaat cagcaggagg attcaagcga gagttgctgg 1500
aattgtggcc gtaaagcgag tgaaacctgc agtggctgta acacagcccg atactgtggc 1560
tcattttgcc agcacaaga ctgggagaag caccatcaca tctgtggaca gaccctgcag 1620
gcccgagcgc agggagacac acctgcagtc agtcctctg tcacgcccac cagcggggtc 1680
gggagcccga tggacacacc accagcagcc actccgaggt caaccacccc gggaaccctc 1740
tccaccatag agacaacccc tcgctagacg tgaactcaga actgtcggag gaaagacaac 1800
acaaccaacg cgaaaccaat tcctcatcct cagatgctca aagttgtttt ttttgtttgt 1860
ttgtttatta gatgaattat cctatttcag tacttcagca agagagaacc taactgtatc 1920
ttgaggtggt agtaaaacac agagggccag taacgggtca taatgactta ttgtggataa 1980
caaagatatc ttttctttag agaactgaaa agagagcaga gaataataca tgaaatgata 2040
gatttgacct cctccctgaa attttcaagt agctgggatt ttaaactaga tgacctcatt 2100
aaccgatgct ttaccaaaca ccaaaccaag agattgctaa ttgctgttga aagcaaaaat 2160
gctaataatta aaagtcacaa tgttctttat atacaataat ggaaaaaaaa aaaaaaa 2217

```

<210> 97
 <211> 231
 <212> PRT
 <213> Homo sapiens

<400> 97
 Ala Ile Lys Ile Thr Val Asp Gly Pro Arg Glu Pro Arg Asn Arg Thr
 1 5 10 15
 Glu Lys His Ser Thr Met Pro Asp Ser Pro Val Asp Val Lys Thr Gln
 20 25 30
 Ser Arg Leu Thr Pro Pro Thr Met Pro Pro Pro Pro Thr Thr Gln Gly
 35 40 45
 Ala Pro Arg Thr Ser Ser Phe Thr Pro Thr Thr Leu Thr Asn Gly Thr
 50 55 60
 Ser His Ser Pro Thr Ala Leu Asn Gly Ala Pro Ser Pro Pro Asn Gly
 65 70 75 80
 Phe Ser Asn Gly Pro Ser Ser Ser Ser Ser Ser Ser Leu Ala Asn Gln
 85 90 95
 Gln Leu Pro Pro Ala Cys Gly Ala Arg Gln Leu Ser Lys Leu Lys Arg
 100 105 110
 Phe Leu Thr Thr Leu Gln Gln Phe Gly Asn Asp Ile Ser Pro Glu Ile
 115 120 125
 Gly Glu Arg Val Arg Thr Leu Val Leu Gly Leu Val Asn Ser Thr Leu
 130 135 140

82/299

Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu Ala Thr Asn Phe Pro
 145 150 155 160

Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Ala Asn Leu Pro Leu Leu
 165 170 175

Gln Arg Glu Leu Leu His Cys Ala Arg Leu Ala Lys Gln Asn Pro Ala
 180 185 190

Gln Tyr Leu Ala Gln His Glu Gln Leu Leu Leu Asp Ala Ser Thr Thr
 195 200 205

Ser Pro Val Asp Ser Ser Glu Leu Leu Leu Asp Val Asn Glu Asn Gly
 210 215 220

Lys Arg Arg Thr Pro Asp Arg
 225 230

<210> 98
 <211> 1412
 <212> DNA
 <213> Homo sapiens

<400> 98
 gccatcaaaa tcacagtgga tgggccccga gaacctcgaa atcgctactga gaagcactcc 60
 acaatgccag actcacctgt ggatgtgaag acgcaatcta ggctgactcc tccaacaatg 120
 ccacctcccc caactactca aggagctcca agaaccagtt catttacacc gacaacgtta 180
 actaatggca cgagccattc tcctacagcc ttgaatggcg cccctcacc acccaatggc 240
 ttcagcaatg ggcttccctc ttcttccctc tcctctctgg ctaatcaaca gctgccccca 300
 gcctgtggtg ccaggcaact cagcaagctg aaaagggttc ttactaccct gcagcagttt 360
 ggcaatgaca ttccaccgga gataggagaa agagtctgca ccctcgttct gggactagt 420
 aactccactt tgacaattga agaatttcat tccaaactgc aagaagctac taacttccca 480
 ctgagacctt ttgtcatccc atttttgaag gccaaactgc ccctgctgca gcgtgagctc 540
 ctccactgcg caagactggc caaacagaac cctgccaggt acctcgcca gcatgaacag 600
 ctgcttctgg atgccagcac cacctcacct gttgactcct cagagctgct tctcgatgtg 660
 aacgaaaacg ggaagaggcg aactccagac aggtgagagg gaggaggagc ctggatgaac 720
 catgaccttt ttccataacc tgtggcatga ggaacattt catgtcacia ttaaaccgct 780
 ggccatgtgc attcttgcac aatagcaata agccattgtg gccatcttga gaactctggc 840
 ctggcctggg attttacaga gttttgaatc tctggcctgg gacagtttgg cttttgtgta 900
 ggttaatctt ttctgcttgt agtattaaag cgaaatggtg aagacgaatg atttttctga 960
 tttgccagt accactgatg gctcttagat gcacatcaat attaaaattc tcattcatta 1020
 tgtaatttaa cccaaccaca tattttactt caatattctg aaattggctg ttcctagttt 1080
 ccttaaaatg tgatggtttg gaagcttgct tgtatgtatt tcttaacaca gtacagtagt 1140
 tatttgtttt gggtgtatat gaactaagag aaaacttctg ggacactaga tgaactgagt 1200
 gaagataaga gttatacagt agagacaata gatggtatatt ttgctgaaaa ttttacttgt 1260
 tagatactgt tctatcagat actgtgctct cataactaag aattctaaga aatgtaaaat 1320
 aaaaccactt ctccattaaa ccctacagag taattgttga ataaagcata cacatgaaat 1380
 ttcaaaaaaa aaaaaaaaaa aagggcggcc gc 1412

<210> 99
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 99
 Ser Phe Thr Leu Thr Ile Thr Val Phe Thr Asn Pro Pro Gln Val Ala

83/299

1 5 10 15
 Thr Tyr His Arg Ala Ile Lys Ile Thr Val Asp Gly Pro Arg Glu Pro
 20 25 30
 Arg Asn Arg Thr Glu Lys His Ser Thr Met Pro Asp Ser Pro Val Asp
 35 40 45
 Val Lys Thr Gln Ser Arg Leu Thr Pro Pro Thr Met Pro Pro Pro Pro
 50 55 60
 Thr Thr Gln Gly Ala Pro Arg Thr Ser Ser Phe Thr Pro Thr Thr Leu
 65 70 75 80
 Thr Asn Gly Thr Ser His Ser Pro Thr Ala Leu Asn Gly Ala Pro Ser
 85 90 95
 Pro Pro Asn Gly Phe Ser Asn Gly Pro Ser Ser Ser Ser Ser Ser Ser
 100 105 110
 Leu Ala Asn Gln Gln Leu Pro Pro Ala Cys Gly Ala Arg Gln Leu Ser
 115 120 125
 Lys Leu Lys Arg Phe Leu Thr Thr Leu Gln Gln Phe Gly Asn Asp Ile
 130 135 140
 Ser Pro Glu Ile Gly Glu Arg Val Arg Thr Leu Val Leu Gly Leu Val
 145 150 155 160
 Asn Ser Thr Leu Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu Ala
 165 170 175
 Thr Asn Phe Pro Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Val Leu
 180 185 190
 His Ser Ser Leu Val Val
 195

<210> 100

<211> 799

<212> DNA

<213> Homo sapiens

<400> 100

aagcttcact ctgaccatca ctgtcttcac aaacccaccg caagtcgcca cctaccacag 60
 agccatcaaa atcacagtgg atgggccccg agaacctcga aatcgctactg agaagcactc 120
 cacaatgcca gactcacctg tggatgtgaa gacgcaatct aggctgactc ctccaacaat 180
 gccacctccc ccaactactc aaggagctcc aagaaccagt tcatttacac cgacaacggt 240
 aactaatggc acgagccatt ctccacagc cttgaatggc gccccctcac caccacatgg 300
 cttcagcaat gggccttctc cttcttctc ctcctctctg gctaatcaac agctgcccc 360
 agcctgtggt gccaggcaac tcagcaagct gaaaagggtc cttactaccc tgcagcagtt 420
 tggcaatgac atttcacccg agataggaga aagagttcgc accctcggtc tgggactagt 480
 gaactccact ttgacaattg aagaatttca ttccaaactg caagaagcta ctaacttccc 540
 actgagacct tttgtcatcc catttttgaa ggtattgcac agttcactgg tcgtgtaaag 600
 tatttttaaac catattgttg ctaggtcata actgtgtgct ttttttagtac atttaggggc 660
 tctttgattt aatttaattg atgaaaacta tctgaatcga ttgtatttat gaccatttcc 720
 taagtagtct gaaaattaca aggagtgttt taaataatta cctgaaaaga agtaaaagttt 780

84/299

gaagaagagt ttagaagtc

799

<210> 101

<211> 237

<212> DNA

<213> Homo sapiens

<400> 101

```

gccccgagaa cctcgaaatc gtactgagaa gcactccaca atgccagact cacctgtgga 60
tgtgaagacg caatctaggc tgactcctcc aacaatgcc aatcccccaa ctactcaagg 120
agctccaaga accagttcat ttacaccgac aacgttaact aatggcacga gccattctcc 180
tacagccttg aatggcgccc cctcaccacc caatggcttc agcaatgggc cttcctc 237

```

<210> 102

<211> 276

<212> DNA

<213> Homo sapiens

<400> 102

```

gaagtggaag agggaaaagc ttactctga ccatcactgt cttcaciaaac ccaccgcaag 60
tcgccaccta ccacagagcc atcaaaatca cagtggatgg gccccgagaa cctcgaaata 120
aaccacctt gaaaaactga ggtgcttaag gagtaaaata atatgttcct ggtggcatcc 180
tccagatcgt actgagaagc actccacaat gccagactca cctgtggatg tgaagacgca 240
atctaggctg actcctccaa caatgccacc tcccc 276

```

<210> 103

<211> 251

<212> PRT

<213> Homo sapiens

<400> 103

```

Ser Phe Thr Leu Thr Ile Thr Val Phe Thr Asn Pro Pro Gln Val Ala
 1              5              10              15

Thr Tyr His Arg Ala Ile Lys Ile Thr Val Asp Gly Pro Arg Glu Pro
      20              25              30

Arg Asn Arg Thr Glu Lys His Ser Thr Met Pro Asp Ser Pro Val Asp
      35              40              45

Val Lys Thr Gln Ser Arg Leu Thr Pro Pro Thr Met Pro Pro Pro Pro
      50              55              60

Thr Thr Gln Gly Ala Pro Arg Thr Ser Ser Phe Thr Pro Thr Thr Leu
      65              70              75              80

Thr Asn Gly Thr Ser His Ser Pro Thr Ala Leu Asn Gly Ala Pro Ser
      85              90              95

Pro Pro Asn Gly Phe Ser Asn Gly Pro Ser Ser Ser Ser Ser Ser Ser
      100              105              110

Leu Ala Asn Gln Gln Leu Pro Pro Ala Cys Gly Ala Arg Gln Leu Ser
      115              120              125

```

85/299

Lys Leu Lys Arg Phe Leu Thr Thr Leu Gln Gln Phe Gly Asn Asp Ile
 130 135 140
 Ser Pro Glu Ile Gly Glu Arg Val Arg Thr Leu Val Leu Gly Leu Val
 145 150 155 160
 Asn Ser Thr Leu Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu Ala
 165 170 175
 Thr Asn Phe Pro Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Ala Asn
 180 185 190
 Leu Pro Leu Leu Gln Arg Glu Leu Leu His Cys Ala Arg Leu Ala Lys
 195 200 205
 Gln Asn Pro Ala Gln Tyr Leu Ala Gln His Glu Gln Leu Leu Leu Asp
 210 215 220
 Ala Ser Thr Thr Ser Pro Val Asp Ser Ser Glu Leu Leu Leu Asp Val
 225 230 235 240
 Asn Glu Asn Gly Lys Arg Arg Thr Pro Asp Arg
 245 250

<210> 104

<211> 1446

<212> DNA

<213> Homo sapiens

<400> 104

```

aagcttcaact ctgaccatca ctgtcttcac aaacccaccg caagtcgccca cctaccacag 60
agccatcaaaa atcacagtgg atgggccccg agaacctcga aatcgctactg agaagcactc 120
cacaatgccca gactcacctg tggatgtgaa gacgcaatct aggctgactc ctccaacaat 180
gccacctccc ccaactactc aaggagctcc aagaaccagt tcattttacac cgacaacggt 240
aactaatggc acgagccatt ctccctacagc cttgaatggc gccccctcac cacccaatgg 300
cttcagcaat gggccttctc cttcttctctc ctctctctctg gctaatacaac agctgcccc 360
agcctgtggg gccaggcaac tcagcaagct gaaaagggttc cttactacc tgcagcagtt 420
tggcaatgac atttcacccg agataggaga aagagttcgc accctcgttc tgggactagt 480
gaactccact ttgacaattg aagaatttca ttccaaactg caagaagcta ctaacttccc 540
actgagacct tttgtcatcc catttttga a ggccaaactg cccctgctgc agcgtgagct 600
cctccactgc gcaagactgg ccaaacagaa cctgcccag tacctcgccc agcatgaaca 660
gctgcttctg gatgccagca ccacctcacc tgttgactcc tcagagctgc ttctcgatgt 720
gaacgaaaac ggggaagaggc gaactccaga caggtgagag ggaggaggag cctggatgaa 780
ccatgacctt tttcccatc ctgtggcatg aggaaacatt tcatgtcaca attaaaccgc 840
tggcctatgt cattcttgca caatagcaat aagccattgt ggccatcttg agaatctggc 900
tctggcctgg gattttacag agttttgaat ctctggcctg ggacagtttg gcttttgtgt 960
aggttaaatct tttctgcttg tagtattaaa gcgaaatggg gaagacgaat gatttttctg 1020
atgtgccaag taccactgat ggctcttaga tgcacatcaa tattaaaatt ctcatcatt 1080
atgtaattta acccaaccac atattttact tcaatattct gaaattggct gttcctagtt 1140
tccttaaaat gtgatggtt ggaagcttgt ctgtatgtat ttcttaacac agtacagtag 1200
ttatttgttt tggttgtata tgaactaaga gaaaacttct gggacactag atgaactgag 1260
tgaagataag agttatacag tagagacaat agatggtatt tttgctgaaa attttacttg 1320
ttagatactg ttctatcaga tactgtgctc tcataactaa gaattctaag aaatgtaaaa 1380
taaaaccact tctccattaa accctacaga gtaattgttg aataaagcat acacatgaaa 1440
tttccc
1446

```

86/299

<210> 105

<211> 1395

<212> PRT

<213> Homo sapiens

<400> 105

```

Met Arg Ile Pro Val Asp Ala Ser Thr Ser Arg Arg Phe Thr Pro Pro
 1              5              10              15

Ser Thr Ala Leu Ser Pro Gly Lys Met Ser Glu Ala Leu Pro Leu Gly
      20              25              30

Ala Pro Asp Ala Gly Ala Ala Leu Ala Gly Lys Leu Arg Ser Gly Asp
      35              40              45

Arg Ser Met Val Glu Val Leu Ala Asp His Pro Gly Glu Leu Val Arg
      50              55              60

Thr Asp Ser Pro Asn Phe Leu Cys Ser Val Leu Pro Thr His Trp Arg
 65              70              75              80

Cys Asn Lys Thr Leu Pro Ile Ala Phe Lys Val Val Ala Leu Gly Asp
      85              90              95

Val Pro Asp Gly Thr Leu Val Thr Val Met Ala Gly Asn Asp Glu Asn
      100              105              110

Tyr Ser Ala Glu Leu Arg Asn Ala Thr Ala Ala Met Lys Asn Gln Val
      115              120              125

Ala Arg Phe Asn Asp Leu Arg Phe Val Gly Arg Ser Gly Arg Gly Lys
      130              135              140

Ser Phe Thr Leu Thr Ile Thr Val Phe Thr Asn Pro Pro Gln Val Ala
      145              150              155              160

Thr Tyr His Arg Ala Ile Lys Ile Thr Val Asp Gly Pro Arg Glu Pro
      165              170              175

Arg Asn Asn Glu Cys Val Tyr Gly Asn Tyr Pro Glu Ile Pro Leu Glu
      180              185              190

Glu Met Pro Asp Ala Asp Gly Val Ala Ser Thr Pro Ser Leu Asn Ile
      195              200              205

Gln Glu Pro Cys Ser Pro Ala Thr Ser Ser Glu Ala Phe Thr Pro Lys
      210              215              220

Glu Gly Ser Pro Tyr Lys Ala Pro Ile Tyr Ile Pro Asp Asp Ile Pro
      225              230              235              240

Ile Pro Ala Glu Phe Glu Leu Arg Glu Ser Asn Met Pro Gly Ala Gly
      245              250              255

Leu Gly Ile Trp Thr Lys Arg Lys Ile Glu Val Gly Glu Lys Phe Gly
      260              265              270

Pro Tyr Val Gly Glu Gln Arg Ser Asn Leu Lys Asp Pro Ser Tyr Gly

```

87/299

275					280					285					
Trp	Glu	Ile	Leu	Asp	Glu	Phe	Tyr	Asn	Val	Lys	Phe	Cys	Ile	Asp	Ala
290					295					300					
Ser	Gln	Pro	Asp	Val	Gly	Ser	Trp	Leu	Lys	Tyr	Ile	Arg	Phe	Ala	Gly
305					310					315					320
Cys	Tyr	Asp	Gln	His	Asn	Leu	Val	Ala	Cys	Gln	Ile	Asn	Asp	Gln	Ile
				325					330					335	
Phe	Tyr	Arg	Val	Val	Ala	Asp	Ile	Ala	Pro	Gly	Glu	Glu	Leu	Leu	Leu
			340					345					350		
Phe	Met	Lys	Ser	Glu	Asp	Tyr	Pro	His	Glu	Thr	Met	Ala	Pro	Asp	Ile
		355					360					365			
His	Glu	Glu	Arg	Gln	Tyr	Arg	Cys	Glu	Asp	Cys	Asp	Gln	Leu	Phe	Glu
	370					375					380				
Ser	Lys	Ala	Glu	Leu	Ala	Asp	His	Gln	Lys	Phe	Pro	Cys	Ser	Thr	Pro
385					390					395					400
His	Ser	Ala	Phe	Ser	Met	Val	Glu	Glu	Asp	Phe	Gln	Gln	Lys	Leu	Glu
				405					410					415	
Ser	Glu	Asn	Asp	Leu	Gln	Glu	Ile	His	Thr	Ile	Gln	Glu	Cys	Lys	Glu
			420				425						430		
Cys	Asp	Gln	Val	Phe	Pro	Asp	Leu	Gln	Ser	Leu	Glu	Lys	His	Met	Leu
	435						440					445			
Ser	His	Thr	Glu	Glu	Arg	Glu	Tyr	Lys	Cys	Asp	Gln	Cys	Pro	Lys	Ala
	450					455					460				
Phe	Asn	Trp	Lys	Ser	Asn	Leu	Ile	Arg	His	Gln	Met	Ser	His	Asp	Ser
465					470					475					480
Gly	Lys	His	Tyr	Glu	Cys	Glu	Asn	Cys	Ala	Lys	Val	Phe	Thr	Asp	Pro
				485					490					495	
Ser	Asn	Leu	Gln	Arg	His	Ile	Arg	Ser	Gln	His	Val	Gly	Ala	Arg	Ala
			500					505					510		
His	Ala	Cys	Pro	Glu	Cys	Gly	Lys	Thr	Phe	Ala	Thr	Ser	Ser	Gly	Leu
	515						520					525			
Lys	Gln	His	Lys	His	Ile	His	Ser	Ser	Val	Lys	Pro	Phe	Ile	Cys	Glu
	530					535					540				
Val	Cys	His	Lys	Ser	Tyr	Thr	Gln	Phe	Ser	Asn	Leu	Cys	Arg	His	Lys
545					550					555					560
Arg	Met	His	Ala	Asp	Cys	Arg	Thr	Gln	Ile	Lys	Cys	Lys	Asp	Cys	Gly
				565					570					575	
Gln	Met	Phe	Ser	Thr	Thr	Ser	Ser	Leu	Asn	Lys	His	Arg	Arg	Phe	Cys
			580					585					590		

88/299

Glu Gly Lys Asn His Phe Ala Ala Gly Gly Phe Phe Gly Gln Gly Ile
 595 600 605
 Ser Leu Pro Gly Thr Pro Ala Met Asp Lys Thr Ser Met Val Asn Met
 610 615 620
 Ser His Ala Asn Pro Gly Leu Ala Asp Tyr Phe Gly Ala Asn Arg His
 625 630 635 640
 Pro Ala Gly Leu Thr Phe Pro Thr Ala Pro Gly Phe Ser Phe Ser Phe
 645 650 655
 Pro Gly Leu Phe Pro Ser Gly Leu Tyr His Arg Pro Pro Leu Ile Pro
 660 665 670
 Ala Ser Ser Pro Val Lys Gly Leu Ser Ser Thr Glu Gln Thr Asn Lys
 675 680 685
 Ser Gln Ser Pro Leu Met Thr His Pro Gln Ile Leu Pro Ala Thr Gln
 690 695 700
 Asp Ile Leu Lys Ala Leu Ser Lys His Pro Ser Val Gly Asp Asn Lys
 705 710 715 720
 Pro Val Glu Leu Gln Pro Glu Arg Ser Ser Glu Glu Arg Pro Phe Glu
 725 730 735
 Lys Ile Ser Asp Gln Ser Glu Ser Ser Asp Leu Asp Asp Val Ser Thr
 740 745 750
 Pro Ser Gly Ser Asp Leu Glu Thr Thr Ser Gly Ser Asp Leu Glu Ser
 755 760 765
 Asp Ile Glu Ser Asp Lys Glu Lys Phe Lys Glu Asn Gly Lys Met Phe
 770 775 780
 Lys Asp Lys Val Ser Pro Leu Gln Asn Leu Ala Ser Ile Asn Asn Lys
 785 790 795 800
 Lys Glu Tyr Ser Asn His Ser Ile Phe Ser Pro Ser Leu Glu Glu Gln
 805 810 815
 Thr Ala Val Ser Gly Ala Val Asn Asp Ser Ile Lys Ala Ile Ala Ser
 820 825 830
 Ile Ala Glu Lys Tyr Phe Gly Ser Thr Gly Leu Val Gly Leu Gln Asp
 835 840 845
 Lys Lys Val Gly Ala Leu Pro Tyr Pro Ser Met Phe Pro Leu Pro Phe
 850 855 860
 Phe Pro Ala Phe Ser Gln Ser Met Tyr Pro Phe Pro Asp Arg Asp Leu
 865 870 875 880
 Arg Ser Leu Pro Leu Lys Met Glu Pro Gln Ser Pro Gly Glu Val Lys
 885 890 895

89/299

Lys Leu Gln Lys Gly Ser Ser Glu Ser Pro Phe Asp Leu Thr Thr Lys
 900 905 910
 Arg Lys Asp Glu Lys Pro Leu Thr Pro Val Pro Ser Lys Pro Pro Val
 915 920 925
 Thr Pro Ala Thr Ser Gln Asp Gln Pro Leu Asp Leu Ser Met Gly Ser
 930 935 940
 Arg Ser Arg Ala Ser Gly Thr Lys Leu Thr Glu Pro Arg Lys Asn His
 945 950 955 960
 Val Phe Gly Gly Lys Lys Gly Ser Asn Val Glu Ser Arg Pro Ala Ser
 965 970 975
 Asp Gly Ser Leu Gln His Ala Arg Pro Thr Pro Phe Phe Met Asp Pro
 980 985 990
 Ile Tyr Arg Val Glu Lys Arg Lys Leu Thr Asp Pro Leu Glu Ala Leu
 995 1000 1005
 Lys Glu Lys Tyr Leu Arg Pro Ser Pro Gly Phe Leu Phe His Pro Gln
 1010 1015 1020
 Met Ser Ala Ile Glu Asn Met Ala Glu Lys Leu Glu Ser Phe Ser Ala
 1025 1030 1035 1040
 Leu Lys Pro Glu Ala Ser Glu Leu Leu Gln Ser Val Pro Ser Met Phe
 1045 1050 1055
 Asn Phe Arg Ala Pro Pro Asn Ala Leu Pro Glu Asn Leu Leu Arg Lys
 1060 1065 1070
 Gly Lys Glu Arg Tyr Thr Cys Arg Tyr Cys Gly Lys Ile Phe Pro Arg
 1075 1080 1085
 Ser Ala Asn Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Gln Pro
 1090 1095 1100
 Tyr Arg Cys Lys Tyr Cys Asp Arg Ser Phe Ser Ile Ser Ser Asn Leu
 1105 1110 1115 1120
 Gln Arg His Val Arg Asn Ile His Asn Lys Glu Lys Pro Phe Lys Cys
 1125 1130 1135
 His Leu Cys Asp Arg Cys Phe Gly Gln Gln Thr Asn Leu Asp Arg His
 1140 1145 1150
 Leu Lys Lys His Glu Asn Gly Asn Met Ser Gly Thr Ala Thr Ser Ser
 1155 1160 1165
 Pro His Ser Glu Leu Glu Ser Thr Gly Ala Ile Leu Asp Asp Lys Glu
 1170 1175 1180
 Asp Ala Tyr Phe Thr Glu Ile Arg Asn Phe Ile Gly Asn Ser Asn His
 1185 1190 1195 1200
 Gly Ser Gln Ser Pro Arg Asn Val Glu Glu Arg Met Asn Gly Ser His

90/299

1205	1210	1215
Phe Lys Asp Glu Lys Ala Leu Val Thr Ser Gln Asn Ser Asp Leu Leu		
1220	1225	1230
Asp Asp Glu Glu Val Glu Asp Glu Val Leu Leu Asp Glu Glu Asp Glu		
1235	1240	1245
Asp Asn Asp Ile Thr Gly Lys Thr Gly Lys Glu Pro Val Thr Ser Asn		
1250	1255	1260
Leu His Glu Gly Asn Pro Glu Asp Asp Tyr Glu Glu Thr Ser Ala Leu		
1265	1270	1275
Glu Met Ser Cys Lys Thr Ser Pro Val Arg Tyr Lys Glu Glu Glu Tyr		
1285	1290	1295
Lys Ser Gly Leu Ser Ala Leu Asp His Ile Arg His Phe Thr Asp Ser		
1300	1305	1310
Leu Lys Met Arg Lys Met Glu Asp Asn Gln Tyr Ser Glu Ala Glu Leu		
1315	1320	1325
Ser Ser Phe Ser Thr Ser His Val Pro Glu Glu Leu Lys Gln Pro Leu		
1330	1335	1340
His Arg Lys Ser Lys Ser Gln Ala Tyr Ala Met Met Leu Ser Leu Ser		
1345	1350	1355
Asp Lys Glu Ser Leu His Ser Thr Ser His Ser Ser Ser Asn Val Trp		
1365	1370	1375
His Ser Met Ala Arg Ala Ala Ala Glu Ser Ser Ala Ile Gln Ser Ile		
1380	1385	1390
Ser His Val		
1395		

<210> 106
 <211> 5938
 <212> DNA
 <213> Homo sapiens

<400> 106
 tttccaggca ctctcattca tagagccagc gggcgcgggc gggacgggag ccccgcgggc 60
 ggacccagcc agggcaccac gctgcccggc cctgcgcgcg caggcacttc tttccggggc 120
 tcctagggac gccagaagga agtcaacctc tgctgcttct ccttggcctg cgttggaact 180
 tccttttttt gttgtttttt tttgtttttc cctttcttct cttttgaatt aactggcttc 240
 ttggctggat gttttcaact tctttcctgg ctgcgaactt tttccccaat tgttttcctt 300
 ttacaacagg gggagaaagt gctctgtggt ccgaggcgag ccgtgaagt gcgtgtgcgt 360
 ggcagtgtgc gtggcaggat gtgcgtgcgt gtgtaaccgc agccgcccga tctgtttcga 420
 tctgcgcgcg ggagccctcc ctcaaggccc gctccacctg cttggcggtt acgcgggcgt 480
 cgtgggtgtt cgtgccttcg gagcagctaa ccggcggttg ctgggagcgt gtggaggagt 540
 atcgcttctc ctgcttgcgc gagtcagggc tgagtcaccc cagctgatgt agacagtggc 600
 tgctttccga agagtgcgtg tttgcatgtg tgtgactctg cggctgctca actcccaaca 660
 aaccagagga ccagccacaa acttaaccaa catccccaaa cccgagttca cagatgtggg 720
 agagctgtag aaccctgagt gtcactgact gggccttctt atgattgttg ttttaagatt 780

agctgaagat	ctctgaaacg	ctgaattttc	tgcactgagc	gtttgacaga	attcattgag	840
agaacagaga	acatgacaag	tacttctagc	tcagcactgc	tccaactact	gaagctgatt	900
ttcaaggcta	cttaaaaaaa	tctgcagcgt	acattaatgg	atttctgttg	tgtttaaatt	960
ctccacagat	tgtattgtaa	atattttatg	aagtagagca	tatgtatata	tttatatata	1020
cgtgcacata	cattagtagc	actacctttg	gaagtctcag	ctcttgcttt	tcgggactga	1080
agccagtttt	gcatgataaa	agtggccttg	ttacggggaga	taattgtgtt	ctgttggggac	1140
tttagacaaa	actcacctgc	aaaaaactga	caggcattaa	ctactggaac	ttccaaataa	1200
tgtgtttgct	gatcgtttta	ctcttcgcat	aaatatttta	ggaagtgtat	gagaattttg	1260
ccttcaggaa	cttttctaac	agccaaagac	agaacttaac	ctctgcaagc	aagattcgtg	1320
gaagatagtc	tccacttttt	aatgcactaa	gcaatcgggt	gctaggagcc	catcctgggt	1380
cagaggccga	tccgcagaac	cagaacgttt	tcccctcctg	gactgttagt	aacttagtct	1440
ccctcctccc	tcaaccaccc	ccgccccccc	ccaccccccg	cagtaataaa	ggcccctgaa	1500
cgtgtatggt	ggtctcccgg	gagctgcttg	ctgaagatcc	gcgcccctgt	cgccgtctgg	1560
taggagctgt	ttgcagggtc	ctaactcaat	cggtctgttg	tgatgcgtat	ccccgtagat	1620
gccagcacga	gccgcgcgtt	cacgcgcgct	tccaccgcgc	tgagcccagg	caagatgagc	1680
gaggcggtgc	cgctggggcg	cccgacgccc	ggcgctgccc	tggccggcaa	gctgaggagc	1740
ggcgaccgca	gcatggtgga	ggtgctggcc	gaccacccgg	gcgagctggt	gcgaccgac	1800
agccccaact	tctctgctc	cgtgctgcct	acgcactggc	gctgcaacaa	gaccctgccc	1860
atcgctttca	aggtggtggc	cctaggggat	gttccagatg	gcactctggt	cactgtgatg	1920
gctggcaatg	atgaaaacta	ctcggctgag	ctgagaaatg	ctaccgcagc	catgaagaac	1980
caggttgcaa	gatttaattga	cctcaggttt	gtcggctgaa	gtggaagagg	gaaaagcttc	2040
actctgacca	tcaactgtctt	cacaaaccca	ccgcaagtcg	ccacctacca	cagagccatt	2100
aaaatcacag	tggatggggc	ccgagaacct	cgaaataatg	agtgtgtata	tggcaactac	2160
cctgaaatac	cttttgaaga	aatgccagat	gcagatggag	tagccagcac	tccctccctc	2220
aatattcaag	agccatgctc	tcttgccaca	tccagtgaag	cattcactcc	aaaggagggt	2280
tctccttaca	aagcccccat	ctacatccct	gatgatattc	ccattcctgc	tgagtttgaa	2340
cttcgagagt	caaatatgcc	tggggcagga	ctaggaatat	ggacccaaaag	gaagatcgaa	2400
gtaggtgaaa	agtttggggc	ttatgtggga	gagcagaggt	caaacctgaa	agaccccagt	2460
tatggatggg	agatcttaga	cgaattttac	aatgtgaagt	tctgcataga	tgccagtcaa	2520
ccagatgttg	gaagctggct	caagtacatt	agattcgtcg	gctgttatga	tcagcacaac	2580
cttgttgcat	gccagataaa	tgatcagata	ttctatagag	tagttgcaga	cattgcgcgc	2640
ggagaggagc	ttctgctgtt	catgaagagc	gaagactatc	cccatgaaac	tatggcgccg	2700
gatatccacg	aagaacggca	atatcgctgc	gaagactgtg	accagctctt	tgaatctaag	2760
gctgaactag	cagatcacca	aaagtttcca	tgcagtactc	ctcactcagc	atttttcaatg	2820
gttgaagagg	actttcagca	aaaactcgaa	agcgagaatg	atctccaaga	gatacacacg	2880
atccaggagt	gtaaggaatg	tgaccaagtt	tttcctgatt	tgcaaagcct	ggagaaacac	2940
atgctgtcac	atactgaaga	gagggaatac	aagtgtgatc	agtgtcccaa	ggcattttaac	3000
tggaaagtcca	attttaattcg	ccaccagatg	tcacatgaca	gtggaaaagca	ctatgaatgt	3060
gaaaactgtg	ccaaggtttt	cacggaccct	agcaaccttc	agcggcacat	tcgctctcag	3120
catgtcgggt	cccgggcccc	tgcatgcccg	gagtggtggc	aaacgttttg	cacttcgtcg	3180
ggcctcaaac	aacacaagca	catccacagc	agtgtgaagc	cctttatctg	tgaggtctcg	3240
cataaatcct	atactcagtt	ttcaaaccct	tgcgctcata	agcgcatgca	tgctgattgc	3300
agaacccaaa	tcaagtgcaa	agactgtgga	caaagtgtca	gcactacgtc	ttccttaaat	3360
aaacacagga	ggtttttgtga	gggcaagaac	cattttgcgg	caggtggatt	ttttggccaa	3420
ggcatttcac	ttcctgggaac	cccagctatg	gataaaacgt	ccatgggttaa	tatgagtcac	3480
gccaaccggg	gccttgctga	ctattttggc	gccaataggc	atcctgctgg	tcttaccttt	3540
ccaacagctc	ctggattttc	tttttagctc	cctggctctg	ttccttcogg	cttgtaccac	3600
aggcctcctt	tgatacctgc	tagttctcct	gttaaaggac	tatcaagtac	tgaacagaca	3660
aacaaaagtc	aaagtccctc	catgacacat	cctcagatac	tgccagctac	acaggatatt	3720
ttgaaggcac	tatctaaaca	cccatctgta	ggggacaata	agccagtggg	gctccagccc	3780
gagaggtcct	ctgaagagag	gccctttgag	aaaatcagtg	accagtcaga	gagtagtgac	3840
cttgatgatg	tcagtacacc	aagtggcagt	gacctggaaa	caacctcggg	ctctgatctg	3900
gaaagtgaca	ttgaaagtga	taaagagaaa	tttaaagaaa	atggtaaaat	gttcaaagac	3960
aaagtaagcc	ctcttcagaa	tctggcttca	ataaataata	agaaagaata	cagcaatcat	4020
tccattttct	caccatcttt	agaggagcag	actgcggtgt	caggagctgt	gaatgattct	4080
ataaaggcta	ttgcttctat	tgctgaaaaa	tactttgggt	caacaggact	ggtggggctg	4140
caagacaaaa	aagttggagc	tttaccttac	ccttccatgt	ttccccctcc	attttttcca	4200
gcattctctc	aatcaatgta	cccatttcct	gatagagact	tgagatcggt	acctttgaaa	4260

92/299

```

atggaacccc aatcaccagg tgaagtaaag aaactgcaga agggcagctc tgagtcccc 4320
tttgaatctca ccactaagcg aaaggatgag aagcccttga ctccagtccc ctccaagcct 4380
ccagtgcacac ctgccacaag ccaagaccag cccctggatc taagtatggg cagtaggagt 4440
agagccagtg ggacaaagct gactgagcct cgaaaaaacc acgtgtttgg gggaaaaaaa 4500
ggaagcaacg tgaatcaag acctgcttca gatggttcct tgcagcatgc aagacccact 4560
cctttcttta tggaccctat ttacagagta gagaaaagaa aactaactga cccacttgaa 4620
gctttaaaag agaaatactt gaggccttct ccaggattct tgtttcacc ccaaattgtca 4680
gctattgaaa acatggcaga aaagctagag agcttcagtg cctgaaacc tgaggccagt 4740
gagctcttac agtcagtgcc ctctatgttc aacttcaggg cgctcccaa tgccttgcca 4800
gagaaccttc tgcggaaggg aaaggagcgc tatacctgca gatactgtgg caagattttt 4860
ccaaggctcg caaacctaac acggcacttg agaaccaca caggagagca gccttacaga 4920
tgcaaatact gtgacagatc atttagcata tcttctaact tgcaaaggca tgttcgcaac 4980
atccacaata aagagaagcc atttaagtgt cacttatgtg ataggtgtt tggccaaca 5040
accaatttag acagacacct aaagaaacat gagaatggga acatgtccg tacagcaaca 5100
tcgtcgctc attctgaact ggaaagtaca ggtgcgattc tggatgacaa agaagatgct 5160
tacttcacag aaattcgaaa ttctattggg aacagcaacc atggcagcca atctcccagg 5220
aatgtggagg agagaatgaa tggcagtcac tttaaagatg aaaaggcttt ggtgaccagt 5280
caaaattcag acttgctgga tgatgaagaa gttgaagatg aggtgttgtt agatgaggag 5340
gatgaagaca atgatattac tggaaaaaca ggaaaggaa cagtgcacaa taatttacat 5400
gaaggaaacc ctgaggatga ctatgaagaa accagtggcc tggagatgag ttgcaagaca 5460
tcccagtgga ggtataaaga ggaagaatat aaaagtggac tttctgctct agatcatata 5520
aggcacttca cagatagcct caaaatgagg aaaatggaag ataatacata ttctgaagct 5580
gagctgtctt cttttagtac ttcccatgtg ccagaggaac ttaagcagcc gttacacaga 5640
aagtccaaat cgcaggcata tgctatgatg ctgtcactgt ctgacaagga gtccctccat 5700
tctacatccc acagttcttc caacgtgtgg cacagtatgg ccagggtctg gcggaatcc 5760
agtgtatccc agtcataag ccacgtatga cgttatcaag gttgaccaga gtgggaccaa 5820
gtccaacagt agcatggctc tttcatatag gactatttac aagactgctg agcagaatgc 5880
cttataaacc tgcagggtca ctcatctaaa gtctagtgcac cttaaactga atgattta 5938

```

<210> 107

<211> 261

<212> PRT

<213> Homo sapiens

<400> 107

```

Met Asn Pro Ser Arg Asp Val His Asp Ala Ser Thr Ser Arg Arg Phe
  1              5              10              15

```

```

Thr Pro Pro Ser Thr Ala Leu Ser Pro Gly Lys Met Ser Glu Ala Leu
      20              25              30

```

```

Pro Leu Gly Ala Pro Asp Ala Gly Ala Ala Leu Ala Gly Lys Leu Arg
    35              40              45

```

```

Ser Gly Asp Arg Ser Met Val Glu Val Leu Ala Asp His Pro Gly Glu
    50              55              60

```

```

Leu Val Arg Thr Asp Ser Pro Asn Phe Leu Cys Ser Val Leu Pro Thr
    65              70              75              80

```

```

His Trp Arg Cys Asn Lys Thr Leu Pro Ile Ala Phe Lys Val Val Ala
      85              90              95

```

```

Leu Gly Asp Val Pro Asp Gly Thr Leu Val Thr Val Met Ala Gly Asn
    100              105              110

```

```

Asp Glu Asn Tyr Ser Ala Glu Leu Arg Asn Ala Thr Ala Ala Met Lys

```

93/299

115	120	125
Asn Gln Val Ala Arg Phe	Asn Asp Leu Arg Phe	Val Gly Arg Ser Gly
130	135	140
Arg Gly Lys Ser Phe Thr	Leu Thr Ile Thr Val	Phe Thr Asn Pro Pro
145	150	155
Gln Val Ala Thr Tyr His	Arg Ala Ile Lys Ile	Thr Val Asp Gly Pro
165	170	175
Arg Glu Pro Arg Arg His	Arg Gln Lys Leu Asp	Asp Gln Thr Lys Pro
180	185	190
Gly Ser Leu Ser Phe Ser	Glu Arg Leu Ser Glu	Leu Glu Gln Leu Arg
195	200	205
Arg Thr Ala Met Arg Val	Ser Pro His His Pro	Ala Pro Thr Pro Asn
210	215	220
Pro Arg Ala Ser Leu Asn	His Ser Thr Ala Phe	Asn Pro Gln Pro Gln
225	230	235
Ser Gln Met Gln Glu Ser	Trp Met Leu Pro Ile	Leu Ser Ser Phe Cys
245	250	255
Lys Lys Gly Ser Lys		
260		

<210> 108
 <211> 1025
 <212> DNA
 <213> Homo sapiens

<400> 108
 atgaatcctt ctagagacgt ccacgatgcc agcacgagcc gccgcttcac gccgccttcc 60
 accgcgctga gccagggcaa gatgagcgag gcgttgccgc tgggcgcccc ggacgcgggc 120
 gctgccctgg ccggcaagct gaggagcggc gaccgcagca tgggtggaggt gctggccgac 180
 caccgcggcg agctgggtgc caccgacagc cccaacttcc tctgctccgt gctgcctacg 240
 cactggcgct gcaacaagac cctgcccacg gctttcaagg tgggtggccct aggggatgtt 300
 ccagatggca ctctggtcac tgtgatggct ggcaatgatg aaaactactc ggctgagctg 360
 agaaatgcta ccgcagccat gaagaaccag gttgcaagat ttaatgacct caggttttgtc 420
 ggtcgaagtg gaagagggaa aagcttccact ctgaccatca ctgtcttcac aaaccaccg 480
 caagtcgcca cctaccacag agccatcaaa atcacagtgg atgggccccg agaacctcga 540
 agacatcggc agaaactaga tgatcagacc aagcccggga gcttgtcctt ttccgagcgg 600
 ctcagtgaac tggagcagct gcggcgacaca gccatgaggg tcagcccaca ccaccagcc 660
 cccacgcccc accctcgtgc ctccctgaac cactccactg cctttaacct tcagcctcag 720
 agtcagatgc aggaatcatg gatgctgcca attttgagca gtttttgcaa gaaaggatca 780
 aagtgaacgg aaaagctggg aaccttggtg gaggggtggg gaccatcgaa aggagcaaga 840
 gcaagatcac cgtgacatcc gaggtgcctt tctccaaaag gtatttgaaa tatctacca 900
 aaaaatattt gaagaagaat aatctacgtg actggttgcg cgtagttgct aacagcaaag 960
 agagttacga attacgttac ttccagatta accaggacga agaagaggag gaagacgagg 1020
 attaa 1025

<210> 109
 <211> 470

94/299

<212> DNA

<213> Homo sapiens

<400> 109

```

tgtcgggtcga agtggaagag ggaaaagctt cactctgacc atcactgtct tcacaaaccc 60
accgcaagtc gccacctacc acagagccat caaaatcaca gtggatgggc cccgagaacc 120
tcgaaaatca tggatgctgc caattttgag cagtttttgc aagaaaggat caaagtgaac 180
ggaaaagctg ggaaccttgg tggaggggtg gtgaccatcg aaaggagcaa gagcaagatc 240
accgtgacat ccgaggtgcc tttctccaaa aggtatttga aatatctcac caaaaaatat 300
ttgaagaaga ataatctacg tgactgggtg cgcgtagttg ctaacagcaa agagagttac 360
gaattacgtt acttcagat taaccaggac gaagaagagg aggaagacga ggattaaatt 420
tcatttatct ggaaaatttt gtatgagttc ttgaataaaa cttgggaacc 470

```

<210> 110

<211> 17

<212> PRT

<213> Homo sapiens

<400> 110

```

Gly Met Gly Gly Ser Asp Arg Gly Gly Phe Asn Lys Phe Gly Gly Ser
 1             5             10             15

```

Gly

<210> 111

<211> 55

<212> DNA

<213> Homo sapiens

<400> 111

```

gtggcatggg cggaagtgac cgtggtggct tcaataaatt tggatggcagt ggcca 55

```

<210> 112

<211> 32

<212> PRT

<213> Homo sapiens

<400> 112

```

Gly Met Gly Arg Trp Lys Leu His Val Leu Ser Ser Asn Leu Ser Ser
 1             5             10             15

```

```

Pro Ala Glu Val Thr Val Val Ala Ser Ile Asn Leu Val Ala Val Ala
      20             25             30

```

<210> 113

<211> 99

<212> DNA

<213> Homo sapiens

<400> 113

```

gtggcatggg ccgttggaag cttcatgtcc tttcttctaa cttgtcttct ccagcgggaag 60
tgaccgtggt ggcttcaata aatttggtgg cagtggcca 99

```

95/299

<210> 114
 <211> 120
 <212> DNA
 <213> Homo sapiens

<400> 114
 atccttttga tcgttggtgc caaggcttgt gtgtgtgtga gtgtgtggga gacaactccg 60
 aacagtcctg agccctatgt ctttatggct actgggtaaa atagtcaagt gagaaattag 120

<210> 115
 <211> 375
 <212> PRT
 <213> Homo sapiens

<400> 115
 Met Ser Ala Ser Ala Pro Ala Ala Glu Gly Glu Gly Thr Pro Thr Gln
 1 5 10 15
 Pro Ala Ser Glu Lys Glu Pro Glu Met Pro Gly Pro Arg Glu Glu Ser
 20 25 30
 Glu Glu Glu Glu Asp Glu Asp Asp Glu Glu Glu Glu Glu Glu Lys
 35 40 45
 Glu Lys Ser Leu Ile Val Glu Gly Lys Arg Glu Lys Lys Lys Val Glu
 50 55 60
 Arg Leu Thr Met Gln Val Ser Ser Leu Gln Arg Glu Pro Phe Thr Ile
 65 70 75 80
 Ala Gln Gly Lys Gly Gln Lys Leu Cys Glu Ile Glu Arg Ile His Phe
 85 90 95
 Phe Leu Ser Lys Lys Lys Thr Asp Glu Leu Arg Asn Leu His Lys Leu
 100 105 110
 Leu Tyr Asn Arg Pro Gly Thr Val Ser Ser Leu Lys Lys Asn Val Gly
 115 120 125
 Gln Phe Ser Gly Phe Pro Phe Glu Lys Gly Ser Val Gln Tyr Lys Lys
 130 135 140
 Lys Glu Glu Met Leu Lys Lys Phe Arg Asn Ala Met Leu Lys Ser Ile
 145 150 155 160
 Cys Glu Val Leu Asp Leu Glu Arg Ser Gly Val Asn Ser Glu Leu Val
 165 170 175
 Lys Arg Ile Leu Asn Phe Leu Met His Pro Lys Pro Ser Gly Lys Pro
 180 185 190
 Leu Pro Lys Ser Lys Lys Thr Cys Ser Lys Gly Ser Lys Lys Glu Arg
 195 200 205
 Asn Ser Ser Gly Met Ala Arg Lys Ala Lys Arg Thr Lys Cys Pro Glu
 210 215 220

96/299

Ile Leu Ser Asp Glu Ser Ser Ser Asp Glu Asp Glu Lys Lys Asn Lys
 225 230 235 240
 Glu Glu Ser Ser Asp Asp Glu Asp Lys Glu Ser Glu Glu Glu Pro Pro
 245 250 255
 Lys Lys Thr Ala Lys Arg Glu Lys Pro Lys Gln Lys Ala Thr Ser Lys
 260 265 270
 Ser Lys Lys Ser Val Lys Ser Ala Asn Val Lys Lys Ala Asp Ser Ser
 275 280 285
 Thr Thr Lys Lys Asn Gln Asn Ser Ser Lys Lys Glu Ser Glu Ser Glu
 290 295 300
 Asp Ser Ser Asp Asp Glu Pro Leu Ile Lys Lys Leu Lys Lys Pro Pro
 305 310 315 320
 Thr Asp Glu Glu Leu Lys Glu Thr Ile Lys Lys Leu Leu Ala Ser Ala
 325 330 335
 Asn Leu Glu Glu Val Thr Met Lys Gln Ile Cys Lys Lys Val Tyr Glu
 340 345 350
 Asn Tyr Pro Thr Tyr Asp Leu Thr Glu Arg Lys Asp Phe Ile Lys Thr
 355 360 365
 Thr Val Lys Glu Leu Ile Ser
 370 375

<210> 116

<211> 2699

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1740)

<223> a, c, t, g, other or unknown

<400> 116

ggcccgcggc ggccgaaatc cgcggttcac agcatgtccg cctcggcccc tgctgcggag 60
 ggggagggaa cccccaccca gccgcgctcc gagaaagaac ccgaaatgcc cgggtcccaga 120
 gaggagagcg aggaggaaga ggacgaggac gacgaggagg aggaggagga ggaaaaagaa 180
 aagagtctca tcgtggaagg caagagggaa aagaaaaaag tagagaggtt gacaatgcaa 240
 gtctcttcct tacagagaga gccatttaca attgcacaag gaaaggggca gaaactttgt 300
 gaaattgaga ggatacattt ttttctaagt aagaagaaaa cogatgaact tagaaatcta 360
 cacaaactgc tttacaacag gccaggcact gtgtcctcat taaagaagaa tgtgggtcag 420
 tttagtggct ttccatttga aaaaggaagt gtccaatata aaaagaagga agaaatgttg 480
 aaaaaattta gaaatgccat gttaaagagc atctgtgagg ttcttgattt ggagagatca 540
 ggtgtaaaata gtgaactagt gaagaggatc ttgaatttct taatgcatcc aaagccttct 600
 ggcaaaccat tgccgaaatc taaaaaaaact tgtagcaaag gcagtaaaaa ggaacggaac 660
 agttctggaa tggcaaggaa ggctaagcga accaaatgtc ctgaaattct gtcagatgaa 720
 tctagtagtg atgaagatga aaagaaaaac aaggaagagt cttcagatga tgaagataaa 780
 gaaagtgaag aggagccacc aaaaaagaca gccaaaagag aaaaacctaa acagaaagct 840
 acttctaaaa gtaaaaaatc tgtgaaaagt gccaatgtta agaaagcaga tagcagcacc 900
 accaagaaga atcaaaacag ttccaaaaaa gaaagtgtgt ctgaggatag ttcagatgat 960

97/299

```

gaaccttttaa ttaaaaagtt gaagaaaccc cctacagatg aagagttaaa ggaaacaata 1020
aagaaattac tggccagtgc taacttggaa gaagtcacaa tgaaacagat ttgcaaaaag 1080
gtctatgaaa attatcctac ttatgattta actgaaagaa aagatttcat aaaaacaact 1140
gtaaaagagc taatttcctg agatagagga cagagaagat gactcgttcc catagatttg 1200
aagatctgat ttataccatt ataccagcaa agagaatgta tttccttttc taaatccttg 1260
ttaagcaacg ttagtagaac ttaactgctga cctttttatc ttgagtgtta tgtgaatttg 1320
agtttgctgt tttaaattgc atttctatgc catttttagt ttaaaatctt gcatggcatt 1380
aattgttcct tgctttttata gttgtatttt gtacattttg gatttcttta tataaggtca 1440
tagattcctg agctgttggt gtttttagtg cacttaatat tagcttgctt aaggcatact 1500
tttaatcaag tagaacaaaa actattatca ccaggattta tacatacaga gattgtagta 1560
tttagtatat gaaatatttt gaatacacat ctctgtcagt gtgaaaattc agcggcagtg 1620
tgtccatcat attaaaaata tacaagctac agttgtccag atcactgaat tggaaacttt 1680
ctctgcacg tgtatatatg tcaaattgtc agcatgacaa aagtgcacaga tgttattttt 1740
gtatttttaa aaaacaattg gttgtatata aagttttttt atttcttttg tgcagatcac 1800
tttttaaaact cacataggta ggtatcttta tagttgtaga ctatggaatg tcagtgttca 1860
gccaaacagt atgatggaac agtgaaagtc aattcagtga tggcaacact gaagggaacag 1920
ttaccctgct ttgcctcgaa agtgtcatca atttgtaatt ttagtattaa ctctgtaaaa 1980
gtgtctgtag gtacgtttta tattatataa ggacagacca aaaatcaacc tatcaaagct 2040
tcaaaaactt tgggaaaggg tgggattaag tacaagcaca tttggcttac agtaaataag 2100
ctgattttta ttaactgctt ttgcccataa aaaatgctga tatttactgg aaacctagcc 2160
agcttcacga ttatgactaa agtaccagat tataatgcca gaatataatg tgcaggcaat 2220
cgtggatgct tctgacaaag tgtgtctcaa aaataatata cttttacatt aaagaaattt 2280
aatgtttctc tggagttggg gctcttggtt ttcagagttt gggttaatcag tgttgattct 2340
agatgatcaa cataatggac cactcctgaa tgagacttaa ttttgtcttt caaatttact 2400
gtcttaaatc agttttattaa atctgaattt taaaacatgc tgtttatgac acaatgacac 2460
atgtgttgca ccaatttaag gttagaaaaa atctttgcat catagaacag aaatatataa 2520
aaatatatgt tgaatgttaa cagggtattt cacaggtttg tttcttgata gttactcaga 2580
cactagggaa aggtaaatac aagtgaacaa aataagcaac taaatgagac ctaataattg 2640
gccttcgatt ttaaatattt gttcttataa accttgtcaa taaaaataaa tctaaatca 2699

```

<210> 117
 <211> 288
 <212> DNA
 <213> Homo sapiens

```

<400> 117
gtcaacagtc gcccaaaatt taaataaaat tattgcaggc ctataataag ttaaataagct 60
aaaattttta ataatgacag attcagtttt tagtgctgac agtggttctt gattttgcaa 120
acaaatgagt atttctcaa tgggaagacg tcttatatgt tctatgctgt gaatagatag 180
gttttagaatt actttcagca ccgttttgc tccattacag ttaattttat ggggtgggaga 240
gcaaaatcta aatggatgca ctgtctgagt accagaatga atggaaaa 288

```

<210> 118
 <211> 277
 <212> PRT
 <213> Homo sapiens

```

<400> 118
Met Ser Ala Gln Ala Ala Lys Val Ser Lys Lys Glu Leu Asn Ser Asn
  1              5              10              15

His Asp Gly Ala Asp Glu Thr Ser Glu Lys Glu Gln Gln Glu Ala Ile
      20              25              30

Glu His Ile Asp Glu Val Gln Asn Glu Ile Asp Arg Leu Asn Glu Gln
      35              40              45

```


98/299

Ala Ser Glu Glu Ile Leu Lys Val Glu Gln Lys Tyr Asn Lys Leu Arg
 50 55 60
 Gln Pro Phe Phe Gln Lys Arg Ser Glu Leu Ile Ala Lys Ile Pro Asn
 65 70 75 80
 Phe Trp Val Thr Thr Phe Val Asn His Pro Gln Val Ser Ala Leu Leu
 85 90 95
 Gly Glu Glu Asp Glu Glu Ala Leu His Tyr Leu Thr Arg Val Glu Val
 100 105 110
 Thr Glu Phe Glu Asp Ile Lys Ser Gly Tyr Arg Ile Asp Phe Tyr Phe
 115 120 125
 Asp Glu Asn Pro Tyr Phe Glu Asn Lys Val Leu Ser Lys Glu Phe His
 130 135 140
 Leu Asn Glu Ser Gly Asp Pro Ser Ser Lys Ser Thr Glu Ile Lys Trp
 145 150 155 160
 Lys Ser Gly Lys Asp Leu Thr Lys Arg Ser Ser Gln Thr Gln Asn Lys
 165 170 175
 Ala Ser Arg Lys Arg Gln His Glu Glu Pro Glu Ser Phe Phe Thr Trp
 180 185 190
 Phe Thr Asp His Ser Asp Ala Gly Ala Asp Glu Leu Gly Glu Val Ile
 195 200 205
 Lys Asp Asp Ile Trp Pro Asn Pro Leu Gln Tyr Tyr Leu Val Pro Asp
 210 215 220
 Met Asp Asp Glu Glu Gly Glu Gly Glu Glu Asp Asp Asp Asp Glu
 225 230 235 240
 Glu Glu Glu Gly Leu Glu Asp Ile Asp Glu Glu Gly Asp Glu Asp Glu
 245 250 255
 Gly Glu Glu Asp Glu Asp Asp Asp Glu Gly Glu Glu Gly Glu Glu Asp
 260 265 270
 Glu Gly Glu Asp Asp
 275

<210> 119

<211> 2577

<212> DNA

<213> Homo sapiens

<400> 119

cacatgtcgg cgcaggcggc caaagtcagt aaaaaggagc tcaactccaa ccacgacggg 60
 gccgacgaga cctcagaaaa agaacagcaa gaagcgattg aacacattga tgaagtacaa 120
 aatgaaatag acagacttaa tgaacaagcc agtgaggaga ttttgaaagt agaacagaaa 180
 tataacaaac tccgccaacc attttttcag aagagggtcag aattgatcgc caaaatccca 240
 aatttttggg taacaacatt tgtcaacat ccacaagtgt ctgcactgct tggggaggaa 300

99/299

```

gatgaagagg cactgcatta tttgaccaga gttgaagtga cagaatttga agatatttaa 360
tcagggttaca gaatagattt ttattttgat gaaaatcctt actttgaaaa taaagtcttc 420
tccaaagaat ttcatctgaa tgagagtggg gatccatctt cgaagtccac cgaaatcaaa 480
tggaatcttg gaaaggattt gacgaaacgt tcgagtcaaa cgcagaataa agccagcagg 540
aagaggcagc atgaggaacc agagagcttc tttacctggg ttactgacca ttctgatgca 600
gggtgctgatg agttaggaga ggtcatcaaa gatgatatct ggccaaaccc attacagtac 660
tacttgggttc ccgatatgga tgatgaagaa ggagaaggag aagaagatga tgatgatgat 720
gaagaggagg aaggattaga agatattgac gaagaagggg atgaggatga aggtgaagaa 780
gatgaagatg atgatgaagg ggaggaagga gaggaggatg aaggagaaga tgactaaata 840
gaacactgat ggattccaac ctcccttttt ttaaattttt tccagtcctt gggagcaagt 900
tgcagtcctt tttttttttt tttttttttt cctctctgtg ctccagtcgc ctgttcttga 960
ggtctctttt ctctactcca tggttctcaa tttatttggg gggaaatacc ttgagcagaa 1020
tacaatggga aaagagtctc tacccttttc tgttcgaagt tcatttttat cccttcctgt 1080
ctgaacaaaa actgtatgga atcaaacacca ccgagctctg tgggaaaaaa gaaaaacctg 1140
ctccctttgc tctgctggaa gctggagggt gctaggcccc tgtgtagtag tgtatagaat 1200
tctagctttt ttctctctt ctctgtatat tgggctcaga gactacactg tgtctctatg 1260
tgaatatgga cagttagcat ttaccaacat gtatctgtct actttctctt gtttaaaaaa 1320
agaaaaaaaa acttaaaaaa atgggggttat agaaggctcag caaaggggtg gggtttgaga 1380
tgtttgggtg ggtagtgagg cattttgaca acatggcttc tcctttggca tgtttaattg 1440
tgatatttga cagacatcct tgcagtttaa gatgacactt ttaaaataaa ttctctccta 1500
atgatgactt gagccctgcc actcaatggg agaatcagca gaacctgtag gatcttattt 1560
ggaattgaca ttctctattg taattttggt cctgtttatt tttgggtttc tttttgttct 1620
actggaaaag aaagatgatg ctccagttta aacgttaaaa gtgtacaagt tgctttgtta 1680
caataaaaact aaatgtgtac acaaaggatt tgatgctttt ctctcagcat aggtatgctt 1740
actatgacct tccaagtttg acttgataaa catcactgtc aaactttgtc accctaactt 1800
cgtatttttt gatacgcact tttgcaggat gacctcaggg ctatgtggat tgagtaatgg 1860
gatttgaatc aatgtattaa tatctccata gctgggaaac gtgggttcaa tttgccattg 1920
gtttctgaaa agtattcaca tcatattggga taccagatag ctcaatactc tctgagtaca 1980
ttgtgccctt gatttttatc tccaagtggc agtttttaaa attggccttt tacctggata 2040
taaaatattt gtgcctgcca ccaccatcca acagacctgg tgctctaata ccaagttata 2100
cacgggacag ttgctggcat gtcttcattg gctctctaaa atgtggccaa gaagataggc 2160
tctcagtaag aagtctgatg gtgagcagta actgtccctg ctttctggta taaagctctc 2220
aaatgtgacc atgtgaatct ggggtgggata atggactcag ctctgtctgc tcaatgccat 2280
tgtgcagaga agcaccctaa tgcataagct ttttaatgct gtaaaatata gtcgctgaaa 2340
ttaaatgcca ctttttcaga ggtgaattaa tggacagtct ggtgaacttc aaaagctttt 2400
tgatgtataa aacttgataa atggaactat tccatcaata ggcaaaagtg taacaaccta 2460
tctagatgga tagtatgtaa tttctgcaca ggtctctgtt tagtaaatac atcactgtat 2520
accgatcagg aatcttgctc caataaagga acataaagat ttaaaaaaaaa aaaaaaa 2577

```

<210> 120

<211> 288

<212> PRT

<213> Homo sapiens

<400> 120

```

Ala Leu Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser
  1             5             10             15

Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln
      20             25             30

Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg
      35             40             45

Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys
      50             55             60

```

100/299

His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
 65 70 75 80
 Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile
 85 90 95
 Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Met Ala Gly Gln Cys
 100 105 110
 Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile Pro Cys
 115 120 125
 Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln Arg Tyr
 130 135 140
 Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala Ile Leu
 145 150 155 160
 Trp Thr Cys Leu Gly Leu Ser Leu Ile Ile Ser Leu Ala Val Phe Val
 165 170 175
 Leu Met Phe Leu Leu Arg Lys Ile Ser Ser Glu Pro Leu Lys Asp Glu
 180 185 190
 Phe Lys Asn Thr Gly Ser Gly Leu Leu Gly Met Ala Asn Ile Asp Leu
 195 200 205
 Glu Lys Ser Arg Thr Gly Asp Glu Ile Ile Leu Pro Arg Gly Leu Glu
 210 215 220
 Tyr Thr Val Glu Glu Cys Thr Cys Glu Asp Cys Ile Lys Ser Lys Pro
 225 230 235 240
 Lys Val Asp Ser Asp His Cys Phe Pro Leu Pro Ala Met Glu Glu Gly
 245 250 255
 Ala Thr Ile Leu Val Thr Thr Lys Thr Asn Asp Tyr Cys Lys Ser Leu
 260 265 270
 Pro Ala Ala Leu Ser Ala Thr Glu Ile Glu Lys Ser Ile Ser Ala Arg
 275 280 285

<210> 121

<211> 1073

<212> DNA

<213> Homo sapiens

<400> 121

gcactaagtc ttgcacttgt cacaaacagt gcacctactt caagttctac aaagaaaaca 60
 cagctacaac tggagcattt actgctggat ttacagatga ttttgaatgg aattaataat 120
 tacaagaatc ccaaactcac caggatgctc acatttaagt tttacatgcc caagaaggcc 180
 acagaactga aacatcttca gtgtctagaa gaagaactca aacctctgga ggaagtgcta 240
 aatttagctc aaagcaaaaa ctttcactta agaccagggy acttaatcag caatatcaac 300
 gtaatatgtc tggaactaaa gatggctggg cagtgtctcc aaaatgaata ttttgacagt 360
 ttgttgcatg cttgcatacc ttgtcaactt cgatgttctt ctaatactcc tcctctaaca 420
 tgtcagcggt attgtaatgc aagtgtgacc aattcagtga aaggaacgaa tgcgattctc 480
 tggacctgtt tgggactgag cttaataatt tctttggcag ttttcgtgct aatgtttttg 540

101/299

```

ctaaggaaga taagctctga accattaaag gacgagttta aaaacacagg atcaggtctc 600
ctgggcatgg ctaacattga cctggaaaag agcaggactg gtgatgaaat tattcttccg 660
agaggcctcg agtacacggg ggaagaatgc acctgtgaag actgcatcaa gagcaaaccg 720
aagggtcgact ctgaccattg ctttccactc ccagctatgg aggaaggcgc aaccattctt 780
gtcaccacga aaacgaatga ctattgcaag agcctgccag ctgctttgag tgctacggag 840
atagagaaat caatttctgc taggtaatta accatttcga ctcgagcagt gccactttaa 900
aaatcttttg tcagaataga tgatgtgtca gatctcttta ggatgactgt atttttcagt 960
tgccgataca gctttttgtc ctctaactgt ggaaactcct tatgttagat atatttctct 1020
aggttactgt tgggagctta atggtagaaa cttccttggg ttctatgatt aaa 1073

```

<210> 122

<211> 26

<212> PRT

<213> Homo sapiens

<400> 122

```

Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu Glu Met Glu Phe Lys
  1             5             10             15

```

```

Arg Ala Lys Ala Asn Leu Asp Lys Asn Lys
      20             25

```

<210> 123

<211> 78

<212> DNA

<213> Homo sapiens

<400> 123

```

gaatttgaag atagagacag gtctcatcgg gaggaatgg agttcaagag ggccaaggcg 60
aacctagaca agaataag                                     78

```

<210> 124

<211> 34

<212> PRT

<213> Homo sapiens

<400> 124

```

Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu Glu Met Glu Val His
  1             5             10             15

```

```

Glu Leu Glu Lys Ser Lys Arg Ala Leu Glu Thr Gln Met Glu Glu Met
      20             25             30

```

Lys Thr

<210> 125

<211> 102

<212> DNA

<213> Homo sapiens

<400> 125

```

gaatttgaag atagagacag gtctcatcgg gaggaatgg aggtccatga gctggagaag 60
tccaagcggg ccctggagac ccagatggag gagatgaaga cg 102

```

102/299

<210> 126

<211> 50

<212> PRT

<213> Homo sapiens

<400> 126

Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu Glu Met Glu Asn Glu
1 5 10 15

Val Glu Ser Val Thr Gly Met Leu Asn Glu Ala Glu Gly Lys Ala Ile
20 25 30

Lys Leu Ala Lys Asp Val Ala Ser Leu Ser Ser Gln Leu Gln Asp Thr
35 40 45

Gln Glu
50

<210> 127

<211> 152

<212> DNA

<213> Homo sapiens

<400> 127

gaatttgaag atagagacag gtctcatcgg gaggaatgg agaatgaagt tgagagcgtc 60
acagggatgc ttaacgaggc cgaggggaag gccattaagc tggccaagga cgtggcgtcc 120
ctcagttccc agctccagga caccaggag tt 152

<210> 128

<211> 1353

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (941)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (1067)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (1077)

<223> a, c, t, g, other or unknown

<400> 128

cttggccaac attctggagg cagtaaagaa agcttataga ataaccacat attagaactt 60
gtgaaggaga aaatatacat atatatatat gtatatatat agtctctcta ttaagtaatt 120
taccataagg ggttttaaata ggaatgtttt ctccaaagtg aatcttgaaa tcttgggtgtt 180
tataattgtc aagcctcttt ttttaaaata gatttgggtca acaggaagta tttttttcta 240
atttttatth tatagaccta gtcaagcttc ttaattgtta aatattgtta taacaatata 300
tctgggcccgg gcgcgggtggc tcaactcctgt aatccagca ctttggggagg ccagggcggg 360

103/299

```

tgaatcacga ggtcaggaga ttgagaccat cctggctaac acaaagaaac cccatctcta 420
ctaaaaatac aaaaaattag ctgggagagg aggagggcgc ctgtagtccc agctactcgg 480
gaggcggagc ttgcggtgag ccaagatcgc gccactgcac tccagcgact ccgtctcaaa 540
aaaaaaaaaa aaaaaacatc tgagtcggta catggttggt agccgaggag aaaaaacatc 600
cttccaaata cgcggatgag agggacagag ctgaggcaga agccaggagg aaggaaacca 660
aggccctgtc cctggctcgg gcccttgaag aggccttggg agccaaagag gaactcgagc 720
ggaccaacaa aatgctcaaa gccgaaatgg aagacctggg cagctccaag gatgacgtgg 780
gcaagaacgt aagtggctct ggggtggtttt tctcgtccat gtttcgcctg cccaccctct 840
gtgtattca ccagtcctatg cgaggctagc tcctggcctt tttcatagcg aactatcctc 900
ggaaatggaa ggaggttttt ggactgggtgc aggggctaaa naggggctga gaatggcagt 960
cgaggatggg tctgagttgg ggggtccgag gataaggctg ggggtctgaac tctcaggggt 1020
catcttgagt cccggccatg catcctgtgg gaggccaaag ccacctnccc tgatctnctt 1080
gaggtgccgc tcacgggtggg tttctcaatc gtcttcatga agttgagcct catagaatgg 1140
ggctgccgcg tctgccggca ggtccatgag ctggagaagt ccaagcgggc cctggagacc 1200
cagatggagg agatgaagac gcagctggaa gagctggagg acgagctgca agccacggag 1260
gacgccaaac tgcggctgga agtcaacatg caggcgtca agggccagtt cgaaagggat 1320
ctccaagccc gggacgagca gaatgaggag aag                                     1353

```

<210> 129

<211> 744

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (326)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (614)

<223> a, c, t, g, other or unknown

<400> 129

```

gcccggctta aaatttagta tcttttagtg attgctagat ctctttgtca gtgagttaat 60
taatctaata ggctgatagc agctgaggat gtccccaaga atacttggtta gctaagagaa 120
gaaaatggag ggatatatgt gatacttggt ttctttgatg ctggttgtaat tcttgatgatt 180
ttcatatatg tgaatacaag acttccacac catgcccttt ctttcgggat ctgtaaaatt 240
tagaagcttt aaaatgtata atgtacattt gttacatttc tgaacctttt tgctcatgct 300
ctttgttccc tgatgtagaa tggtcnatct tgtccgtcaa ggcccaacct gaatgttgct 360
attaaatgtc aggcctttcc tcagtctctg ggggtctgaac tgctcagggg tcatcttgag 420
tcccggccat gcactctgtg ggaggccaaa gccacctccc tgatctcctg aggtgccgct 480
cacggtgggt ttctcaatcg tcttcatgaa gttgagcctc atagaatggg gctgcccgtc 540
ctgccggcag gtccatgagc tggagaagtc caagcggggc ctggagaccc agatggagga 600
gatgaagacg cagntggaag agctggagga cgagctgcaa gccacggagg acgccaaact 660
gcggctggaa gtcaacatgc aggcgctcaa gggccagttc gaaagggatc tccaagcccc 720
ggacgagcag aatgaggaga agag                                     744

```

<210> 130

<211> 29

<212> PRT

<213> Homo sapiens

<400> 130

```

Arg Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu Glu Met Glu Glu
  1                      5                      10                      15

```

104/299

Leu Leu Gln Glu Glu Thr Arg Gln Lys Leu Asn Val Ser
 20 25

<210> 131
 <211> 89
 <212> DNA
 <213> Homo sapiens

<400> 131
 acgcgaattt gaagatagag acaggtctca tcgggaggaa atggaggagc tgcttcaaga 60
 agaaaccggg cagaagctca acgtgtcta 89

<210> 132
 <211> 452
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Ser Glu Thr Pro Ala Gln Cys Ser Ile Lys Gln Glu Arg Ile Ser
 1 5 10 15
 Tyr Thr Pro Pro Glu Ser Pro Val Pro Ser Tyr Ala Ser Ser Thr Pro
 20 25 30
 Leu His Val Pro Val Pro Arg Ala Leu Arg Met Glu Glu Asp Ser Ile
 35 40 45
 Arg Leu Pro Ala His Leu Arg Leu Gln Pro Ile Tyr Trp Ser Arg Asp
 50 55 60
 Asp Val Ala Gln Trp Leu Lys Trp Ala Glu Asn Glu Phe Ser Leu Arg
 65 70 75 80
 Pro Ile Asp Ser Asn Thr Phe Glu Met Asn Gly Lys Ala Leu Leu Leu
 85 90 95
 Leu Thr Lys Glu Asp Phe Arg Tyr Arg Ser Pro His Ser Gly Asp Val
 100 105 110
 Leu Tyr Glu Leu Leu Gln His Ile Leu Lys Gln Arg Lys Pro Arg Ile
 115 120 125
 Leu Phe Ser Pro Phe Phe His Pro Gly Asn Ser Ile His Thr Gln Pro
 130 135 140
 Glu Val Ile Leu His Gln Asn His Glu Glu Asp Asn Cys Val Gln Arg
 145 150 155 160
 Thr Pro Arg Pro Ser Val Asp Asn Val His His Asn Pro Pro Thr Ile
 165 170 175
 Glu Leu Leu His Arg Ser Arg Ser Pro Ile Thr Thr Asn His Arg Pro
 180 185 190
 Ser Pro Asp Pro Glu Gln Arg Pro Leu Arg Ser Pro Leu Asp Asn Met

105/299

195	200	205
Ile Arg Arg Leu Ser Pro	Ala Glu Arg Ala Gln Gly	Pro Arg Pro His
210	215	220
Gln Glu Asn Asn His	Gln Glu Ser Tyr Pro	Leu Ser Val Ser Pro Met
225	230	235 240
Glu Asn Asn His Cys	Pro Ala Ser Ser Glu	Ser His Pro Lys Pro Ser
245	250	255
Ser Pro Arg Gln Glu	Ser Thr Arg Val Ile	Gln Leu Met Pro Ser Pro
260	265	270
Ile Met His Pro Leu	Ile Leu Asn Pro Arg	His Ser Val Asp Phe Lys
275	280	285
Gln Ser Arg Leu Ser	Glu Asp Gly Leu His	Arg Glu Gly Lys Pro Ile
290	295	300
Asn Leu Ser His Arg	Glu Asp Leu Ala Tyr	Met Asn His Ile Met Val
305	310	315 320
Ser Val Ser Pro Pro	Glu Glu His Ala Met	Pro Ile Gly Arg Ile Ala
325	330	335
Asp Cys Arg Leu Leu	Trp Asp Tyr Val Tyr	Gln Leu Leu Ser Asp Ser
340	345	350
Arg Tyr Glu Asn Phe	Ile Arg Trp Glu Asp	Lys Glu Ser Lys Ile Phe
355	360	365
Arg Ile Val Asp Pro	Asn Gly Leu Ala Arg	Leu Trp Gly Asn His Lys
370	375	380
Asn Arg Thr Asn Met	Thr Tyr Glu Lys Met	Ser Arg Ala Leu Arg His
385	390	395 400
Tyr Tyr Lys Leu Asn	Ile Ile Arg Lys Glu	Pro Gly Gln Arg Leu Leu
405	410	415
Phe Arg Phe Met Lys	Thr Pro Asp Glu Ile	Met Ser Gly Arg Thr Asp
420	425	430
Arg Leu Glu His Leu	Glu Ser Gln Glu Leu	Asp Glu Gln Ile Tyr Gln
435	440	445
Glu Asp Glu Cys		
450		

<210> 133

<211> 1956

<212> DNA

<213> Homo sapiens

<400> 133

tcctgatctc tctcgctgtg agacatgtct gagactcctg ctcagtgtag cattaagcag 60

106/299

```

gaacgaattt catatacacc tccagagagc ccagtgccga gttacgcttc ctcgacgcca 120
cttcatgttc cagtgcctcg agcgctcagg atggaggaag actcgatccg cctgcctgcg 180
cacctgcgct tgcagccaat ttactggagc agggatgacg tagcccagtg gctcaagtgg 240
gctgaaaatg agttttcttt aaggccaatt gacagcaaca cgtttgaaat gaatggcaaa 300
gctctcctgc tgctgaccaa agaggacttt cgtatcgtat ctcctcattc aggtgatgtg 360
ctctatgaac tccttcagca tattctgaag cagaggaaac ctcggattct tttttcacca 420
ttcttccacc ctggaaactc tatacacaca cagccggagg tcatactgca tcagaaccat 480
gaagaagata actgtgtcca gaggaccccc aggccatccg tggataatgt gcaccataac 540
cctcccacca ttgaactgtt gcaccgctcc aggtcaccta tcacgacaaa tcaccggcct 600
tctcctgacc ccgagcagcg gcccctccgg tccccctggg acaacatgat ccgcgcctc 660
tccccggctg agagagctca gggacccagg ccgcaccagg agaacaacca ccaggagtcc 720
tacctctgtt cagtgtctcc catggagaat aatcactgcc cagcgtcctc cgagtcccac 780
ccgaagccat ccagcccccg gcaggagagc acacgcgtga tccagctgat gccagcccc 840
atcatgcacc ctctgatcct gaacccccgg cactccgtgg atttcaaaca gtccaggctc 900
tccgaggacg ggctgcatag ggaagggaag cccatcaacc tctctcatcg ggaagacctg 960
gcttacatga accacatcat ggtctctgtc tccccgcctg aagagcacgc catgcccatt 1020
gggagaatag cagactgtag actgctttgg gattacgtct atcagttgct ttctgacagc 1080
cggtagcaaa acttcatccg atgggaggac aaagaatcca aaatattccg gatagtggat 1140
cccaacggac tggctcgact gtggggaaac cataagaaca gaacaaacat gacctatgag 1200
aaaatgtcca gagccctgcg ccactactac aaactaaaca ttatcaggaa ggagccagga 1260
caaaggcctt tgttcaggtt tatgaaaacc ccagatgaaa tcatgagtgg ccgaacagac 1320
cgtctggagc acctagagtc ccaggagctg gatgaacaaa tataccaaga agatgaatgc 1380
tgaaggaacc aacagtccac ctcagcgggc cagcagccca gggaaaccct gccaccagg 1440
attgctggaa gtgtgacgga gcaggcgggc tgaggagagt ggaaaaggaa gcgaccaga 1500
aatggcaggg acacttctct tgcagaccaa gagggaccct ggagcacctt agacaaacta 1560
ccagcacagc gcggggctgg aattctggcg gatggcacga gcctgggact ccatgtcacg 1620
tttcttctg atttggaatc tctccatctg taattcctca cctcaccct tccaccgtt 1680
ttagtatcat ggtgtttttg tttttgtttt tgttttaaga acctgcagtt tgactcttca 1740
tcgttcatct aggggaagac atctgatgtt gtttctctat ggaaatatat atctattata 1800
tatatatatt ttttgcaaat ctcacaaagt gcggcaagcc cagctgggtca ggaaagagaa 1860
tacttgcaga ggggttcagg ttctctttt tcttgccacg tggatcaggt ctgttctgt 1920
tactgttggg tcttggctga aaaaaaaaaa aaaaaa 1956

```

<210> 134

<211> 452

<212> PRT

<213> Homo sapiens

<400> 134

```

Met Ser Glu Thr Pro Ala Gln Cys Ser Ile Lys Gln Glu Arg Ile Ser
  1             5             10             15

Tyr Thr Pro Pro Glu Ser Pro Val Pro Ser Tyr Ala Ser Ser Thr Pro
          20             25             30

Leu His Val Pro Val Pro Arg Ala Leu Arg Met Glu Glu Asp Ser Ile
          35             40             45

Arg Leu Pro Ala His Leu Arg Leu Gln Pro Ile Tyr Trp Ser Arg Asp
  50             55             60

Asp Val Ala Gln Trp Leu Lys Trp Ala Glu Asn Glu Phe Ser Leu Arg
  65             70             75             80

Pro Ile Asp Ser Asn Thr Phe Glu Met Asn Gly Lys Ala Leu Leu Leu
          85             90             95

```

107/299

Leu Thr Lys Glu Asp Phe Arg Tyr Arg Ser Pro His Ser Gly Asp Val
 100 105 110
 Leu Tyr Glu Leu Leu Gln His Ile Leu Lys Gln Arg Lys Pro Arg Ile
 115 120 125
 Leu Phe Ser Pro Phe Phe His Pro Gly Asn Ser Ile His Thr Gln Pro
 130 135 140
 Glu Val Ile Leu His Gln Asn His Glu Glu Asp Asn Cys Val Gln Arg
 145 150 155 160
 Thr Pro Arg Pro Ser Val Asp Asn Val His His Asn Pro Pro Thr Ile
 165 170 175
 Glu Leu Leu His Arg Ser Arg Ser Pro Ile Thr Thr Asn His Arg Pro
 180 185 190
 Ser Pro Asp Pro Glu Gln Arg Pro Leu Arg Ser Pro Leu Asp Asn Met
 195 200 205
 Ile Arg Arg Leu Ser Pro Ala Glu Arg Ala Gln Gly Pro Arg Pro His
 210 215 220
 Gln Glu Asn Asn His Gln Glu Ser Tyr Pro Leu Ser Val Ser Pro Met
 225 230 235 240
 Glu Asn Asn His Cys Pro Ala Ser Ser Glu Ser His Pro Lys Pro Ser
 245 250 255
 Ser Pro Arg Gln Glu Ser Thr Arg Val Ile Gln Leu Met Pro Ser Pro
 260 265 270
 Ile Met His Pro Leu Ile Leu Asn Pro Arg His Ser Val Asp Phe Lys
 275 280 285
 Gln Ser Arg Leu Ser Glu Asp Gly Leu His Arg Glu Gly Lys Pro Ile
 290 295 300
 Asn Leu Ser His Arg Glu Asp Leu Ala Tyr Met Asn His Ile Met Val
 305 310 315 320
 Ser Val Ser Pro Pro Glu Glu His Ala Met Pro Ile Gly Arg Ile Ala
 325 330 335
 Asp Cys Arg Leu Leu Trp Asp Tyr Val Tyr Gln Leu Leu Ser Asp Ser
 340 345 350
 Arg Tyr Glu Asn Phe Ile Arg Trp Glu Asp Lys Glu Ser Lys Ile Phe
 355 360 365
 Arg Ile Val Asp Pro Asn Gly Leu Ala Arg Leu Trp Gly Asn His Lys
 370 375 380
 Asn Arg Thr Asn Met Thr Tyr Glu Lys Met Ser Arg Ala Leu Arg His
 385 390 395 400
 Tyr Tyr Lys Leu Asn Ile Ile Arg Lys Glu Pro Gly Gln Arg Leu Leu

108/299

	405		410		415
Phe Arg Phe Met Lys Thr Pro Asp Glu Ile Met Ser Gly Arg Thr Asp					
	420		425		430
Arg Leu Glu His Leu Glu Ser Gln Glu Leu Asp Glu Gln Ile Tyr Gln					
	435		440		445
Glu Asp Glu Cys					
	450				

<210> 135
 <211> 1580
 <212> DNA
 <213> Homo sapiens

<400> 135

tcctgatctc	tctcgctgtg	agacatgtct	gagactcctg	ctcagtgtag	cattaagcag	60
gaacgaattt	catatacacc	tccagagagc	ccagtgccga	gttacgcttc	ctcgacgcca	120
cttcatgttc	cagtgcctcg	agcgcacagg	atggaggaag	actcgatccg	cctgcctgcg	180
cacctgcgct	tcagccaat	ttactggagc	agggatgacg	tagcccagtg	gctcaagtgg	240
gctgaaaatg	agttttcttt	aaggccaatt	gacagcaaca	cgtttgaaat	gaatggcaaa	300
gctctcctgc	tgctgaccaa	agaggacttt	cgctatcgat	ctcctcattc	aggtgatgtg	360
ctctatgaac	tccttcagca	tattctgaag	cagaggaaac	ctcggattct	tttttcacca	420
ttcttccacc	ctggaaactc	tatacacaca	cagccggagg	tcatactgca	tcagaaccat	480
gaagaagata	actgtgtcca	gaggaccccc	aggccatccg	tggataatgt	gcaccataac	540
cctcccacca	ttgaactgtt	gcaccgctcc	aggtcaccta	tcacgacaaa	tcaccggcct	600
tctcctgacc	ccgagcagcg	gccccctccg	tccccctgg	acaacatgat	ccgccgcctc	660
tccccggctg	agagagctca	gggacccagg	ccgcaccagg	agaacaacca	ccaggagtcc	720
taccctctgt	cagtgtctcc	catggagaat	aatcactgcc	cagcgtcctc	cgagtccac	780
ccgaagccat	ccagcccccg	gcaggagagc	acacgcgtga	tccagctgat	gcccagcccc	840
atcatgcacc	ctctgatcct	gaaccccccg	cactccgtgg	atttcaaaca	gtccaggctc	900
tccgaggacg	ggctgcatag	ggaaggggaag	cccatcaacc	tctctcatcg	ggaagacctg	960
gcttacatga	accacatcat	ggtctctgtc	tccccgcctg	aagagcacgc	catgcccatt	1020
gggagaatag	cagactgtag	actgcttttg	gattacgtct	atcagttgct	ttctgacagc	1080
cggtagcaaa	acttcatccg	atgggaggac	aaagaatcca	aaatattccg	gatagtggat	1140
cccaacggac	tggtctgact	gtggggaaac	cataagaaca	gaacaaacat	gacctatgag	1200
aaaatgtoca	gagccctgcg	ccactactac	aaactaaaca	ttatcaggaa	ggagccaggac	1260
caaaggcttt	tgttcaggtt	tatgaaaacc	ccagatgaaa	tcatgagtgg	ccgaacagac	1320
cgtctggagc	acctagagtc	ccaggagctg	gatgaacaaa	tataccaaga	agatgaatgc	1380
tgaagggaacc	aacagtccac	ctcagcgggc	cagcagccca	gggaacccct	gcccaccagg	1440
attgctggaa	gtgtgacgga	gcaggcgggc	tgaggagagt	ggaaaaggaa	gcgacccaga	1500
aatggcaggg	acatttctct	tgacagacaa	gagggaccct	ggagcacctt	agacaaaacta	1560
cccagcacag	gcggggctgg					1580

<210> 136
 <211> 1451
 <212> DNA
 <213> Homo sapiens

<400> 136

ccctcgtggc	cgccctggtc	ctggctttct	ccggcatcat	gattggtgag	tgacacagagc	60
cccagggact	ccaaggggg	caggaaggca	ggactgaata	gtgtctcagg	ctgtgccaca	120
ggtgccaagg	tgctacttcg	ttatgctagt	ccctggaatt	gggtggggtg	gtgattaggg	180
cagcccaggc	caagccaaaa	cggaagctcc	caaccttccc	cccaccagag	cagctgcagt	240
tccttgagga	gcccttgatt	ctgcacctca	gccccgtgtg	tatcctcctg	gtgatcagg	300

109/299

```

gggtggggag ctccttcagt gtccatcacg atgggtgaaag ctgcgccccca cccctagacg 360
tcacttctag ctcccacatg ctccaccgg cgcagctcct gtttggtcc caccctatgt 420
aatgcactag cccactcttc cccaaaccag ccctccacca ccctccaggc agagagatag 480
gaaaatcggg ttctgagtat atttctgttc agcctgtgag ccaagggtgag ctgacctgca 540
ggtcacagag aactcagtgt ggtcccaacc agctcttact gctggcagag acatgccag 600
gacagatggg cagaggcttg aaaagggcag agggaaaggc tcttgagagc cctcgaggc 660
caggccccctg caggcaaagg gatctgccgg tagaaggagg atggcagcac acactgtgtc 720
cccataatggt gccatccctc aaagggacag gataatagga gctaacactt gttgcatggt 780
tactacgtgc tcggcaatct acacatttca attcattcga tcctcaggta accctaactc 840
gatcacgggc ggtccattgc atagaggagg gaactgagca catagcgggt gactcatttg 900
ccctggccca tgtgttgggg ggctgggctt tacacacaga atctacccac tgaatcaca 960
ttttgttctg gcttccatgg agtttgctt ccagaacatc ctacatgta ggagtataa 1020
tgggtcactca cattgggtaga gctctttagg atttttcaaa accattttat gttggtgaat 1080
tcatttcatt gacaacccta gaggggtgggg agtggcagcg gttagggaag cagggcagga 1140
gttaccatcc ctgctacag agagggaac tgcagtccaa agaggctctg tgacctggtc 1200
ctcatggctc agcttgtaag taacaagagg cggaattaga gcacagatcc ccagacacca 1260
attcagatcc taggaagtct cagtttttag agtatttact atcagtgttc ttttttttc 1320
tgacttcttg ctgcttgagt ttataatgt ctaataaatt gtatttttagc tgtggaggaa 1380
gatgcagagt cagaagatga agaggaggag gatgtgaaac tcttaagtat atctggaaag 1440
cggctctgcc c 1451

```

<210> 137

<211> 1565

<212> DNA

<213> Homo sapiens

<400> 137

```

tcccttgggg gctttgaaat aacaccacca gtggtcttaa ggttgaagtg tgggtcaggg 60
ccagtgcata ttagtggaca gcacttagta ggtatgttat tttatataat tatactactt 120
agtttgtcct ctttagtgca gttgcttggg tccagtttg gacttaaagc atgggtatag 180
tactactgtc tttttaatag gttccaatgt gagtctagaa attggagagg acaataaat 240
ttttggggcg ggggtggggg gaggaatct tgctgtcacc caggctagag tacagtggca 300
cgatcttggc tcaactggaac ctctccggga ttcaagagat cctcctgtct cagcctcccc 360
agtagctggg gccacagacg tgcaccacca agtccagttg cgtttcatag ttttagtaga 420
gaaggggttt cgtgatgttg gccaggccga tcttgaactc ctggccttaa gctgatctgc 480
acgccctggc ctgtgaaagt gctagtatta cacgtgtcag cactgtgcc tggcctaaaa 540
attatttttt aataaagaca gtctcattat aacggctgga gtgcagtgat gtgatcatag 600
cttgctatat cctcgaactg ctactgggtt cacctcagcc tctggaatag ctagaactac 660
aggcacactc cagcctggc taattttttt tgtatatgtg cagatggggg ctcagtatgt 720
tgcccagatt ggactcttgg cctcaagtgg tccgccttgg cctcccaaaa gtgagattac 780
aggcatgagc caccctcccc aggcctcttg catttaaaac aactatagga aacacaactg 840
accaagatcc cagctgcacc ctcaaatcca ctgctgtgat tgcactgaag ctgccctacc 900
caatggctga gcacagcaga aatactaagg caggccaatt cctgggagtc atgggactcc 960
tctgatgact gactttgggt ccagaacccc ttagggcctt gctgaaactt ccttaggctc 1020
cattggcacc cagggtgctt ccaccaaac ttcctcctt ccctcgttca cgtgggttga 1080
tacttgcaac acagtctgct ggttcaccca gccttcctg gctccctccc catttcctct 1140
catgggcatt tctcctaata aaatctgcag accatatgg gtctaatacc atctccagtc 1200
tgcttcttgg aggaaccaga ctaacatgac tctgccctat ataatacaaa taattatttt 1260
ccatataatc gattttttagc tttgcattta ctttaaatca tgcttcaatt aaagacacac 1320
cttctttaat cattttatta gtatttctaa gtatgatgga aagggtcaga gctcagggga 1380
ggatatggag atccaggagg gcttcctgta ggaagtggcc tgtgtagtgc ttcaagggcc 1440
aggctgccag gccatgttgc agctgaccac ccacctgcag tgtaccgcc gaagcaccag 1500
gagctgcaag ccatgcagat ggagctgcag agccctgagt acaagctgag caagtcogca 1560
cctcg 1565

```

<210> 138

110/299

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 138

```
tcccttgggg gctttgaaat aacaccacca gtggtcttaa ggttgaagtg tgggttcagg 60
ccagtgcata ttagtggaac gcacttagta ggtatgttat ttttatatat tatactactt 120
agtttgcctt ctttagtgca gttgcttggt tcccagtttg gacttaaagc atgggtatag 180
tactactgtc tttttaatag gttccaatgt gagtctagaa attggagagg acaaataaat 240
ttttggggcg ggggggagag gaatcttgct gtcacccagg ctagagtaca gtggcacgat 300
cttggctcac tggaacctct ccgggattca agagatcctc ctgtctcagc ctccccagta 360
gctggggcca cagacgtgca ccaccaagtc cagttgcgtt tcatagttat agtagagaag 420
gggtttcgtg atgttggcca ggcgatctt gaactcctgg ccttaagctg atctgcacgc 480
cctggcctgt gaaagtgcta gtattacacg tgtcagccac tgtgcctggc ctaaaaatta 540
ttttttaata aagacagtct cattataacg gctggagtgc agtgatgtga tcatagcttg 600
ctatatcctc gaactgctac tgggttcacc tcagcctctg gaatagctag aactacaggc 660
acactccacg cctggctaata tttttttgta tatgtgcaga tggggctctca gtatgttgcc 720
cagattggac tcttgacctc aagtggctcg ccttggcctc cccaaagtga gattacaggc 780
atgagccacc ctccccaggc ttcttgctt taaaacctgg cagtgaacat taggcctcaa 840
aatacttttg ttaaaaagtt ctttttccca tgtgctcttt tttttttttt ttttttaaat 900
agaatagaag tctcagtttt tagagtcatt tactatcagt gttctttttt ttctgacccc 960
tgggccagct gcacctcaa atccactgct gtgattgcac tgaagctgcc ctaccaatg 1020
gctgagcaca gcagaaatac taaggcaggc caattcctgg gagtcatggg actcctctga 1080
tgactgactt tggctccaga accccttagg gccttgctga aacttcctta ggctccatgg 1140
caccagggt gcttcaccc aaccttccct cctccctcg ttcacgtggg gttatacttg 1200
caacacagtc tgctggttca ccagccttc cctggctccc tccccatttc ctctcatggg 1260
catttctcct aataaaatct gcagaccgta ttgggtctaa tcccatctcc agtctgcttc 1320
ttggaggaac cagactaaca tgactctgcc ctatataata caaataatta tttccatat 1380
atctgatttt tagcttttga tttactttaa atcatgcttc aattaaagac acaccttctt 1440
taatcatttt attagtattt ctaagtatga tggaaagggt cagagctcag gggaggatat 1500
ggagatccag ggagccttc ttaggaagt ggcctgtgta gtgcttcaag ggccaggctg 1560
ccaggccatg ttgcagctga ccaaccacct gcagtgtacc gccggaagca ccaggagctg 1620
caagccatgc agatggagct gcagagccct gagtacaagc tgagcaagtc cgcacctcg 1679
```

<210> 139

<211> 680

<212> PRT

<213> Homo sapiens

<400> 139

```
Met Glu Asp Ser Met Asp Met Asp Met Ser Pro Leu Arg Pro Gln Asn
  1                      5                      10                      15

Tyr Leu Phe Gly Cys Glu Leu Lys Ala Asp Lys Asp Tyr His Phe Lys
    20                      25                      30

Val Asp Asn Asp Glu Asn Glu His Gln Leu Ser Leu Arg Thr Val Ser
    35                      40                      45

Leu Gly Ala Gly Ala Lys Asp Glu Leu His Ile Val Glu Ala Glu Ala
    50                      55                      60

Met Asn Tyr Glu Gly Ser Pro Ile Lys Val Thr Leu Ala Thr Leu Lys
    65                      70                      75                      80

Met Ser Val Gln Pro Thr Val Ser Leu Gly Gly Phe Glu Ile Thr Pro
    85                      90                      95
```

111/299

Pro Val Val Leu Arg Leu Lys Cys Gly Ser Gly Pro Val His Ile Ser
 100 105 110
 Gly Gln His Leu Val Val Tyr Arg Arg Lys His Gln Glu Leu Gln Ala
 115 120 125
 Met Gln Met Glu Leu Gln Ser Pro Glu Tyr Lys Leu Ser Lys Leu Arg
 130 135 140
 Thr Ser Thr Ile Met Thr Asp Tyr Asn Pro Asn Tyr Cys Phe Ala Gly
 145 150 155 160
 Lys Thr Ser Ser Ile Ser Asp Leu Lys Glu Val Pro Arg Lys Asn Ile
 165 170 175
 Thr Leu Ile Arg Gly Leu Gly His Gly Ala Phe Gly Glu Val Tyr Glu
 180 185 190
 Gly Gln Val Ser Gly Met Pro Asn Asp Pro Ser Pro Leu Gln Val Ala
 195 200 205
 Val Lys Thr Leu Pro Glu Val Cys Ser Glu Gln Asp Glu Leu Asp Phe
 210 215 220
 Leu Met Glu Ala Leu Ile Ile Ser Lys Phe Asn His Gln Asn Ile Val
 225 230 235 240
 Arg Cys Ile Gly Val Ser Leu Gln Ser Leu Pro Arg Phe Ile Leu Leu
 245 250 255
 Glu Leu Met Ala Gly Gly Asp Leu Lys Ser Phe Leu Arg Glu Thr Arg
 260 265 270
 Pro Arg Pro Ser Gln Pro Ser Ser Leu Ala Met Leu Asp Leu Leu His
 275 280 285
 Val Ala Arg Asp Ile Ala Cys Gly Cys Gln Tyr Leu Glu Glu Asn His
 290 295 300
 Phe Ile His Arg Asp Ile Ala Ala Arg Asn Cys Leu Leu Thr Cys Pro
 305 310 315 320
 Gly Pro Gly Arg Val Ala Lys Ile Gly Asp Phe Gly Met Ala Arg Asp
 325 330 335
 Ile Tyr Arg Ala Ser Tyr Tyr Arg Lys Gly Gly Cys Ala Met Leu Pro
 340 345 350
 Val Lys Trp Met Pro Pro Glu Ala Phe Met Glu Gly Ile Phe Thr Ser
 355 360 365
 Lys Thr Asp Thr Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser
 370 375 380
 Leu Gly Tyr Met Pro Tyr Pro Ser Lys Ser Asn Gln Glu Val Leu Glu
 385 390 395 400

112/299

Phe Val Thr Ser Gly Gly Arg Met Asp Pro Pro Lys Asn Cys Pro Gly
 405 410 415
 Pro Val Tyr Arg Ile Met Thr Gln Cys Trp Gln His Gln Pro Glu Asp
 420 425 430
 Arg Pro Asn Phe Ala Ile Ile Leu Glu Arg Ile Glu Tyr Cys Thr Gln
 435 440 445
 Asp Pro Asp Val Ile Asn Thr Ala Leu Pro Ile Glu Tyr Gly Pro Leu
 450 455 460
 Val Glu Glu Glu Glu Lys Val Pro Val Arg Pro Lys Asp Pro Glu Gly
 465 470 475 480
 Val Pro Pro Leu Leu Val Ser Gln Gln Ala Lys Arg Glu Glu Glu Arg
 485 490 495
 Ser Pro Ala Ala Pro Pro Pro Leu Pro Thr Thr Ser Ser Gly Lys Ala
 500 505 510
 Ala Lys Lys Pro Thr Ala Ala Glu Val Ser Val Arg Val Pro Arg Gly
 515 520 525
 Pro Ala Val Glu Gly Gly His Val Asn Met Ala Phe Ser Gln Ser Asn
 530 535 540
 Pro Pro Ser Glu Leu His Lys Val His Gly Ser Arg Asn Lys Pro Thr
 545 550 555 560
 Ser Leu Trp Asn Pro Thr Tyr Gly Ser Trp Phe Thr Glu Lys Pro Thr
 565 570 575
 Lys Lys Asn Asn Pro Ile Ala Lys Lys Glu Pro His Asp Arg Gly Asn
 580 585 590
 Leu Gly Leu Glu Gly Ser Cys Thr Val Pro Pro Asn Val Ala Thr Gly
 595 600 605
 Arg Leu Pro Gly Ala Ser Leu Leu Leu Glu Pro Ser Ser Leu Thr Ala
 610 615 620
 Asn Met Lys Glu Val Pro Leu Phe Arg Leu Arg His Phe Pro Cys Gly
 625 630 635 640
 Asn Val Asn Tyr Gly Tyr Gln Gln Gln Gly Leu Pro Leu Glu Ala Ala
 645 650 655
 Thr Ala Pro Gly Ala Gly His Tyr Glu Asp Thr Ile Leu Lys Ser Lys
 660 665 670
 Asn Ser Met Asn Gln Pro Gly Pro
 675 680

<210> 140

<211> 2043

<212> DNA

113/299

<213> Homo sapiens

<400> 140

```
atggaagatt cgatggacat ggacatgagc cccttgaggg cccagaacta tcttttcggg 60
tgtgaactaa aggcggacaa agattatcac ttaagggtgg ataatgatga aaatgagcac 120
cagttatctt taagaacggg cagtttaggg gctggtgcaa aggatgagtt gcacattgtt 180
gaagcagagg caatgaatta cgaaggcagt ccaattaaag taacactggc aactttgaaa 240
atgtctgtac agccaacggg ttcccttggg ggctttgaaa taacaccacc agtgggtctta 300
agggttgaagt gtggttcagg gccagtgcac attagtggac agcacttagt agtggtaccg 360
cggaagcacc aggagctgca agccatgcag atggagctgc agagccctga gtacaagctg 420
agcaagctcc gcacctcgac catcatgacc gactacaacc ccaactactg ctttgctggc 480
aagacctcct ccacagtgga cctgaaggag gtgccggcga aaaacatcac cctcattcgg 540
ggctctgggc atggcgctt tggggagggt tatgaaggcc aggtgtccgg aatgccaac 600
gaccaagcc cctgcaagt ggctgtgaag acgtgcctg aagtgtgctc tgaacaggac 660
gaactggatt tcctcatgga agccctgatc atcagcaaat tcaaccacca gaacattgtt 720
cgctgcattg gggtagcct gcaatccctg ccccggttca tcctgctgga gctcatggcg 780
gggggagacc tcaagtcctt cctccgagag acccgccctc gcccgagcca gccctcctcc 840
ctggccatgc tggaccttct gcacgtggct cgggacattg cctgtggctg tcagtatttg 900
gaggaanaacc acttcatcca ccgagacatt gctgccagaa actgcctctt gacctgtcca 960
ggccctggaa gagtggccaa gattggagac ttcgggatgg cccgagacat ctacagggcg 1020
agctactata gaaaggagg ctgtgccatg ctgccagtta agtgatgcc cccagaggcc 1080
ttcatggaag gaatttcac ttctaaaaca gacacatggg ctttgaggat gctgctatgg 1140
gaaatctttt ctcttgata tatgccata cccagcaaaa gcaaccagga agttctggag 1200
tttgtaacca gtggaggccg gatggacca cccaagaact gccctgggcc tgtataccgg 1260
ataatgactc agtgctggca acatcagcct gaagacaggc ccaactttgc catcattttg 1320
gagaggattg aatactgcac ccaggaccg gatgtaatca acaccgcttt gccgatagaa 1380
tatgggtcac ttgtggaaga ggaagagaaa gtgcctgtga ggccaagga cctgagggg 1440
gttcctcctc tcctggtctc tcaacaggca aaacgggagg aggagcgcag cccagctgcc 1500
ccaccacctc tgcctaccac ctctctggc aaggctgcaa agaaaccac agctgcagag 1560
gtctctgttc gactccctag agggccggcc gtggaagggg gacacgtgaa tatggcattc 1620
tctcagtcac accctcctc ggagttgcac aaggtccacg gatccagaaa caagcccacc 1680
agcttggtga acccaacgta cggctcctgg ttacagaga aaccaccaa aaagaataat 1740
cctatagcaa agaaggagcc acacgacagg ggtaacctgg ggctggaggg aagctgtact 1800
gtccaccta acgttgcaac tgggagactt ccgggggcct cactgctcct agagccctct 1860
tcgctgactg ccaatatgaa ggaggtacct ctgttcaggc tacgtcactt cccttggtgg 1920
aatgtcaatt acggctacca gcaacagggc ttgcccttag aagccgctac tgcccctgga 1980
gctgggtcatt acgaggatac cattctgaaa agcaagaata gcatgaacca gcctggggcc 2040
tga 2043
```

<210> 141

<211> 180

<212> DNA

<213> Homo sapiens

<400> 141

```
caggaccacc ccagtagcat ggggtgtttat gggcaggagt ctggaggatt ttccggacca 60
ggagagaacc ggagcatgag tggccctgca tggaggacac ataaagggtt cctggagggt 120
gacaatcaca gttaccctct catactcaca tgcaaggacg aggaacttgt ttccctattac 180
```

<210> 142

<211> 180

<212> DNA

<213> Homo sapiens

<400> 142

```
aagggtgtat attgaggaaa tttagcaag ctgccctgaa gaaaggcata gtgacaagat 60
```


114/299

gagagagatg cattgttttg agatgtgttt agccagtgcc cttcttcccc acgatcaggt 120
 tcctggagct taggatgtgt gatgcagaag aagtctggaa aggtaagaaa cagaattgta 180

<210> 143

<211> 427

<212> DNA

<213> Homo sapiens

<400> 143

tcaatggcac tctcatccct tagcatcagg ctcaagctcc tgagaagcag caggacttaa 60
 ctactcttgc cttcacagtc agcagccact ctctcagagc tgggtgtggga atccaaagtg 120
 aataaatcag agccctcaag acaactgaatg ccaggagcat ggtctgaggg acagtgtgct 180
 ataatagaga tacatatgga ggaagcggag gaggaaggag cagattgtgt ttgagaatgg 240
 cttaagcaga gttgaagcta tttctcaggg ttatcaactt ccaccagagg aactggaatt 300
 tggtgtatct ctctctaaat attgatggtg aacatttatg tttagaaatc tcctcttagt 360
 gcctttacat tactaaacat taagagatga ttgaagggaa aatgcacttt agaccaggtg 420
 aaattag 427

<210> 144

<211> 438

<212> DNA

<213> Homo sapiens

<400> 144

gatccactca tcagagggga gtccacagtc cccacagagg gccggcatgt gtgggaggtt 60
 aggaaatgtc agcactgccc tgaaacaaat caggcgtggc ccttgccgag cacctggcac 120
 atagtaggtg ctaaataaat atttgttgaa tggatgaatt gttaggtaag tagaaataga 180
 gagataggta ggtaggtagg taggtaggta ggtagataga tagagacaga taaataaatg 240
 gggtgacaga tgtgtggatt ggatgagtg atgggtgagt tgggtggatag atggattgga 300
 ttgtatagat gaattgaatg gatggttgaa tggatggata gatggatgga tgggtggaat 360
 agatggatgg acggatggat ggatggatgg atggatggat ggatggatga tgkatggatg 420
 gacggacaga cggacgga 438

<210> 145

<211> 135

<212> DNA

<213> Homo sapiens

<400> 145

gtactagata gtgtcccact tggcccaact acgacatgca gaaaccaaca atgccaaccc 60
 ttggagctag accttgatt caggagcttg atcccctaca actgctctgg tatgtcaata 120
 tacctcttcg gatga 135

<210> 146

<211> 476

<212> PRT

<213> Homo sapiens

<400> 146

Met Ala Ser Thr Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln
 1 5 10 15
 Gly Tyr Ser Ala Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr
 20 25 30

115/299

Thr Gln Ala Tyr Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr
 35 40 45
 Asp Val Ser Tyr Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr
 50 55 60
 Ala Tyr Ala Thr Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro
 65 70 75 80
 Thr Ala Pro Gln Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly
 85 90 95
 Ala Tyr Asp Thr Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr
 100 105 110
 Ala Ala Gln Ser Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly
 115 120 125
 Gln Gln Pro Ala Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys
 130 135 140
 Pro Thr Glu Thr Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln
 145 150 155 160
 Pro Ser Leu Gly Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro
 165 170 175
 Gly Ser Tyr Pro Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro
 180 185 190
 Thr Ser Tyr Ser Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr
 195 200 205
 Ser Gln Gln Asn Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser
 210 215 220
 Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr
 225 230 235 240
 Pro Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln
 245 250 255
 Gln Ser Ser Ser Tyr Gly Gln Gln Ser Pro Pro Leu Gly Gly Ala Gln
 260 265 270
 Thr Ile Ser Lys Asn Thr Glu Gln Arg Pro Gln Pro Asp Pro Tyr Gln
 275 280 285
 Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala Asn Pro Gly Ser Gly Gln
 290 295 300
 Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Ser Asp Ser Ala Asn
 305 310 315 320
 Ala Ser Cys Ile Thr Trp Glu Gly Thr Asn Gly Glu Phe Lys Met Thr
 325 330 335

116/299

Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Gln Arg Lys Ser Lys Pro
 340 345 350
 Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala Leu Arg Tyr Tyr Tyr Asp
 355 360 365
 Lys Asn Ile Met Thr Lys Val His Gly Lys Arg Tyr Ala Tyr Lys Phe
 370 375 380
 Asp Phe His Gly Ile Ala Gln Ala Leu Gln Pro His Pro Thr Glu Ser
 385 390 395 400
 Ser Met Tyr Lys Tyr Pro Ser Asp Ile Ser Tyr Met Pro Ser Tyr His
 405 410 415
 Ala His Gln Gln Lys Val Asn Phe Val Pro Pro His Pro Ser Ser Met
 420 425 430
 Pro Val Thr Ser Ser Ser Phe Phe Gly Ala Ala Ser Gln Tyr Trp Thr
 435 440 445
 Ser Pro Thr Gly Gly Ile Tyr Pro Asn Pro Asn Val Pro Arg His Pro
 450 455 460
 Asn Thr His Val Pro Ser His Leu Gly Ser Tyr Tyr
 465 470 475

<210> 147

<211> 1431

<212> DNA

<213> Homo sapiens

<400> 147

```

atggcggtcca cggattacag tacctatagc caagctgcag cgcagcaggg ctacagtgt 60
tacaccgccc agcccactca aggatatgca cagaccaccc aggcataatgg gcaacaaagc 120
tatggaacct atggacagcc cactgatgtc agctataccc aggctcagac cactgcaacc 180
tatgggcaga ccgcctatgc aacttcttat ggacagcctc cactgggtta tactactcca 240
actgcccccc aggcatacag ccagcctgtc caggggtatg gcactgggtg ttatgatacc 300
accactgcta cagtcaccac caccagggc tcctatgcag ctcagtctgc atatggcact 360
cagcctgctt atccagccta tgggcagcag ccagcagcca ctgcacctac aagaccgcag 420
gatggaaaca agcccactga gactagtcaa cctcaatcta gcacaggggg ttacaaccag 480
cccagcctag gatattggaca gagtaactac agttatcccc aggtacctgg gagctacccc 540
atgcagccag tcaatgcacc tccatcctac cctcctacca gctattcctc tacacagccg 600
actagttatg atcagagcag ttactctcag cagaacacct atgggcaacc gagcagctat 660
ggacagcaga gtagctatgg tcaacaaagc agctatgggc agcagcctcc cactagttac 720
ccaccccaaa ctggatccta cagccaagct ccaagtcaat atagccaaca gagcagcagc 780
tacgggcagc agagtccctc ccttggaggg gcacaaacga tcagtaagaa tacagagcaa 840
cggccccagc cagatccgta tcagatcctg ggcccagcca gcagtcgcct agccaaccct 900
ggaagcgggc agatccagct gtggcaattc ctccctggagc tgctctccga cagcgccaac 960
gccagctgta tcacctggga ggggaccaac ggggagttca aaatgacgga ccccgatgag 1020
gtggccaggc gctgggggca gcggaaaagc aagcccaaca tgaattacga caagctgagc 1080
cgggcccctc gttattacta tgataaaaac attatgaoca aagtgcacgg caaaagatat 1140
gcttacaaat ttgacttcca cggcattgcc caggctctgc agccacatcc gaccgagtcg 1200
tccatgtaca agtacccttc tgacatctcc tacatgcctt cctaccatgc ccaccagcag 1260
aaggtgaact ttgtccctcc ccatccatcc tccatgcctg tcacttcctc cagcttcttt 1320
ggagccgcac caaatactg gacctcccc acggggggaa tctaccccaa ccccaacgctc 1380
ccccgccatc ctaacaccca cgtgccttca cacttaggca gctactacta g 1431

```

117/299

<210> 148

<211> 154

<212> PRT

<213> Homo sapiens

<400> 148

Met Asp Leu Pro Tyr Tyr His Gly Arg Leu Thr Lys Gln Asp Cys Glu
 1 5 10 15

Thr Leu Leu Leu Lys Glu Gly Val Asp Gly Asn Phe Leu Leu Arg Asp
 20 25 30

Ser Glu Ser Ile Pro Gly Val Leu Cys Leu Cys Val Ser Phe Lys Asn
 35 40 45

Ile Val Tyr Thr Tyr Arg Ile Phe Arg Glu Lys His Gly Tyr Tyr Arg
 50 55 60

Ile Gln Pro Ile Lys Arg Thr Ser Pro Ser Leu Arg Trp Arg Gly Ser
 65 70 75 80

Lys Leu Glu Leu Glu Ala Phe Met Thr Ala Glu Gly Ser Pro Lys Gln
 85 90 95

Val Phe Pro Ser Leu Lys Glu Leu Ile Ser Lys Phe Glu Lys Pro Asn
 100 105 110

Gln Gly Met Val Val His Leu Leu Lys Pro Ile Lys Arg Thr Ser Pro
 115 120 125

Ser Leu Arg Trp Arg Gly Leu Lys Leu Glu Leu Glu Thr Phe Val Asn
 130 135 140

Ser Asn Ser Asp Tyr Val Asp Val Leu Pro
 145 150

<210> 149

<211> 465

<212> DNA

<213> Homo sapiens

<400> 149

atggatctgc cttactacca tggacgtctg accaagcaag actgtgagac cttgctgctc 60
 aaggaagggg tggatggcaa ctttctttta agagacagcg agtcgatacc aggagtcctg 120
 tgcctctgtg tctcgtttta aaatattgtc tacacatacc gaatcttcag agagaaacac 180
 gggattaca ggatacagcc aataaagaga accagcccca gcttgagatg gagaggatcg 240
 aaattagagt tggaagcatt tatgactgca gaaggttctc caaaacaggt ctttccaagc 300
 ctaaaggaac tgatctccaa atttgaaaaa ccaaatacagg ggatgggtggg tcacctttta 360
 aagccaataa agagaaccag cccagcttg agatggagag gattgaaatt agagttggaa 420
 acatttgtga acagtaacag cgattatgtg gatgtcttgc cttga 465

<210> 150

<211> 132

<212> PRT

118/299

<213> Homo sapiens

<400> 150

```

Met Asp Leu Pro Tyr Tyr His Gly Arg Leu Thr Lys Gln Asp Cys Glu
 1             5             10             15

Thr Leu Leu Leu Lys Glu Gly Val Asp Gly Asn Phe Leu Leu Arg Asp
      20             25             30

Ser Glu Ser Ile Pro Gly Val Leu Cys Leu Cys Val Ser Phe Lys Asn
      35             40             45

Ile Val Tyr Thr Tyr Arg Ile Phe Arg Glu Lys His Gly Tyr Tyr Arg
      50             55             60

Ile Gln Thr Ala Glu Gly Ser Pro Lys Gln Val Phe Pro Ser Leu Lys
      65             70             75             80

Glu Leu Ile Ser Lys Phe Glu Lys Pro Asn Gln Gly Met Val Val His
      85             90             95

Leu Leu Lys Pro Ile Lys Arg Thr Ser Pro Ser Leu Arg Trp Arg Gly
      100            105            110

Leu Lys Leu Glu Leu Glu Thr Phe Val Asn Ser Asn Ser Asp Tyr Val
      115            120            125

Asp Val Leu Pro
      130

```

<210> 151

<211> 420

<212> DNA

<213> Homo sapiens

<400> 151

```

atggatctgc cttactacca tggacgtctg accaagcaag actgtgagac cttgctgctc 60
aaggaagggg tggatggcaa ctttctttta agagacagcg agtcgatacc aggagtcctg 120
tgcctctgtg tctcgtttta aaatattgtc tacacatacc gaatcttcag agagaaacac 180
gggtattaca ggatacagac tgcagaagg tctccaaaac aggtctttcc aagcctaaag 240
gaactgatct ccaaatttga aaaaccaa atcaggggatgg tggttcacct tttaaagcca 300
ataaagagaa ccagccccag cttgagatgg agaggattga aattagagtt ggaaacattt 360
gtgaacagta acagcgatta tgtggatgtc ttgccttgaa gataaggctg ccggacaaa 420

```

<210> 152

<211> 45

<212> PRT

<213> Homo sapiens

<400> 152

```

Met Asp Leu Pro Tyr Tyr His Gly Arg Leu Thr Lys Gln Asp Cys Glu
 1             5             10             15

Thr Leu Leu Leu Lys Glu Gly Val Asp Gly Asn Phe Leu Leu Arg Asp
      20             25             30

```

119/299

Ser Glu Ser Ile Pro Gly Val Leu Cys Leu Cys Val Ser
 35 40 45

<210> 153
 <211> 136
 <212> DNA
 <213> Homo sapiens

<400> 153
 atggatctgc cttactacca tggacgtctg accaagcaag actgtgagac cttgctgctc 60
 aaggaagggg tggatggcaa ctttctttta agagacagcg agtcgatacc aggagtcctg 120
 tgcctctgtg tctcgt 136

<210> 154
 <211> 132
 <212> PRT
 <213> Mus musculus

<400> 154
 Met Asp Leu Pro Tyr Tyr His Gly Cys Leu Thr Lys Arg Glu Cys Glu
 1 5 10 15
 Ala Leu Leu Leu Lys Gly Gly Val Asp Gly Asn Phe Leu Ile Arg Asp
 20 25 30
 Ser Glu Ser Val Pro Gly Ala Leu Cys Leu Cys Val Ser Phe Lys Lys
 35 40 45
 Leu Val Tyr Ser Tyr Arg Ile Phe Arg Glu Lys His Gly Tyr Tyr Arg
 50 55 60
 Ile Glu Thr Asp Ala His Thr Pro Arg Thr Ile Phe Pro Asn Leu Gln
 65 70 75 80
 Glu Leu Val Ser Lys Tyr Gly Lys Pro Gly Gln Gly Leu Val Val His
 85 90 95
 Leu Ser Asn Pro Ile Met Arg Asn Asn Leu Cys Gln Arg Gly Arg Arg
 100 105 110
 Met Glu Leu Glu Leu Asn Val Tyr Glu Asn Thr Asp Glu Glu Tyr Val
 115 120 125
 Asp Val Leu Pro
 130

<210> 155
 <211> 399
 <212> DNA
 <213> Mus musculus

<400> 155
 atggatctgc cttactacca tggctgcctg accaagcgag agtgtgaagc cctgctcctc 60
 aagggagggtg tggatggcaa ctttctgata agagacagcg agtctgtgcc aggagccctg 120
 tgcctctgtg tctcgtttta aaagcttgctc tacagctacc gaatcttcag agagaaacat 180

120/299

ggatattaca ggatagagac tgatgctcat actccaagaa cgatctttcc aaacctacag 240
gaattgggtct ccaaatatgg aaaaccgggt caaggattgg tggttcacct ttcaaacca 300
ataatgagaa acaacctatg ccaaagaggg agaagaatgg agttagagct gaatgtttat 360
gagaacactg atgaggagta tgtggacgtc ttgcottga 399

<210> 156
<211> 76
<212> PRT
<213> Homo sapiens

<400> 156
Pro Thr Ser Tyr Pro Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser
1 5 10 15
Gln Tyr Ser Gln Gln Ser Ser Ser Tyr Gly Gln Gln Asn Pro Tyr Gln
20 25 30
Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala Asn Pro Gly Ser Gly Gln
35 40 45
Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Ser Asp Ser Ala Asn
50 55 60
Ala Ser Cys Ile Thr Trp Glu Gly Thr Asn Gly Glu
65 70 75

<210> 157
<211> 229
<212> DNA
<213> Homo sapiens

<400> 157
cccactagtt acccacccca aactggatcc tacagccaag ctccaagtca atatagccaa 60
cagagcagca gctacgggca gcagaatccg tatcagatcc tgggcccgac cagcagtcgc 120
ctagccaacc ctggaagcgg gcagatccag ctgtggcaat tcctcctgga gctgctctcc 180
gacagcgcca acgccagctg tatcacctgg gaggggacca acggggagt 229

<210> 158
<211> 100
<212> DNA
<213> Homo sapiens

<400> 158
tacgggcagc agagttcact gctggcctat aatacaacct cccacaccga ccaatcctca 60
cgattgagtg tcaaagaaga cccttcttat gactcagtca 100

<210> 159
<211> 20
<212> PRT
<213> Homo sapiens

<400> 159
Ser Gln Gln Ser Ser Ser Tyr Gly Gln Gln Ser Pro Pro Leu Gly Gly
1 5 10 15

121/299

Ala Gln Thr Ile
20

<210> 160
<211> 60
<212> DNA
<213> Homo sapiens

<400> 160
agccaacaga gcagcagcta cgggcagcag agtcctcccc ttggaggggc acaaacgata 60

<210> 161
<211> 447
<212> DNA
<213> Homo sapiens

<400> 161
agatagagct ggagacctac aaactgaagt gcaaggcact gcaggaggag aaccgcgacc 60
tgcgcaaagc cagcggtacc atcatactgg agaacaggcc atctgttctg tttctacctg 120
tcccctggag gctgccaga aaccggccct cgctggactc catggagaac caggtctccg 180
tggatgcctt caagatcctg gaggatccaa agtgggaatt ccctcggaag aacttggttc 240
ttggaaaaac tctaggagaa ggcgaatttg gaaaagtggg caaggcaacg gccttccatc 300
tgaaaggcag agcagggtac accacgggtg ccgtgaagat gctgaaagag aacgcctccc 360
cgagtgcgct tcgagacctg ctgtcagagt tcaacgtcct gaagcaggtc aaccacccac 420
atgtcatcaa attgtatggg gcctgca 447

<210> 162
<211> 585
<212> PRT
<213> Homo sapiens

<400> 162
Met Ala Asp Ser Ala Ser Glu Ser Asp Thr Asp Gly Ala Gly Gly Asn
1 5 10 15
Ser Ser Ser Ser Ala Ala Met Gln Ser Ser Cys Ser Ser Thr Ser Gly
20 25 30
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Lys Ser Gly Gly
35 40 45
Ile Val Ile Ser Pro Phe Arg Leu Glu Glu Leu Thr Asn Arg Leu Ala
50 55 60
Ser Leu Gln Gln Glu Asn Lys Val Leu Lys Ile Glu Leu Glu Thr Tyr
65 70 75 80
Lys Leu Lys Cys Lys Ala Leu Gln Glu Glu Asn Arg Asp Leu Arg Lys
85 90 95
Ala Ser Val Thr Ile Gln Ala Arg Ala Glu Gln Glu Glu Glu Phe Ile
100 105 110
Ser Asn Thr Leu Phe Lys Lys Ile Gln Ala Leu Gln Lys Glu Lys Glu

122/299

115					120					125					
Thr	Leu	Ala	Val	Asn	Tyr	Glu	Lys	Glu	Glu	Glu	Phe	Leu	Thr	Asn	Glu
130						135					140				
Leu	Ser	Arg	Lys	Leu	Met	Gln	Leu	Gln	His	Glu	Lys	Gly	Glu	Leu	Glu
145				150						155					160
Gln	His	Leu	Glu	Gln	Glu	Gln	Glu	Phe	Gln	Val	Asn	Lys	Leu	Met	Lys
			165					170						175	
Lys	Ile	Lys	Lys	Leu	Glu	Asn	Asp	Thr	Ile	Ser	Lys	Gln	Leu	Thr	Leu
			180					185						190	
Glu	Gln	Leu	Arg	Arg	Glu	Lys	Ile	Asp	Leu	Glu	Asn	Thr	Leu	Glu	Gln
		195					200					205			
Glu	Gln	Glu	Ala	Leu	Val	Asn	Arg	Leu	Trp	Lys	Arg	Met	Asp	Lys	Leu
		210				215					220				
Glu	Ala	Glu	Thr	Arg	Ile	Leu	Gln	Glu	Lys	Leu	Asp	Gln	Pro	Val	Ser
225					230					235					240
Ala	Pro	Pro	Ser	Pro	Arg	Asp	Ile	Ser	Met	Glu	Ile	Asp	Ser	Pro	Glu
				245					250					255	
Asn	Met	Met	Arg	His	Ile	Arg	Phe	Leu	Lys	Asn	Glu	Val	Glu	Arg	Leu
			260					265					270		
Lys	Lys	Gln	Leu	Arg	Ala	Ala	Gln	Leu	Gln	His	Ser	Glu	Lys	Met	Ala
		275					280					285			
Gln	Tyr	Leu	Glu	Glu	Glu	Arg	His	Met	Arg	Glu	Glu	Asn	Leu	Arg	Leu
	290					295						300			
Gln	Arg	Lys	Leu	Gln	Arg	Glu	Met	Glu	Arg	Arg	Glu	Ala	Leu	Cys	Arg
305					310					315					320
Gln	Leu	Ser	Glu	Ser	Glu	Ser	Ser	Leu	Glu	Met	Asp	Asp	Glu	Arg	Tyr
			325						330					335	
Phe	Asn	Glu	Met	Ser	Ala	Gln	Gly	Leu	Arg	Pro	Arg	Thr	Val	Ser	Ser
			340					345					350		
Pro	Ile	Pro	Tyr	Thr	Pro	Ser	Pro	Ser	Ser	Ser	Arg	Pro	Ile	Ser	Pro
		355					360					365			
Gly	Leu	Ser	Tyr	Ala	Ser	His	Thr	Val	Gly	Phe	Thr	Pro	Pro	Thr	Ser
	370					375					380				
Leu	Thr	Arg	Ala	Gly	Met	Ser	Tyr	Tyr	Asn	Ser	Pro	Gly	Leu	His	Val
385					390					395					400
Gln	His	Met	Gly	Thr	Ser	His	Gly	Ile	Thr	Arg	Pro	Ser	Pro	Arg	Arg
			405					410						415	
Ser	Asn	Ser	Pro	Asp	Lys	Phe	Lys	Arg	Pro	Thr	Pro	Pro	Pro	Ser	Pro
			420					425						430	

123/299

Asn Thr Gln Thr Pro Val Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro
 435 440 445

Met Gln Pro Thr Val Pro Ser Gly Ser His Leu Ala Ala Tyr Ser Phe
 450 455 460

Ala Thr Phe Gly Ala His Leu Leu Pro Ala Leu Met His Glu Leu Ser
 465 470 475 480

Leu Asn Phe Lys Leu Gly Leu Ile Gln Trp Ser Arg Leu Leu Asn Ala
 485 490 495

Lys Gly Ser Phe Ser Gly Ile Phe Gly Tyr Asp Leu Phe Ala Leu Arg
 500 505 510

Leu Ser Arg Leu His Tyr Pro Leu Cys Cys Lys Cys Leu Ser Glu Met
 515 520 525

Gln Pro Val Leu Trp Val Tyr Asn Thr Asn Gln Thr Thr Phe Ser Ile
 530 535 540

Ser Val Leu Leu Glu Ser Ser Cys Thr Ser Ile Pro Trp Leu Glu Pro
 545 550 555 560

Ser Leu Phe Gly Ile Trp Tyr Phe Ser Ser Ser Val Gln Phe Leu Leu
 565 570 575

Gly Pro Glu Leu His Ser Pro Gly Phe
 580 585

<210> 163

<211> 3011

<212> DNA

<213> Homo sapiens

<400> 163

ctgctgctcc tcttcctttc ccagcccgcc gcggccatgg cggacagcgc cagcgagagc 60
 gacacggacg gggcgggggg caacagcagc agctcggccg ccatgcagtc gtctgctcg 120
 tcgacctcg ggcggcgcg tggcgggcg ggaggcgcg gcggtgggaa gtcggggggc 180
 attgtcatct cgccgttccg cctggaggag ctccaccaacc gcctggcctc gctgcagcaa 240
 gagaacaagg tgctgaagat agagctggag acctacaaac tgaagtgc aa ggcactgcag 300
 gaggagaacc gcgacctgcg caaagccagc gttaccatcc aagccagggc tgagcaggaa 360
 gaagaattca ttagtaacac tttattcaag aaaattcagg ctttgcagaa ggagaaagaa 420
 acccttgctg taaattatga gaaagaagaa gaattcctca ctaatgagct ctccagaaaa 480
 ttgatgcagt tgcagcatga gaaaggcgaa ctagaacagc atcttgaaca agagcaggaa 540
 tttcaggtca acaaaactgat gaagaaaatt aaaaaactgg agaattgacac catttctaag 600
 caacttacat tagaacagtt gagacgggag aagattgacc ttgaaaatac attggaacaa 660
 gaacaagaag cactagttaa tcgcctctgg aaaaggatgg ataagcttga agctgaaacg 720
 cgaatcctgc aggaaaaatt agaccagccc gtctctgctc caccatcgcc tagagatatc 780
 tccatggaga ttgattctcc agaaaatatg atgcgtcaca tcagggtttt aaagaatgaa 840
 gtggaacggc tgaagaagca actgagagct gtcaggttac agcattcaga gaaaatggca 900
 cagtatctgg aggaggaacg tcacatgaga gaagagaact tgaggctcca gaggaagctg 960
 cagaggggaga tggagagacg agaagccctc tgctcgacagc tctccgagag tgagtccagc 1020
 ttagaaatgg acgacgaaaag gtattttaat gagatgtctg cacaaggatt aagacctcga 1080
 actgtgtcca gcccgatccc ttacacacct tctccgagtt caagcaggcc tatatcacct 1140
 ggtctatcat atgcaagtca cacggttggt ttacagccac caacttcact gactagagct 1200

124/299

```

ggaatgtctt attacaattc cccgggtctt cactgtcagc acatgggaac atcccatggt 1260
atcacaaaggc cttcaccacg gagaagcaac agtcctgaca aattcaaacg gccacgccc 1320
cctccatctc ccaacacaca gacccagtc cagccacctc cactccacc tccgccaccc 1380
atgcagccca cgggtccctc aggcagccac ctgcagcct actccttcgc aacattcggc 1440
gcacacctcc tcccagcctt aatgcatgag cttagtctga atttcaagtt gggactcatc 1500
caatggagcc gtctactcaa cgccaaaggc tccttctctg gcataatttg atatgactta 1560
tttgactga ggttatctag gcttactat ccattgtgtt gtaaattgtt gtcagaaatg 1620
cagccagtgt tgtgggtcta caacactaac cagacgactt tttocatcag tgttttactt 1680
gaatcttcat gtacgtccat tccctggctg gaaccttcgc tgtttgggtat ttggtatttc 1740
agcagcagtg tgcaattttt gcttggccca gagcttcatt ctccctggctt ttaggtttgt 1800
aaaagaaaaa gggatatctt tttatatatt ttttccatga atctgcagaa aataactaag 1860
ctgttgtaac cctoctataa ttataatagt gtttacaac aataccaata attcagcact 1920
acaattcaga cctttgaaaa tctggctttc agtgtagaac agaaagttag atgaatcagt 1980
gccccagaca tatttctgtt ttaacagaa tttctacaga tacatttttt acaggttatt 2040
ttcatttgtt tattgacatc catgtctctc gtaaacagag gtcccaaagt aatgaatcat 2100
gtggcgtagc ttctccacat aaatggatgg ataattacgt atattaagat gtgattctct 2160
tttttatcct taatgttaat ctacttaacc tggcccccct taacatgagt cgataaatgt 2220
tgtcctactc accggtgggt tcaatggcta attagaatgt gttatttgat ttctgctgca 2280
gaaggcagtg tgattgtaac aaaaacaatg cggcttcccc ctttctgact tcatttgtgt 2340
tctcttaaaa tagagtttga acaaatattt taaagggtgca aaataccatt agaaaatact 2400
atttgaaatg gacattatcg cattatcttg gcataatggc cagaaaatat tgtattgctt 2460
ggcagaaaaa aaaataaggt ctaaaggaaa gtagcacatt agcattgatg gctgttcatt 2520
tcaccagta taagcaagtg tacaaagaag tatattctga atacattatt tccattcatt 2580
tagcacaaat aaatcatttg gtttacttt gcagtggaa actgagtcac tcttttctta 2640
atacgtgcaa catcttaatt tttgtttttc agcagttgct gttttgtact ttggtagtga 2700
agtgattttt accacctgtg tttgcatatt tatatatgct gtggatgaaa ataacttact 2760
agagaatgta tattttatga caagaatgtg tatctgttgg gatataatca gagaactgaa 2820
aagtaattta tcagtaattt ttaagagtcc atgttttgtg acaaccatct ctaatagcca 2880
actctttatt aaacacactc ctaaaaataa ggaaccatga cgattgtaga tatttaatat 2940
tgtacagtat agaaacctcc gatttttgcc ttogaatgca gtatttaaga gttaacagaa 3000
aaaaaaaaa a 3011

```

<210> 164
 <211> 447
 <212> DNA
 <213> Homo sapiens

```

<400> 164
gatcaggggg ctcggaggcc ctcccttgga acacgtgtgg ctggcgagct ggtgggtgcg 60
gggcagtcct tggctttccc gcacccgcag tgccctgcgc ttcccagccc gcccggtggtc 120
accagacggc ggcgggcggg tcccggagct ttcagccagc tttgctgggc ggcctaggga 180
gcgcgcccag cccggctgga gcgagcccca gtgcaatact gcccaagccc gggcggggtc 240
tctgttctct ggagaggag gtcccttggc agcgggaggc gccctctctt tctctcgccg 300
ccgctccgag tctgcgccct ggtgccaggc gctcagctcg gcgctcccc tctctcgccc 360
ggcgccact cattcgagc ccggccttcg tcgcgcgcgc ctccctgctg ctccctctcc 420
tttccccagc ccgcgcggc catggcg 447

```

<210> 165
 <211> 585
 <212> PRT
 <213> Homo sapiens

```

<400> 165
Met Ala Asp Ser Ala Ser Glu Ser Asp Thr Asp Gly Ala Gly Gly Asn
1           5           10           15

```

125/299

Ser Ser Ser Ser Ala Ala Met Gln Ser Ser Cys Ser Ser Thr Ser Gly
 20 25 30
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Lys Ser Gly Gly
 35 40 45
 Ile Val Ile Ser Pro Phe Arg Leu Glu Glu Leu Thr Asn Arg Leu Ala
 50 55 60
 Ser Leu Gln Gln Glu Asn Lys Val Leu Lys Ile Glu Leu Glu Thr Tyr
 65 70 75 80
 Lys Leu Lys Cys Lys Ala Leu Gln Glu Glu Asn Arg Asp Leu Arg Lys
 85 90 95
 Ala Ser Val Thr Ile Gln Ala Arg Ala Glu Gln Glu Glu Glu Phe Ile
 100 105 110
 Ser Asn Thr Leu Phe Lys Lys Ile Gln Ala Leu Gln Lys Glu Lys Glu
 115 120 125
 Thr Leu Ala Val Asn Tyr Glu Lys Glu Glu Glu Phe Leu Thr Asn Glu
 130 135 140
 Leu Ser Arg Lys Leu Met Gln Leu Gln His Glu Lys Gly Glu Leu Glu
 145 150 155 160
 Gln His Leu Glu Gln Glu Gln Glu Phe Gln Val Asn Lys Leu Met Lys
 165 170 175
 Lys Ile Lys Lys Leu Glu Asn Asp Thr Ile Ser Lys Gln Leu Thr Leu
 180 185 190
 Glu Gln Leu Arg Arg Glu Lys Ile Asp Leu Glu Asn Thr Leu Glu Gln
 195 200 205
 Glu Gln Glu Ala Leu Val Asn Arg Leu Trp Lys Arg Met Asp Lys Leu
 210 215 220
 Glu Ala Glu Thr Arg Ile Leu Gln Glu Lys Leu Asp Gln Pro Val Ser
 225 230 235 240
 Ala Pro Pro Ser Pro Arg Asp Ile Ser Met Glu Ile Asp Ser Pro Glu
 245 250 255
 Asn Met Met Arg His Ile Arg Phe Leu Lys Asn Glu Val Glu Arg Leu
 260 265 270
 Lys Lys Gln Leu Arg Ala Ala Gln Leu Gln His Ser Glu Lys Met Ala
 275 280 285
 Gln Tyr Leu Glu Glu Glu Arg His Met Arg Glu Glu Asn Leu Arg Leu
 290 295 300
 Gln Arg Lys Leu Gln Arg Glu Met Glu Arg Arg Glu Ala Leu Cys Arg
 305 310 315 320
 Gln Leu Ser Glu Ser Glu Ser Ser Leu Glu Met Asp Asp Glu Arg Tyr

126/299

325	330	335
Phe Asn Glu Met Ser Ala Gln Gly Leu Arg Pro Arg Thr Val Ser Ser		
340	345	350
Pro Ile Pro Tyr Thr Pro Ser Pro Ser Ser Ser Arg Pro Ile Ser Pro		
355	360	365
Gly Leu Ser Tyr Ala Ser His Thr Val Gly Phe Thr Pro Pro Thr Ser		
370	375	380
Leu Thr Arg Ala Gly Met Ser Tyr Tyr Asn Ser Pro Gly Leu His Val		
385	390	395
Gln His Met Gly Thr Ser His Gly Ile Thr Arg Pro Ser Pro Arg Arg		
405	410	415
Ser Asn Ser Pro Asp Lys Phe Lys Arg Pro Thr Pro Pro Pro Ser Pro		
420	425	430
Asn Thr Gln Thr Pro Val Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro		
435	440	445
Met Gln Pro Thr Val Pro Ser Gly Ser His Leu Ala Ala Tyr Ser Phe		
450	455	460
Ala Thr Phe Gly Ala His Leu Leu Pro Ala Leu Met His Glu Leu Ser		
465	470	475
Leu Asn Phe Lys Leu Gly Leu Ile Gln Trp Ser Arg Leu Leu Asn Ala		
485	490	495
Lys Gly Ser Phe Ser Gly Ile Phe Gly Tyr Asp Leu Phe Ala Leu Arg		
500	505	510
Leu Ser Arg Leu His Tyr Pro Leu Cys Cys Lys Cys Leu Ser Glu Met		
515	520	525
Gln Pro Val Leu Trp Val Tyr Asn Thr Asn Gln Thr Thr Phe Ser Ile		
530	535	540
Ser Val Leu Leu Glu Ser Ser Cys Thr Ser Ile Pro Trp Leu Glu Pro		
545	550	555
Ser Leu Phe Gly Ile Trp Tyr Phe Ser Ser Ser Val Gln Phe Leu Leu		
565	570	575
Gly Pro Glu Leu His Ser Pro Gly Phe		
580	585	

<210> 166

<211> 3011

<212> DNA

<213> Homo sapiens

<400> 166

ctgctgctcc tcctcctttc ccagcccgcc gcggccatgg cggacagcgc cagcgagagc 60

127/299

```

gacacggacg gggcgggggg caacagcagc agctcgggcg ccatgcagtc gtcctgctcg 120
tcgacctcgg gcggcgggcg tggcgggcgg ggaggcgggc gcggtgggaa gtcggggggc 180
attgtcatct cgccgttccg cctggaggag ctcaccaacc gcctggcctc gctgcagcaa 240
gagaaacaag tgctgaagat agagctggag acctacaaac tgaagtgcag ggcactgcag 300
gaggagaacc gcgacctgcg caaagccagc gttaccatcc aagccagggc tgagcaggaa 360
gaagaattca ttagtaacac tttattcaag aaaattcagg ctttgcagaa ggagaaagaa 420
acccttgctg taaattatga gaaagaagaa gaattcctca ctaatgagct ctccagaaaa 480
ttgatgcagt tgcagcatga gaaagggcga ctagaacagc atcttgaaca agagcaggaa 540
tttcagggtca acaaaactgat gaagaaaatt aaaaaactgg agaatgacac catttctaag 600
caacttacat tagaacagtt gagacgggag aagattgacc ttgaaaatac attggaacaa 660
gaacaagaag cactagttaa tcgcctctgg aaaaggatgg ataagcttga agctgaaacg 720
cgaatcctgc agggaaaaatt agaccagccc gtctctgctc caccatcgcc tagagatc 780
tccatggaga ttgattctcc agaaaatatg atgcgtcaca tcagggtttt aaagaatgaa 840
gtggaacggc tgaagaagca actgagagct gctcagttac agcattcaga gaaaatggca 900
cagtatctgg aggaggaacg tcacatgaga gaagagaact tgaggctcca gaggaagctg 960
cagagggaga tggagagacg agaagccctc tgtcgacagc tctccgagag tgagtccagc 1020
ttagaaatgg acgacgaaag gtattttaat gagatgtctg cacaaggatt aagacctcga 1080
actgtgtcca gcccgatccc ttacacacct tctccgagtt caagcaggcc tatatcacct 1140
ggtctatcat atgcaagtca cacggttggg ttcacgccac caacttcaact gactagagct 1200
ggaatgtctt attacaattc cccgggtctt cacgtgcagc acatgggaac atcccattgg 1260
atcacaaggg cttcaccacg gagaagcaac agtcttgaca aattcaaacg gccacgccc 1320
cctccatctc ccaacacaca gacccagtc cagccacctc cacctccacc tccgccacc 1380
atgcagccca cggtcacctc aggcagccac ctgcagcct actccttcgc aacattcgcc 1440
gcacacctcc tccagcctt aatgcatgag cttagtctga atttcaagtt gggactcatc 1500
caatggagcc gtctactcaa cgccaaaggt tcttctctg gcataatttg atatgactta 1560
tttgcactga ggttatctag gcttactat ccattgtgtt gtaaattggt gtcagaaatg 1620
cagccagtg tgtgggtcta caacactaac cagacgactt tttccatcag tgttttactt 1680
gaatcttcat gtacgtccat tcctggctg gaaccttcgc tgtttggtat ttggtatttc 1740
agcagcagtg tgcaattttt gcttggccca gagcttcatt ctctgggtt ttaggtttgt 1800
aaaagaaaaa gggatatctt ttttatattt ttttccatga atctgcagaa aataactaag 1860
ctgttgtaac cctoctataa ttataatagt gtttacaac aataccaata attcagact 1920
acaattcaga ctttgaaaaa tctggctttc agtgtagaac agaaagttag atgaatcagt 1980
gcccaagaca tatttctctg ttaacagaac tttctacaga tacatttttt acaggttatt 2040
ttcatttgtt tattgacatc catgtctctc gtaaacagag gtcccaaagt aatgaatcat 2100
gtggcgatcc ttctccacat aaatggatgg ataattacgt atattaagat gtgattctct 2160
tttttatcct taatgttaat ctacttaacc tggccccctc taacatgagt cgataaatgt 2220
tgtcctactc accggtgggt tcaatggcta attagaatgt gttatttgat ttctgctgca 2280
gaaggcagtg tgattgtaac aaaaacaatg cggttcccc ctttcgtact tcatttgtgt 2340
tctcttaaaa tagagtttga acaaatattt taaaggtgca aaataccatt agaaaatact 2400
atttgaaatg gacattatcg cattatcttg gcataatggc cagaaaatat tgtattgctt 2460
ggcagaaaag aaaataaggt ctaaaaggaaa gtagcacatt agcattgatg gctgttcatt 2520
tcacccagta taagcaagtg tacaagaag tatattctga atacattatt tccattcatt 2580
tagcacaat aaatcatttg gtttcacttt gcagtggaa actgagtcac tcttttctta 2640
atacgtgcaa catcttaatt tttgtttttc agcagttgct gttttgtact ttggtagtga 2700
agtgattttt accacctgtg tttgcatatt tatatatgct gtggatgaaa ataacttact 2760
agagaatgta tattttatga caagaatgtg tatctgttgg gatataatca gagaactgaa 2820
aagtaattta tcagtaattt ttaagagtcc atgttttgtg acaaccatct ctaatagcca 2880
actctttatt aaacacactc ctaaaaaataa ggaaccatga cgattgtaga tatttaatat 2940
tgtacagtat agaaacctcc gatttttgcc ttcgaatgca gtatttaaga gttacagaa 3000
aaaaaaaaa a 3011

```

<210> 167

<211> 808

<212> DNA

<213> Homo sapiens

<400> 167

128/299

```

agatcttcac tgaccatggt tgattttgca gcatttggga ttttgacagc tntagccatg 60
gcagtgtcga cactgacctt gactgtgggt tcccaggga tgtggggcca gaccaggaca 120
gcccaggagc aggagacctg gggtagcgga tgcccagagc tggcacatca agggagggtt 180
cctggatcat ggcaggcttt ggctccctgg tcagagttca agtactgggg gccagggttg 240
gggtctcgga aggcattccc agcagtccca agtgggcccc aatgtgtgga tagaactttg 300
gtggagggca gggtagtagt gccagcagca gggtagagcg gtgcgtgagg gccagtgcag 360
cccttgagga gcagtgattc cacactctga ggcggaacat ggtgggcgct ttctttgcag 420
gggtggctat gtagagaagt tgtcctggac acttcactg tagtcggagg tcctgggctg 480
ggcctgggtc tcatttagtc ctggggcagg ggtcagggga gacagtagac caggaaccag 540
agagggtcga agtactgagt ccaagccatg ctgtgaccac acctgtcatg tagcagcttt 600
caggggcctg gctgtggggg cccgcccagg gcagagacag gcaggttcgg ctggctcaga 660
tgacagccgg ttctctgcac attggaactt gtccatgggg cctcctttaa gggctcttgc 720
ttcttcctcc cctgtcatcc tcacactttt cccccccttt ccccccttc ctcatttcc 780
aacataggag gatccaaagt ggaatttc 808

```

<210> 168

<211> 271

<212> PRT

<213> Homo sapiens

<400> 168

```

Met Glu Asp Ser His Lys Ser Thr Thr Ser Glu Thr Ala Pro Gln Pro
  1                      5                      10                      15

Gly Ser Ala Val Gln Gly Ala His Ile Ser His Ile Ala Gln Gln Val
          20                      25                      30

Ser Ser Leu Ser Glu Ser Glu Glu Ser Gln Asp Ser Ser Asp Ser Ile
      35                      40                      45

Gly Ser Ser Gln Lys Ala His Gly Ile Leu Ala Arg Arg Pro Ser Tyr
      50                      55                      60

Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu Asp Thr Arg Gly Arg Lys
      65                      70                      75                      80

Gly Asp Gly Glu Asn Ser Gly Val Ser Ala Ala Val Thr Ser Met Ser
          85                      90                      95

Val Pro Thr Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile
      100                      105                      110

Ala Pro Asn Gly Ala Leu Gln Leu Ala Ser Pro Gly Thr Asp Gly Val
      115                      120                      125

Gln Gly Leu Gln Thr Leu Thr Met Thr Asn Ser Gly Ser Thr Gln Gln
      130                      135                      140

Gly Thr Thr Ile Leu Gln Tyr Ala Gln Thr Ser Asp Gly Gln Gln Ile
      145                      150                      155                      160

Leu Val Pro Ser Asn Gln Val Val Val Gln Thr Ala Ser Gly Asp Met
          165                      170                      175

Gln Thr Tyr Gln Ile Arg Thr Thr Pro Ser Ala Thr Ser Leu Pro Gln
      180                      185                      190

```

129/299

Thr Val Val Met Thr Ser Pro Val Thr Leu Thr Ser Gln Thr Thr Lys
 195 200 205

Thr Asp Asp Pro Gln Leu Lys Arg Glu Ile Arg Leu Met Lys Asn Arg
 210 215 220

Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys
 225 230 235 240

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile
 245 250 255

Glu Glu Leu Lys Thr Leu Lys Asp Leu Tyr Ser Asn Lys Ser Val
 260 265 270

<210> 169
 <211> 816
 <212> DNA
 <213> Homo sapiens

<400> 169
 atggaagatt cccacaagag taccacgtca gagacagcac ctcaacctgg ttcagcagtt 60
 caggagagctc acattttctca tattgctcaa cagggtatcat ctttatcaga aagtgaggag 120
 tcccaggact catccgacag cataggctcc tcacagaaag cccacgggat cctagcacgg 180
 cgcccatctt acagaaaaat tttgaaagac ttatottctg aagatacacg gggcagaaaa 240
 ggagacggag aaaattcttg agtttctgct gctgtcactt ctatgtctgt tccaactccc 300
 atctatcaga ctacgacgg acagtacatt gccattgccc caaatggagc cttacagttg 360
 gcaagtccag gcacagatgg agtacaggga cttcagacat taaccatgac aaattcaggc 420
 agtactcagc aaggtacaac tattcttcag tatgcacaga cctctgatgg acagcagata 480
 cttgtgccc gcaatcaggt ggtcgtacaa actgcatcag gagatatgca aacatatcag 540
 atccgaacta cacccttcagc tacttctctg ccacaaactg tggatgatgac atctcctgtg 600
 actctcacct ctcagacaac taagacagat gacccccaat tgaaaagaga aataagggtta 660
 atgaaaaaca gagaagctgc tcgagaatgt cgcagaaaga agaaagaata tgtgaaatgc 720
 ctggaaaacc gaggttgcagt cctggaaaat caaaataaaa ctctaataga agagttaaaa 780
 actttgaagg atctttattc caataaaagt gtttga 816

<210> 170
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 170
 Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln Gln Ser Ser
 1 5 10 15

Ser Tyr Gly Gln Gln Ile Ala Ile Ala Pro Asn Gly Ala Leu Gln Leu
 20 25 30

Ala Ser Pro Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu Thr Met
 35 40 45

Thr Asn Ser Gly Ser Thr Gln Gln Gly Thr Thr Ile Leu Gln Tyr Ala
 50 55 60

Gln Thr Ser Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln Val Val
 65 70 75 80

130/299

Val Gln Thr Ala Ser Gly Asp Met Pro Thr Tyr Gln Ile Arg Thr Thr
 85 90 95

Pro Ser Ala Thr Ser Leu Pro Gln Thr Val Val Met Thr Ser Pro Val
 100 105 110

Thr Leu Thr Ser Gln
 115

<210> 171
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 171
 aactggatcc tacagccaag ctccaagtca atatagccaa cagagcagca gctacgggca 60
 gcagattgcc attgccccaa atggagcctt acagttggca agtccaggca cagatggagt 120
 acagggactt cagacattaa ccatagacaaa ttcaggcagt actcagcaag gtacaactat 180
 tcttcagtat gcacagacct ctgatggaca gcagatactt gtgcccagca atcaggtggt 240
 cgtacaaact gcatacaggag atatgccaac atatcagatc cgaactacac cttcagctac 300
 ttctctgcca caaactgtgg tgatgacatc tcctgtgact ctcacctctc aga 353

<210> 172
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 172
 taagtgccac ggagaaagct aaagcagaga aaggaatgga gaatgttcag gatggaggtc 60
 agagtgttac atcaggtggt caggaattac cttaggtaat tcctccactc caaacccctc 120
 agtgacttcc atgacatgaa ataggaagtc attggagggt ttgagcagag gaatgacctg 180
 ttttaaaagg ctacttcagg ctgctgtatg tggaatagag ttgcgaacag aggccatagg 240
 ataacagggt tttgttgaga aagtggtttc attttgaggg ctaggtggaa agacctgagg 300
 ttgtaaccag tagtggagag ggaaggaaaa ttaactcagg gggagtgaat ctgtagacct 360
 acttgagata agatactcgc tgggttaggt aggaggggca gataggatat ctaggcttgg 420
 agaggctggt aactcaaata taatggatag ttaatttttt tttttttttt tgcaggggtg 480
 agcagagaca ggatcgcagg 500

<210> 173
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 173
 cccctaaacc agatggccca ggagggggac caggtggctc tcacatgggt aagaaaggca 60
 gacctggtgc tagggagctg ggaccaaaga atccttaatt tttcagcggg gaggctcggg 120
 gaacataggg gaatgggaat atgatagatc ttgtttcttt tgtcctaggg ggtaactacg 180
 gggatgatcg tcgtggtggc agaggaggct atgatcgagg cggctaccgg ggccgcggcg 240
 gggaccgtgg aggcctccga gggggccggg gtggtgggga cagaggtggc tttggccctg 300
 gcaagatgga ttccagacct tctgcagtca gaaagtttct gcagtaattt agagatggta 360
 gtgaattgat ctagattgga aacaatggaa ttagaagtgt ttagattctt ctaagcaaag 420
 gtttttaaaa ctcattttta aagaatgagt taagggccgg gcatgggtggc tcacacctgt 480
 aatcccagca ctttgggaga ccagaggtgg gtggatcacc t 521

131/299

<210> 174

<211> 75

<212> PRT

<213> Homo sapiens

<400> 174

Tyr Ser Gln Gln Ser Ser Gln Pro Tyr Gly Gln Gln Ser Tyr Ser Gly
 1 5 10 15

Tyr Ser Gln Ser Thr Asp Thr Ser Gly Tyr Gly Gln Ser Ser Tyr Ser
 20 25 30

Ser Tyr Gly Gln Ser Gln Asn Met Phe Lys Lys Glu Val Tyr Leu His
 35 40 45

Thr Ser Pro His Leu Lys Ala Asp Val Leu Phe Gln Thr Asp Pro Thr
 50 55 60

Ala Glu Met Ala Ala Glu Ser Leu Pro Phe Ser
 65 70 75

<210> 175

<211> 225

<212> DNA

<213> Homo sapiens

<400> 175

tattcccagc agagcagtc gccctacgga cagcagagtt acagtgggta tagccagtcc 60
 acggacactt caggctatgg ccagagcagc tattcttctt atggccagag ccagaacatg 120
 ttcaagaagg aagtgtatct tcatacatca ccacacctga aagcagatgt gcttttccag 180
 actgatccaa ctgcagagat ggcagctgag tcattgcctt tctcc 225

<210> 176

<211> 78

<212> PRT

<213> Homo sapiens

<400> 176

Gly Asp Trp Lys Cys Pro Asn Pro Thr Cys Glu Asn Met Asn Phe Ser
 1 5 10 15

Trp Arg Asn Glu Cys Asn Gln Cys Lys Ala Pro Lys Pro Asp Gly Pro
 20 25 30

Gly Gly Gly Pro Gly Gly Ser His Met Gly Val Phe Lys Lys Glu Val
 35 40 45

Tyr Leu His Thr Ser Pro His Leu Lys Ala Asp Val Leu Phe Gln Thr
 50 55 60

Asp Pro Thr Ala Glu Met Ala Ala Glu Ser Leu Pro Phe Ser
 65 70 75

<210> 177

132/299

<211> 235

<212> DNA

<213> Homo sapiens

<400> 177

```

tggtgactgg aagtgtccta atccacactg tgagaatatg aacttctctt ggaggaatga 60
atgcaaccag tgtaaggccc ctaaaccaga tggcccagga gggggaccag gtggctctca 120
catgggggtg ttcaagaagg aagtgtatct tcatacatca ccacacctga aagcagatgt 180
gcttttccag actgatccaa ctgcagagat ggcagctgag tcattgcctt tctcc      235

```

<210> 178

<211> 526

<212> PRT

<213> Homo sapiens

<400> 178

```

Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr Gln Ser Tyr Gly Ala
  1           5           10           15

Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln Gln Ser Ser Gln Pro
      20           25           30

Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Ser Gln Ser Thr Asp Thr Ser
      35           40           45

Gly Tyr Gly Gln Ser Ser Tyr Ser Ser Tyr Gly Gln Ser Gln Asn Thr
      50           55           60

Gly Tyr Gly Thr Gln Ser Thr Pro Gln Gly Tyr Gly Ser Thr Gly Gly
      65           70           75           80

Tyr Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr Gly Gln Gln Ser Ser
      85           90           95

Tyr Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser Ser Thr Ser Gly Ser
      100          105          110

Tyr Gly Ser Ser Ser Gln Ser Ser Ser Tyr Gly Gln Pro Gln Ser Gly
      115          120          125

Ser Tyr Ser Gln Gln Pro Ser Tyr Gly Gly Gln Gln Gln Ser Tyr Gly
      130          135          140

Gln Gln Gln Ser Tyr Asn Pro Pro Gln Gly Tyr Gly Gln Gln Asn Gln
      145          150          155          160

Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn
      165          170          175

Tyr Gly Gln Asp Gln Ser Ser Met Ser Ser Gly Gly Gly Ser Gly Gly
      180          185          190

Gly Tyr Gly Asn Gln Asp Gln Ser Gly Gly Gly Gly Ser Gly Gly Tyr
      195          200          205

Gly Gln Gln Asp Arg Gly Gly Arg Gly Arg Gly Gly Ser Gly Gly Gly
      210          215          220

```

133/299

Gly Gly Gly Gly Gly Gly Gly Tyr Asn Arg Ser Ser Gly Gly Tyr Glu
 225 230 235 240
 Pro Arg Gly Arg Gly Gly Gly Arg Gly Gly Arg Gly Gly Met Gly Gly
 245 250 255
 Ser Asp Arg Gly Gly Phe Asn Lys Phe Gly Gly Pro Arg Asp Gln Gly
 260 265 270
 Ser Arg His Asp Ser Glu Gln Asp Asn Ser Asp Asn Asn Thr Ile Phe
 275 280 285
 Val Gln Gly Leu Gly Glu Asn Val Thr Ile Glu Ser Val Ala Asp Tyr
 290 295 300
 Phe Lys Gln Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Gln Pro
 305 310 315 320
 Met Ile Asn Leu Tyr Thr Asp Arg Glu Thr Gly Lys Leu Lys Gly Glu
 325 330 335
 Ala Thr Val Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp
 340 345 350
 Trp Phe Asp Gly Lys Glu Phe Ser Gly Asn Pro Ile Lys Val Ser Phe
 355 360 365
 Ala Thr Arg Arg Ala Asp Phe Asn Arg Gly Gly Gly Asn Gly Arg Gly
 370 375 380
 Gly Arg Gly Arg Gly Gly Pro Met Gly Arg Gly Gly Tyr Gly Gly Gly
 385 390 395 400
 Gly Ser Gly Gly Gly Gly Arg Gly Gly Phe Pro Ser Gly Gly Gly Gly
 405 410 415
 Gly Gly Gly Gln Gln Arg Ala Gly Asp Trp Lys Cys Pro Asn Pro Thr
 420 425 430
 Cys Glu Asn Met Asn Phe Ser Trp Arg Asn Glu Cys Asn Gln Cys Lys
 435 440 445
 Ala Pro Lys Pro Asp Gly Pro Gly Gly Gly Pro Gly Gly Ser His Met
 450 455 460
 Gly Gly Asn Tyr Gly Asp Asp Arg Arg Gly Gly Arg Gly Gly Tyr Asp
 465 470 475 480
 Arg Gly Gly Tyr Arg Gly Arg Gly Gly Asp Arg Gly Gly Phe Arg Gly
 485 490 495
 Gly Arg Gly Gly Gly Asp Arg Gly Gly Phe Gly Pro Gly Lys Met Asp
 500 505 510
 Ser Arg Gly Glu His Arg Gln Asp Arg Arg Glu Arg Pro Tyr
 515 520 525

134/299

<210> 179
 <211> 1824
 <212> DNA
 <213> Homo sapiens

<400> 179
 atgctcagtc ctccaggcgt cgggtgctcag cgggtgttggg acttcggtgc ttgcttgcc 60
 gtgcgcgcgt gcgcggacat ggcctcaaac gattataccc aacaagcaac ccaaagctat 120
 ggggcctacc ccaccagcc cgggcagggc tattcccagc agagcagtc gccctacgga 180
 cagcagagtt acagtggta tagccagtc acggacactt caggctatgg ccagagcagc 240
 tattcttctt atggccagag ccagaacaca ggctatggaa ctcagtcac tccccaggga 300
 tatggctcga ctggcggcta tggcagtagc cagagctccc aatcgtctta cgggcagcag 360
 tcctcctacc ctggctatgg ccagcagcca gctcccagca gcacctcggg aagttacggt 420
 agcagttctc agagcagcag ctatgggcag cccagagtg ggagctacag ccagcagcct 480
 agctatggtg gacagcagca aagctatgga cagcagcaaa gctataatcc ccctcagggc 540
 tatggacagc agaaccagta caacagcagc agtggtggtg gaggtggagg tggaggtgga 600
 ggtaactatg gccaaagatca atcctccatg agtagtggtg gtggcagtggt tggcgggttat 660
 ggcaatcaag accagagtggt tggaggtggc agcgggtggt atggacagca ggaccgtgga 720
 ggccgcggcg ggggtggcag tgggtggcggc ggcggcggcg gcggtggtgg ttacaaccgc 780
 agcagtggtg gctatgaacc cagaggtcgt ggaggtggcc gtggaggcag aggtggcctg 840
 ggcggaagtg accgtggtgg cttcaataaa tttggtggcc ctcgggacca aggatcacgt 900
 catgactccg aacaggataa ttcagacaac aacaccatct ttgtgcaagg cctgggtgag 960
 aatgttaca ttgagtctgt ggctgattac ttcaagcaga ttggtattat taagacaaac 1020
 aagaaaacgg gacagcccat gattaatttg tacacagaca gggaaactgg caagctgaag 1080
 ggagaggcaa cggctctctt tgatgaccca ccttcagcta aagcagctat tgactgggtt 1140
 gatggtaaag aattctcctg aaatcctatc aaggtctcat ttgctactcg cgggcagac 1200
 tttaatcggg gtggtggcaa tggctgtgga ggcgaggggc gaggaggacc catgggcccgt 1260
 ggaggtatg gaggtggtgg cagtgggtgt ggtggccgag gaggatttcc cagtggagggt 1320
 ggtggcgggt gaggacagca gcgagctggt gactggaagt gtctaatacc cacctgtgag 1380
 aatatgaact tctcttgag gaatgaatgc aaccagtgt aggccctaa accagatggc 1440
 ccaggagggg gaccaggtgg ctctcacatg gggggtaaact acggggatga tcgtcgtggt 1500
 ggcagaggag gctatgatcg aggcggctac cggggccgcg gcggggaccg tggaggcttc 1560
 cgagggggcc ggggtggtgg ggacagaggt ggctttggcc ctggcaagat ggattccagg 1620
 ggtgagcaca gacaggatcg caggagagg ccgtattaat tagcctggct cccaggttc 1680
 tggaaacagct tttgtcctg taccagtggt taccctcgtt attttgaac cttccaattc 1740
 ctgatcacc aagggtttt tttgtgtcgg actatgtaat tgtaactata cctctggttc 1800
 ccattaaaag tgaccatttt agtt 1824

<210> 180
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 180
 Gln Ser Ser Gln Ser Ser Tyr Gly Gln Gln Ser Ser Tyr Pro Gly Tyr
 1 5 10 15
 Gly Gln Gln Pro Ala Pro Ser Ser Thr Ser Gly Ser Tyr Gly Ser Ser
 20 25 30
 Ser Gln Ser Ser Ser Tyr Gly Gln Pro Gln Ser Gly Ser Tyr Ser Gln
 35 40 45
 Gln Pro Ser Tyr Gly Gly Gln Gln Gln Ser Tyr Gly Gln Gln Gln Ser
 50 55 60

135/299

Tyr Asn Pro Pro Gln Gly Tyr Gly Gln Gln Asn Gln Tyr Asn Ser Ser
 65 70 75 80
 Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn Tyr Gly Gln Asp
 85 90 95
 Gln Ser Ser Met Ser Ser Gly Gly Gly Ser Gly Gly Gly Tyr Gly Asn
 100 105 110
 Gln Asp Gln Ser Gly Gly Gly Gly Ser Gly Gly Tyr Gly Gln Gln Asp
 115 120 125
 Arg Gly Gly Arg Gly Arg Gly Gly Ser Gly Gly Gly Gly Ala Ala Ala
 130 135 140
 Val Val Val Thr Thr Ala Ala Val Val Ala Met Asn Pro Glu Val Val
 145 150 155 160
 Glu Val Ala Val Glu Ala Glu Val Ala Trp Ala Glu Val Thr Val Val
 165 170 175
 Ala Ser Ile Asn Leu Val Cys Ser Arg Arg Lys Cys Ile Phe Ile His
 180 185 190
 His His Ser
 195

<210> 181
 <211> 652
 <212> DNA
 <213> Homo sapiens

<400> 181
 cagagctccc aatcgtctta cgggcagcag tcctcctacc ctggctatgg ccagcagcca 60
 gctcccagca gcacctcggg aagttacggt agcagttctc agagcagcag ctatgggcag 120
 cccagagtg ggagctacag ccagcagcct agctatgggt gacagcagca aagctatgga 180
 cagcagcaaa gctataatcc ccctcagggc tatggacagc agaaccagta caacagcagc 240
 agtgggtggtg gaggtggagg tggaggtgga ggtaactatg gccaaagatca atcctccatg 300
 agtagtggtg gtggcagtggt tggcggttat ggcaatcaag accagagtggt tggaggtggc 360
 agcgggtggct atggacagca ggaccgtgga ggccgcggca ggggtggcag tgggtggcggc 420
 ggggcggcgg cggtggtggt tacaaccgca gcagtgggtg ctatgaaccc agaggtcgtg 480
 gaggtggccg tggaggcaga ggtggcatgg gcggaagtga ccgtgggtggc ttcaataaat 540
 ttggtgtggt caagaaggaa gtgtatcttc atacatcacc actcctgaaa gcagatgtgc 600
 ttttccagac tgatccaact gcagagatgg cagctgagtc attgcctttc tc 652

<210> 182
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 182
 Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr Gln Ser Tyr Gly Ala
 1 5 10 15
 Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln Gln Ser Ser Gln Pro
 20 25 30

136/299

Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Ser Gln Ser Thr Asp Thr Ser
 35 40 45
 Gly Tyr Gly Gln Ser Ser Tyr Ser Ser Tyr Gly Gln Ser Gln Asn Thr
 50 55 60
 Gly Tyr Gly Thr Gln Ser Thr Pro Gln Gly Tyr Gly Ser Thr Gly Gly
 65 70 75 80
 Tyr Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr Gly Gln Gln Ser Ser
 85 90 95
 Tyr Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser Ser Thr Ser Gly Ser
 100 105 110
 Tyr Gly Ser Ser Ser Gln Ser Ser Tyr Gly Gln Pro Gln Ser Gly
 115 120 125
 Ser Tyr Ser Gln Gln Pro Ser Tyr Gly Gly Gln Gln Gln Ser Tyr Gly
 130 135 140
 Gln Gln Gln Ser Tyr Asn Pro Pro Gln Gly Tyr Gly Gln Gln Asn Gln
 145 150 155 160
 Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn
 165 170 175
 Tyr Gly Gln Asp Gln Ser Ser Met Ser Ser Gly Gly Gly Ser Gly Gly
 180 185 190
 Gly Tyr Gly Asn Gln Asp Gln Ser Gly Gly Gly Gly Ser Gly Gly Tyr
 195 200 205
 Gly Gln Gln Asp Arg Gly Gly Arg Gly Arg Gly Gly Ser Gly Gly Gly
 210 215 220
 Gly Gly Gly Gly Gly Gly Gly Tyr Asn Arg Ser Ser Gly Gly Tyr Glu
 225 230 235 240
 Pro Arg Gly Arg Gly Gly Gly Arg Gly Gly Arg Gly Gly Met Gly Gly
 245 250 255
 Ser Asp Arg Gly Gly Phe Asn Lys Phe Gly Val Phe Lys Lys Glu Val
 260 265 270
 Tyr Leu His Thr Ser Pro His Leu Lys Ala Asp Val Leu Phe Gln Thr
 275 280 285
 Asp Pro Thr Ala Glu Met Ala Ala Glu Ser Leu Pro Phe Ser Phe Gly
 290 295 300
 Thr Leu Ser Ser Trp Glu Leu Glu Ala Trp Tyr Glu Asp Leu Gln Glu
 305 310 315 320
 Val Leu Ser Ser Asp Glu Asn Gly Gly Thr Tyr Val Ser Pro Pro Gly
 325 330 335

137/299

Asn Glu Glu Glu Glu Ser Lys Ile Phe Thr Thr Leu Asp Pro Ala Ser
 340 345 350
 Leu Ala Trp Leu Thr Glu Glu Glu Pro Glu Pro Ala Glu Val Thr Ser
 355 360 365
 Thr Ser Gln Ser Pro His Ser Pro Asp Ser Ser Gln Ser Ser Leu Ala
 370 375 380
 Gln Glu Glu Glu Glu Glu Asp Gln Gly Arg Thr Arg Lys Arg Lys Gln
 385 390 395 400
 Ser Gly His Ser Pro Ala Arg Ala Gly Lys Gln Arg Met Lys Glu Lys
 405 410 415
 Glu Gln Glu Asn Glu Arg Lys Val Ala Gln Leu Ala Glu Glu Asn Glu
 420 425 430
 Arg Leu Lys Gln Glu Ile Glu Arg Leu Thr Arg Glu Val Glu Ala Thr
 435 440 445
 Arg Arg Ala Leu Ile Asp Arg Met Val Asn Leu His Gln Ala
 450 455 460

<210> 183
 <211> 1678
 <212> DNA
 <213> Homo sapiens

<400> 183
 gcggccgctg tcgggtgctca gcgggtgttg aacttcgttg cttgcttgcc tgtgcgcgag 60
 tgcgcggaca tggcctcaaa cgattataacc caacaagcaa cccaaagcta tggggcctac 120
 cccaccagc ccgggcaggg ctattcccag cagagcagtc agccctacgg acagcagagt 180
 tacagtgggt atagccagtc cacggacact tcaggctatg gccagagcag ctattcttct 240
 tatggccaga gccagaacac aggctatgga actcagtc aaatccccagg atagggctcg 300
 actggcggtc atggcagtag ccagagctcc caatcgtctt acgggcagca gtccctctac 360
 cctggctatg gccagcagcc agctcccagc agcacctcgg gaagttacgg tagcagttct 420
 cagagcagca gctatgggca gcccagagt gggagctaca gccagcagcc tagctatggt 480
 ggacagcagc aaagctatgg acagcagcaa agctataatc cccctcagg ctatggacag 540
 cagaaccagt acaacagcag cagtgggtgg ggaggtggag gtggaggtgg aggttaactat 600
 ggccaagatc aatcctccat gtagtagtgt ggtggcagtg gtggcggtta tggcaatcaa 660
 gaccagagtg gtggaggtgg cagcgggtgg tatggacagc aggaccgtgg aggcgcggc 720
 aggggtggca gtgggtggcg cggcggcggg ggcgggtggt gttacaaccg cagcagtggt 780
 ggctatgaac ccagaggtcg tggaggtggc cgtggaggca gaggtggcat gggcggaggt 840
 gaccgtggtg gcttcaataa atttggtgtg ttcaagaagg aagtgtatct tcatacatca 900
 ccacacctga aagcagatgt gcttttcag actgatccaa ctgcagagat ggcagctgag 960
 tcattgcctt tctccttcgg gacactgtcc agctgggagc tggaagcctg gtatgaggac 1020
 ctgcaagagg tcctgtcttc agatgaaaat ggggtacct atgtttcacc tcctggaaat 1080
 gaagaggaag aatcaaaaat cttcaccact cttgaccctg cttctctggc ttggctgact 1140
 gaggaggagc cagaaccagc agaggtcaca agcacctccc agagccctca ctctccagat 1200
 tccagtcaga gctccctggc tcaggaggaa gaggaggaag accaaggag aaccaggaaa 1260
 cggaaacaga gtggtcatc cccagcccg gctggaaagc agcgcatgaa ggagaaagaa 1320
 caggagaatg aaaggaaagt ggcacagcta gctgaagaga atgaacggct caagcaggaa 1380
 atcgagcgcc tgaccaggga agtagaggcg actcgccgag ctctgattga ccgaatggtg 1440
 aatctgcacc aagcatgaac aattgggagc atcagtcacc cacttgggcc aactaccca 1500
 cctttcccag aagtggctac tgactaccc ctcactagt ccaatgatgt gacctcaat 1560
 cccacatacg cagggggaag gcttggagta gacaaaagga aaggtctcag cttgtatata 1620

138/299

gagattgtac atttatttat tactgtccct atctattaaa gtgactttct atgaaaaa 1678

<210> 184

<211> 525

<212> PRT

<213> Homo sapiens

<400> 184

```

Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr Gln Ser Tyr Gly Ala
 1             5             10             15

Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln Gln Ser Ser Gln Pro
          20          25          30

Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Ser Gln Ser Thr Asp Thr Ser
          35          40          45

Gly Tyr Gly Gln Ser Ser Tyr Ser Ser Tyr Gly Gln Ser Gln Asn Ser
          50          55          60

Tyr Gly Thr Gln Ser Thr Pro Gln Gly Tyr Gly Ser Thr Gly Gly Tyr
          65          70          75          80

Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr Gly Gln Gln Ser Ser Tyr
          85          90          95

Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser Ser Thr Ser Gly Ser Tyr
          100          105          110

Gly Ser Ser Ser Gln Ser Ser Ser Tyr Gly Gln Pro Gln Ser Gly Ser
          115          120          125

Tyr Ser Gln Gln Pro Ser Tyr Gly Gly Gln Gln Gln Ser Tyr Gly Gln
          130          135          140

Gln Gln Ser Tyr Asn Pro Pro Gln Gly Tyr Gly Gln Gln Asn Gln Tyr
          145          150          155          160

Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn Tyr
          165          170          175

Gly Gln Asp Gln Ser Ser Met Ser Ser Gly Gly Gly Ser Gly Gly Gly
          180          185          190

Tyr Gly Asn Gln Asp Gln Ser Gly Gly Gly Gly Ser Gly Gly Tyr Gly
          195          200          205

Gln Gln Asp Arg Gly Gly Arg Gly Arg Gly Gly Ser Gly Gly Gly Gly
          210          215          220

Gly Gly Gly Gly Gly Gly Tyr Asn Arg Ser Ser Gly Gly Tyr Glu Pro
          225          230          235          240

Arg Gly Arg Gly Gly Gly Arg Gly Gly Arg Gly Gly Met Gly Gly Ser
          245          250          255

Asp Arg Gly Gly Phe Asn Lys Phe Gly Gly Pro Arg Asp Gln Gly Ser

```

139/299

260										265					270				
Arg	His	Asp	Ser	Glu	Gln	Asp	Asn	Ser	Asp	Asn	Asn	Thr	Ile	Phe	Val				
		275						280				285							
Gln	Gly	Leu	Gly	Glu	Asn	Val	Thr	Ile	Glu	Ser	Val	Ala	Asp	Tyr	Phe				
	290					295					300								
Lys	Gln	Ile	Gly	Ile	Ile	Lys	Thr	Asn	Lys	Lys	Thr	Gly	Gln	Pro	Met				
305					310					315					320				
Ile	Asn	Leu	Tyr	Thr	Asp	Arg	Glu	Thr	Gly	Lys	Leu	Lys	Gly	Glu	Ala				
				325					330					335					
Thr	Val	Ser	Phe	Asp	Asp	Pro	Pro	Ser	Ala	Lys	Ala	Ala	Ile	Asp	Trp				
			340					345					350						
Phe	Asp	Gly	Lys	Glu	Phe	Ser	Gly	Asn	Pro	Ile	Lys	Val	Ser	Phe	Ala				
		355					360					365							
Thr	Arg	Arg	Ala	Asp	Phe	Asn	Arg	Gly	Gly	Gly	Asn	Gly	Arg	Gly	Gly				
	370					375					380								
Arg	Gly	Arg	Gly	Gly	Pro	Met	Gly	Arg	Gly	Gly	Tyr	Gly	Gly	Gly	Gly				
385					390					395					400				
Ser	Gly	Gly	Gly	Gly	Arg	Gly	Gly	Phe	Pro	Ser	Gly	Gly	Gly	Gly	Gly				
				405					410					415					
Gly	Gly	Gln	Gln	Arg	Ala	Gly	Asp	Trp	Lys	Cys	Pro	Asn	Pro	Thr	Cys				
		420						425					430						
Glu	Asn	Met	Asn	Phe	Ser	Trp	Arg	Asn	Glu	Cys	Asn	Gln	Cys	Lys	Ala				
		435					440					445							
Pro	Lys	Pro	Asp	Gly	Pro	Gly	Gly	Gly	Pro	Gly	Gly	Ser	His	Met	Gly				
	450					455					460								
Gly	Asn	Tyr	Gly	Asp	Asp	Arg	Arg	Gly	Gly	Arg	Gly	Gly	Tyr	Asp	Arg				
465					470					475					480				
Gly	Gly	Tyr	Arg	Gly	Arg	Gly	Gly	Asp	Arg	Gly	Gly	Phe	Arg	Gly	Gly				
				485				490						495					
Arg	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Phe	Gly	Pro	Gly	Lys	Met	Asp	Ser				
			500					505					510						
Arg	Gly	Glu	His	Arg	Gln	Asp	Arg	Arg	Glu	Arg	Pro	Tyr							
	515					520						525							

<210> 185

<211> 1822

<212> DNA

<213> Homo sapiens

<400> 185

gcggccgctg gcgtcggtgc tcagcgggtg tggaaactcg ttgcttgctt gctgtgcgc 60

140/299

```
gcgtgcgcgg acatggcctc aaacgattat acccaacaag caacccaaag ctatggggcc 120
taccaccacc agcccgggca gggctattcc cagcagagca gtcagcccta cggacagcag 180
agttacagtg gttatagcca gtccacggac acttcaggct atggccagag cagctattct 240
tcttatggcc agagccagaa cagctatgga actcagtcaa ctcccaggg atatggctcg 300
actggcggct atggcagtag ccagagctcc caatcgtctt acgggcagca gtccctctat 360
cctggctatg gccagcagcc agctcccagc agcacctcgg gaagttacgg tagcagttct 420
cagagcagca gctatgggca gcccagagt gggagctaca gccagcagcc tagctatggg 480
ggacagcagc aaagctatgg acagcagcaa agctataatc cccctcaggg ctatggacag 540
cagaaccagt acaacagcag cagtgggtgg ggaggtggag gtggaggtgg aggttaactat 600
ggccaagatc aatcctccat gagtagtggt ggtggcagtg gtggcgggta tggcaatcaa 660
gaccagagtg gtggaggtgg cagcgggtggc tatggacagc aggaccgtgg aggcccgggc 720
aggggtggca gtgggtggcg cggcggcgcc ggccgtgggtg gttacaaccg cagcagtggt 780
ggctatgaac ccagaggtcg tggaggtggc cgtggaggca gaggtggcat gggcggaagt 840
gaccgtggtg gcttcaataa atttgggtggc cctcgggacc aaggatcacg tcatgactcc 900
gaacaggata attcagacaa caacaccatc tttgtgcaag gcctgggtga gaatgttaca 960
attgagtctg tggctgatta cttcaagcag attggtatta ttaagacaaa caagaaaacg 1020
ggacagccca tgattaatct gtacacagac agggaaactg gcaagctgaa gggagaggca 1080
acggtctctt ttgatgaccc accttcagct aaagcagcta ttgactggtt tgatggtaaa 1140
gaattctccg gaaatcctat caaggtctca tttgctactc gccgggcaga ctttaatcgg 1200
ggtggtggca atggtcgtgg aggccgaggg cgaggaggac ccattgggccg tggaggctat 1260
ggaggtggtg gcagtgggtg tgggtggccga ggaggatttc ccagtggagg tgggtggcgg 1320
ggaggacagc agcagctgg tgactggaag tgtcctaate ccacctgtga gaatatgaac 1380
ttctcttggg ggaatgaatg caaccagtgt aaggccctta aaccagatgg cccaggaggg 1440
ggaccaggtg gctctcacat ggggggtaac tacggggatg atcgtcgtgg tggcagagga 1500
ggctatgacg gaggcggcta ccggggccgc ggccgggacc gtggaggctt ccgagggggc 1560
cggggtggtg gggacagagg tggctttggc cctggcaaga tggattccag gggtgagcac 1620
agacaggatc gcaggagag gccgtattaa ttagcctggc tcccaggtt ctggaacagc 1680
tttttgtcct gtaccagtg ttacctcgt tattttgtaa ccttccaatt cctgatcacc 1740
caagggtttt tttgtgtcgg actatgtaat tgtaactata cctctggttc ccattaaaag 1800
tgaccatttt agttaaaaa aa 1822
```

<210> 186
<211> 120
<212> DNA
<213> Homo sapiens

<400> 186
tggtttctaa agatgaaatt aagaattggt ccacaagggt taagtgtctg gtggtaaagt 60
tgggctcgga ggcctacagt aacccaaata taagtccac ggagaaagct aaagcagaga 120

<210> 187
<211> 118
<212> DNA
<213> Homo sapiens

<400> 187
tgagtgtgtg ggagacaact ccgaatgttt aattctggaa gagggatgta acattgccct 60
gaggattcga gatggtagtg aattgatcta gattggaaac aatggaatta gaagtgtt 118

<210> 188
<211> 120
<212> DNA
<213> Homo sapiens

<400> 188

141/299

gtgtggggaga caactccgaa tggtttaattc tggaagaggg atgtaacatt gccctgagga 60
 tgggtggctca cacctgtaat cccagcactt tgggagacca gaggtgggtg gatcaccctg 120

<210> 189
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 189
 Gln Ser Ser Gln Ser Tyr Gly Gln Gln Ser Ser Tyr Pro Gly Tyr
 1 5 10 15
 Gly Gln Gln Pro Ala Pro Ser Ser Thr Ser Gly Ser Tyr Gly Ser Ser
 20 25 30
 Ser Gln Ser Ser Ser Tyr Gly Gln Pro Gln Ser Gly Ser Tyr Ser Gln
 35 40 45
 Gln Pro Ser Tyr Gly Gly Gln Gln Gln Ser Tyr Gly Gln Gln Gln Ser
 50 55 60
 Tyr Asn Pro Pro Gln Gly Tyr Gly Gln Gln Asn Gln Tyr Asn Ser Ser
 65 70 75 80
 Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Val Phe Lys Lys Glu Val
 85 90 95
 Tyr Leu His Thr Ser Pro Leu Leu Lys Ala Asp Val Leu Phe Gln Thr
 100 105 110
 Asp Pro Thr Ala Glu Met Ala Ala Glu Ser Leu Pro Phe Ser
 115 120 125

<210> 190
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 190
 cagagctccc aatcgtctta cgggcagcag tcctcctacc ctggctatgg ccagcagcca 60
 gctcccagca gcacctcggg aagttacggg agcagttctc agagcagcag ctatggggcag 120
 cccagagtg ggagctacag ccagcagcct agctatgggtg gacagcagca aagctatgga 180
 cagcagcaaa gctataatcc ccctcagggc tatggacagc agaaccagta caacagcagc 240
 agtgggtgggtg gaggtggagg tggaggtgga gtgttcaaga aggaagtgta tcttcataca 300
 tcaccactcc tgaaagcaga tgtgcttttc cagactgatc caactgcaga gatggcagct 360
 gagtcattgc ctttctc 377

<210> 191
 <211> 689
 <212> PRT
 <213> Homo sapiens

<400> 191
 Pro Ser Val Ser Ser Ile Ser Arg Ile Leu Arg Ser Lys Phe Gly Lys
 1 5 10 15

142/299

Gly Glu Glu Glu Glu Ala Asp Leu Glu Arg Lys Glu Ala Glu Glu Ser
 20 25 30
 Glu Lys Lys Ala Lys His Ser Ile Asp Gly Ile Leu Ser Glu Arg Ala
 35 40 45
 Ser Ala Pro Gln Ser Asp Glu Gly Ser Asp Ile Asp Ser Glu Pro Asp
 50 55 60
 Leu Pro Leu Lys Arg Lys Gln Arg Arg Ser Arg Thr Thr Phe Thr Ala
 65 70 75 80
 Glu Gln Leu Glu Glu Leu Glu His Val Ala Phe Glu Arg Thr His Tyr
 85 90 95
 Pro Asp Ile Tyr Thr Arg Glu Glu Leu Ala Gln Arg Ala Lys Leu Thr
 100 105 110
 Glu Ala Arg Val Gln Val Trp Phe Ser Asn Arg Arg Ala Arg Trp Arg
 115 120 125
 Lys Gln Ala Gly Ala Asn Gln Leu Met Ala Phe Asn His Leu Ile Pro
 130 135 140
 Gly Gly Phe Pro Pro Thr Ala Met Pro Thr Leu Pro Thr Tyr Gln Leu
 145 150 155 160
 Ser Glu His Ser Tyr Gln Pro Thr Ser Ile Pro Gln Ala Val Ser Asp
 165 170 175
 Pro Ser Ser Thr Val His Arg Pro Gln Pro Leu Pro Pro Ser Thr Val
 180 185 190
 His Gln Ser Thr Ile Pro Ser Asn Pro Asp Ser Ser Ser Ala Tyr Cys
 195 200 205
 Leu Pro Ser Thr Arg His Gly Phe Ser Ser Tyr Thr Asp Ser Phe Val
 210 215 220
 Pro Pro Ser Gly Pro Ser Asn Pro Met Asn Pro Thr Ile Gly Asn Gly
 225 230 235 240
 Leu Ser Pro Gln Asn Ser Ile Arg His Asn Leu Ser Leu His Ser Lys
 245 250 255
 Phe Ile Arg Val Gln Asn Glu Gly Thr Gly Lys Ser Ser Trp Trp Met
 260 265 270
 Leu Asn Pro Glu Gly Gly Lys Ser Gly Lys Ser Pro Arg Arg Arg Ala
 275 280 285
 Ala Ser Met Asp Asn Asn Ser Lys Phe Ala Lys Ser Arg Ser Arg Ala
 290 295 300
 Ala Lys Lys Lys Ala Ser Leu Gln Ser Gly Gln Glu Gly Ala Gly Asp
 305 310 315 320

143/299

Ser Pro Gly Ser Gln Phe Ser Lys Trp Pro Ala Ser Pro Gly Ser His
 325 330 335
 Ser Asn Asp Asp Phe Asp Asn Trp Ser Thr Phe Arg Pro Arg Thr Ser
 340 345 350
 Ser Asn Ala Ser Thr Ile Ser Gly Arg Leu Ser Pro Ile Met Thr Glu
 355 360 365
 Gln Asp Asp Leu Gly Glu Gly Asp Val His Ser Met Val Tyr Pro Pro
 370 375 380
 Ser Ala Ala Lys Met Ala Ser Thr Leu Pro Ser Leu Ser Glu Ile Ser
 385 390 395 400
 Asn Pro Glu Asn Met Glu Asn Leu Leu Asp Asn Leu Asn Leu Leu Ser
 405 410 415
 Ser Pro Thr Ser Leu Thr Val Ser Thr Gln Ser Ser Pro Gly Thr Met
 420 425 430
 Met Gln Gln Thr Pro Cys Tyr Ser Phe Ala Pro Pro Asn Thr Ser Leu
 435 440 445
 Asn Ser Pro Ser Pro Asn Tyr Gln Lys Tyr Thr Tyr Gly Gln Ser Ser
 450 455 460
 Met Ser Pro Leu Pro Gln Met Pro Ile Gln Thr Leu Gln Asp Asn Lys
 465 470 475 480
 Ser Ser Tyr Gly Gly Met Ser Gln Tyr Asn Cys Ala Pro Gly Leu Leu
 485 490 495
 Lys Glu Leu Leu Thr Ser Asp Ser Pro Pro His Asn Asp Ile Met Thr
 500 505 510
 Pro Val Asp Pro Gly Val Ala Gln Pro Asn Ser Arg Val Leu Gly Gln
 515 520 525
 Asn Val Met Met Gly Pro Asn Ser Val Met Ser Thr Tyr Gly Ser Gln
 530 535 540
 Ala Ser His Asn Lys Met Met Asn Pro Ser Ser His Thr His Pro Gly
 545 550 555 560
 His Ala Gln Gln Thr Ser Ala Val Asn Gly Arg Pro Leu Pro His Thr
 565 570 575
 Val Ser Thr Met Pro His Thr Ser Gly Met Asn Arg Leu Thr Gln Val
 580 585 590
 Lys Thr Pro Val Gln Val Pro Leu Pro His Pro Met Gln Met Ser Ala
 595 600 605
 Leu Gly Gly Tyr Ser Ser Val Ser Ser Cys Asn Gly Tyr Gly Arg Met
 610 615 620
 Gly Leu Leu His Gln Glu Lys Leu Pro Ser Asp Leu Asp Gly Met Phe

144/299

625	630	635	640
Ile Glu Arg Leu Asp Cys Asp Met Glu Ser Ile Ile Arg Asn Asp Leu			
645	650	655	
Met Asp Gly Asp Thr Leu Asp Phe Asn Phe Asp Asn Val Leu Pro Asn			
660	665	670	
Gln Ser Phe Pro His Ser Val Lys Thr Thr Thr His Ser Trp Val Ser			
675	680	685	

Gly

<210> 192

<211> 3517

<212> DNA

<213> Homo sapiens

<400> 192

```

ccgtcagtga gttccatcag ccgcctcctg agaagtaaat tcgggaaagg tgaagaggag 60
gaggccgact tggagaggaa ggaggcagag gaaagcgaga agaaggccaa acacagcatc 120
gacggcatcc tgagcgagcg agcctcagca cccaatcag atgaaggctc tgatattgac 180
tctgaaccag atttaccact aaagaggaaa cagcgcagaa gccgaaccac cttcacagca 240
gaacagctgg aggaactgga gcacgttgct tttgagagaa ctcattacc cttacatttat 300
actagggagg aactggccca gagggcgaag ctcaccgagg cccgagtaca ggtctgggtt 360
agcaaccgcc gtgcaagatg gaggaagcaa gctggggcca atcaactgat ggctttcaac 420
catctcattc ccgggggatt cctccctact gccatgccga ccttgccaac gtaccagctg 480
tcggagcact cttaccagcc cacatctatt ccacaagctg tgtcagatcc cagcagcacc 540
gttcacagac ctcaaccgct cctccaagc actgtacacc aaagcacgat tccttccaac 600
ccagacagca gctctgccta ctgcctcccc agcaccaggc atggattttc cagctataca 660
gacagctttg tgctccgtc ggggcccctc aaccccatga accccaccat tggcaatggc 720
ctctcacctc agaattcaat tcgtcataat ctgtccctac acagcaagtt cattcgtgtg 780
cagaatgaag gaactggaaa aagttcttgg tggatgctca atccagaggg tggcaagagc 840
gggaaatctc ctaggagaag agctgcattc atggacaaca acagtaaat tgctaagagc 900
cgaagccgag ctgccaaaga gaaagcatct ctccagctct gccaggaggg tgctggggac 960
agccctggat cacagttttc caaatggcct gcaagccctg gctctcacag caatgatgac 1020
tttgataact ggagtacatt tcgcccctga actagctcaa atgctagtac tattagtggg 1080
agactctcac ccattatgac cgaacaggat gatcttggag aaggggatgt gcattctatg 1140
gtgtaccgcg catctgcccgc aaagatggcc tctactttac ccagtctgtc tgagataagc 1200
aatcccgaaa acatggaaaa tcttttggat aatctcaacc ttctctcatc accaacatca 1260
ttaactgttt cgaccagtc ctcacctggc accatgatgc agcagacgcc gtgctactcg 1320
tttgcgccac caaacaccag tttgaattca ccagcccaa actacaaaa atatacatat 1380
ggccaatcca gcatgagccc tttgccccag atgcctatac aaacacttca ggacaataag 1440
tcgagttatg gaggtatgag tcagtataac tgtgcgcctg gactcttgaa ggagttgctg 1500
acttctgact ctctcccca taatgacatt atgacaccag ttgatcctgg ggtagcccag 1560
cccaacagcc gggttctggg ccagaacgtc atgatgggccc ctaattcggg catgtcaacc 1620
tatggcagcc aggcattctc taacaaaatg atgaatccca gctcccatc ccacctgga 1680
catgctcagc agacatctgc agtcaacggg cgtccctgac ccacacggg aagcaccatg 1740
ccccacacct cgggtatgaa ccgcctgacc caagtgaaga cacctgtaca agtgccctc 1800
ccccaccca tgcagatgag tgccctgggg ggctactcct ccgtgagcag ctgcaatggc 1860
tatggcagaa tgggcttctt ccaccaggag aagctcccaa gtgacttggg tggcatgttc 1920
attgagcgct tagactgtga catggaatcc atcattcgga atgacctcat ggatggagat 1980
acattggatt ttaactttga caatgtgttg cccaacccaa gcttcccaca cagtgtcaag 2040
acaacgacac atagctgggt gtcaggctga gggtagtgga gcagggtaca cttaaaagta 2100
cttcagattg tctgacagca ggaactgaga gaagcagtc aaagatgtct ttcaccaact 2160
cccttttagt tttcttgggt aaaaaaaaaa acaaaaaaaaaa aaacctcct tttttcctt 2220
cgtcagactt ggcagcaaag acatttttcc tgtacaggat gtttgcccaa tgtgtgcagg 2280

```

145/299

```

ttatgtgctg ctgtagataa ggactgtgcc attggaaatt tcattacaat gaagtgccaa 2340
actcactaca ccatataatt gcagaaaaga ttttcagatc ctggtgtgct ttcaagtttt 2400
gtatataagc agtagataca gattgtatatt gtgtgtgttt ttgggtttttc taaatatcca 2460
attgggtccaa ggaaagttta tactcttttt gtaataactgt gatggggctc atgtcttgat 2520
aagttaaact tttgtttgta ctacctgttt tctgcggaac tgacggatca caaagaactg 2580
aatctccatt ctgcatctcc attgaacagc cttggacctg ttcacgttgc cacagaattc 2640
acatgagaac caagtagcct gttatcaatc tgctaaatta atggacttgt taaacttttg 2700
gaaaaaaaaa gattaaatgc cagctttgta caggctcttt ctattttttt ttgtttattt 2760
tgttatttgc aaatttgtac aaacatttaa atgggttctaa tttccagata aatgattttt 2820
gatgttattg ttgggactta agaacatttt tgggaatagat attgaactgt aataatgttt 2880
tcttaaaaact agagtctact ttgttacata gtcagcttgt aaattttgtg gaaccacagg 2940
tatttggggg cagcattcat aattttcatt ttgtattcta actggattag tactaatttt 3000
atacatgctt aactggtttg tacactttgg gatgctactt agtgatgttt ctgactaatc 3060
ttaaatcatt gtaattagta cttgcatatt caacgtttca ggccctgggt gggcaggaaa 3120
gtgatgtata gttatggaca ctttgcgttt cttatttagg ataacttaat atgtttttat 3180
gtatgtattt taaagaaatt tctactgttc tctgaactat gcgtactgca tagcatcaag 3240
tcttctctag agacctctgt agtcctggga ggccctcataa tgtttgtaga tacagaaagg 3300
gagactgcat ctaaagcaat ggtcctttgt caaacgaggg attttgatcc acttcaccat 3360
tttgagttga gctttagcaa aagtttccct cataattctt tgctcttggt tcagtcagg 3420
tggaggttgg tttttagatt ctgccttgag gaattatgtc aacactcata cttcatctca 3480
ttctcccttc tgccctgcag attagattac ttagcac 3517

```

<210> 193

<211> 55

<212> PRT

<213> Homo sapiens

<400> 193

```

Pro Tyr Gly Tyr Asp Gln Ser Pro Phe Met Cys Asn Lys Arg Ala Glu
  1                      5                      10          15

```

```

Asp Phe Gln Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln
      20                      25          30

```

```

Val Glu Arg Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro
    35                      40          45

```

```

Lys Ile Met Pro Lys Lys Pro
    50                      55

```

<210> 194

<211> 165

<212> DNA

<213> Homo sapiens

<400> 194

```

ccttatggat atgaccagtc tcctttcatg tgtaataaac gggccgaaga cttccagggg 60
aatgatttgg ataatgacct taaccgtggg aatcaggttg aacgtcctca gatgactttc 120
ggcaggctcc agggaatctc cccgaagatc atgcccaaga agcca 165

```

<210> 195

<211> 188

<212> PRT

<213> Homo sapiens

146/299

<400> 195

```

Met Asn Gly Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln
 1             5             10             15

Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
      20             25             30

Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
      35             40             45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
      50             55             60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
      65             70             75             80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
      85             90             95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
      100            105            110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
      115            120            125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
      130            135            140

Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
      145            150            155            160

Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile
      165            170            175

Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
      180            185

```

<210> 196

<211> 766

<212> DNA

<213> Homo sapiens

<400> 196

```

ctctcttttcg attcttccat actcagagta cgcacggtct gattttctct ttggattctt 60
ccaaaatcag agtcagactg ctcccgggtgc catgaacgga gacgacgcct ttgcaaggag 120
acccacgggtt ggtgctcaaa taccagagaa gatccaaaag gccttcgatg atattgccaa 180
atacttctct aaggaagagt gggaaaagat gaaagcctcg gagaaaatct tctatgtgta 240
tatgaagaga aagtatgagg ctatgactaa actagggtttc aaggccaccc tcccaccttt 300
catgtgtaat aaacgggccg aagacttcca ggggaatgat ttggataatg accctaaccg 360
tggaatcag gttgaacgtc ctcagatgac ttctggcagg ctccaggga tctccccgaa 420
gatcatgccc aagaagccag cagaggaagg aaatgattcg gaggaagtgc cagaagcatc 480
tggcccacaa aatgatggga aagagctgtg ccccccggga aaaccaacta cctctgagaa 540
gattcacgag agatctggac caaaagggg ggaacatgcc tggaccaca gactgcgtga 600
gagaaaacag ctggtgattt atgaagagat cagcgaccct gaggaagatg acgagtaact 660
cccctcaggg atacgacaca tgcccagatg gagaagcaga acgtggtgac ctttcacgaa 720
catgggcatg gctgcggacc cctcgtcatc aggtgcatag caagtg 766

```

147/299

<210> 197
 <211> 548
 <212> DNA
 <213> Homo sapiens

<400> 197
 tgaaaattca ttgggtgatt cctgtgtaca acgtaaaagt tctgtcatta actgaatagc 60
 cataaaaagc ctttaaatct ccgtaaagct acaaaaattc gtccggccatg ttgggtgcaca 120
 cctgtagtcc cagctaccga ggaggctgag gtggggagaat cgcttgaacc tgggaagggtgg 180
 aggttgtaat gagccaagat tatgccactg cactccagcc tgggcaacag agtgatactc 240
 tgtctcaaaa aaaaaaaaaat gtgtgtgtat atatatatgt gtgtatatat atacacacac 300
 atatatgtat atatatgcgt atgtatatat acacacatat gtgtatgtgc gtgtgtacac 360
 acacgtgtgt gtgcgtgcgt acacacacac gtgtgtgcgc gtgtgtatgt gtatatatgt 420
 gtgtatatat gtatatatgt gtgtatatat gtatatatgt atatgtgtat atatataatc 480
 ttgccaaata ctacaaatct tataaatcgt tcctttactg gctgttttgt gatatatctt 540
 ttatatgc 548

<210> 198
 <211> 13589
 <212> DNA
 <213> Homo sapiens

<400> 198
 gtgagtgagt tcccctctcg ccgctccagc atcatgggga cctgacaaag tcccactctc 60
 ccctgtgatc tttgcagcca gcctcgcacc attcccaatt aggcgcacct caaggctctc 120
 tgagggcaat tggaggcttc tgcttggatg aggcataatc cctaattggct tgggttaatga 180
 gccgtggga tggagtagtt aatgagcctc agaaatgtta agaaacaaat gtcctacgtc 240
 cagcttacaa ggagagtcac atcagaatca aggctaagcg aaaacattta aaataaaagg 300
 tttatgagca tgctaattggc cctgtcctga agtttccagc agctaattaa tgaccagaca 360
 cagcataaag aagctttgtc tcagattcag gcctgtaatt ccattcctgtg agcggtaacg 420
 ccattgcagc ttcaccttag gagcgggtag gagaggaaaa caggattatg gtattggagg 480
 caggtgttgc tggggccattt ggacagagga aaccactccc agattctctt tcattttatta 540
 taagaagccc aaatttgctt acttaaggga agaaaccagt ggaaaccagt gggaaaaata 600
 tctacacatt gtctgtttcc taggatgtc ataatttaca tgaactcatt ctccagaagc 660
 ttaattcctc aacctgtgta caaggtagc tcttttcgta gagcatttct ccattagata 720
 tttgttgagc acctgctgtg tacaataaaa tgcattagga gtagggatac agagctagtt 780
 taacatgcaa tatctttttc cccaaggaa ttagaatata gtgggagaga caaagggtga 840
 aaccactaag atataaggca gaatgaagtc agccccattt ccatttcatt ttatgtacca 900
 gcattcattg agcacctact gtctgccaga gtaataaagc gctgtagaag caaagcagaa 960
 ggaagggtgt ttttgactgg agggaccaag caaggctttg caggggagag agcctgatac 1020
 tgaagtgact gtgctttcga tagtggaag gaggcctgga ggcaggagag aacggacctg 1080
 ttcagggaag ggtgagaaat gcccctcct ccctgagccc atgaccoggt gagagctcta 1140
 gctgaccatc aagggtgctgc catgctgatg gcagtggaag aacaggctcc tacaagccta 1200
 ctttacttct gccttgaggc actgtccctt tttttttttt ttttccacac tctgttgccc 1260
 aggtcggagt gcagtgcagg aatctcggct cactgcaagc tccgcccccc ggggttcacgt 1320
 cattctcctg cctcggcctc ctgagtagct gogactacag gcgcccgc caatgcccgg 1380
 ctaatttttt tcatattttt agtagagacg gggtttcacc atgttagoca ggatggctct 1440
 gatctcctga cctcgcgatc cgctgcgtc ggccctccta agtgctagga ttacaggcgt 1500
 gagccaccgc gccyggccgg tactgtccct tttttattta aatcatgtat ttctagattt 1560
 ttctctggcc ccaagtgcac caccagtgtt gtctcartt cactgttata aatcatttac 1620
 atcagggatg ttgaatcyag aaaataaaat ggcaaacaaa aatgacttat atgtttttaa 1680
 aactatgaaa aaggaaatga tatatgtttg ggattccatt caaaacgatc ctgcagagtt 1740
 agggggtgag atgtgggtgg ggcctacata aaacaaggct agccatcacc agctagtggc 1800
 tatatgtctg ggtgatagat gcatgggggt taatattatt gatctctctg cttttacctg 1860
 tacatttagt tgttttaatc agaaaaatgaa aaaataaaac tgggggaaaa aagaatagta 1920
 gataaagaag caaagagctt gggcaaaaaca tgtgaatttc cccaaataat tggagaagga 1980

ggatgaggtc	agtgtattgc	tgtgaattct	ataaatgacc	catctcgtgc	tttccaggca	2040
atacccttct	tgtctgtata	cctctcgtc	ttgtttcttg	catggtgtgt	gcagcagact	2100
tgacattttg	cagatacctt	ttgcttggtt	ataattctca	ggaccgctct	ttaaggtagc	2160
tcatgaactg	agtattcatc	ttatgtggaa	gggtcatttg	tacaggggaa	accacagagg	2220
aaactgagcc	ccagagaggg	aaaggccttt	gccaaaggta	gatagggggc	ccatgaccga	2280
ggtgtgcagg	acaacccttg	ctgcccgtgg	ctgctgtcca	tagtgcctgc	ctcgtggggc	2340
tggcttgctt	cccaagatct	ctcctgtcta	cctcccagggt	gacactgcct	tcaccacttc	2400
ttgggaatct	accataagcc	catgaatcaa	gaaagacaca	tggtttagac	ttgaggcggt	2460
atttttccct	tatttagtag	gtttgtaaat	ttcaaaatat	tagtctctta	aaattatatt	2520
actttttttt	ttgagacaga	gtctctgtca	cccaggtctga	agttcagtga	tgcaatctctg	2580
gctcattgca	acctctgcgt	cctagggtca	agtgtattctc	gtgcctcagc	ctcctgagta	2640
gcaggggatta	caggcacacg	ccaccatgcc	tggcgaattt	ttttgtattt	ttagttaaaga	2700
cgggggtttca	ccgtgtttgg	caggctgggtc	ttgaactcct	gacctcaagt	gatctgcctg	2760
ccttggcctc	ctaaattgct	gggattacag	gcatgaacca	ctgcaccag	cctatactac	2820
tatttttttc	atctcattcc	ccaatatcag	tggttgatga	tggatgcggc	ctcatcggtt	2880
aggaagcttg	gtggaatact	gcaccaccca	aatgatagcc	tgggtgtcta	tgggtgcccg	2940
ctctctcaag	ggcacacaga	aataggcaat	atgtgctttt	cttgatggct	cttaggaagt	3000
caagaatatt	catgtaaaat	aaccctgggg	cctagatctt	ttgggggaat	gcgttaactc	3060
cttcagtata	acaaatgtc	ctaaaactaa	ttaccagtgc	tataatggca	tattcaaaag	3120
tttttaaatc	tcccaatata	tattttaact	aatgcaacca	aatccaaatt	taactcattc	3180
cactgaaagg	cattgttttt	ctccgaagaa	ggtaggactg	aatcatccct	aaagttcctt	3240
ccagctctgc	cagtctgtag	tctgacagtc	ttgattctgt	aaccctccca	agaaaacaca	3300
agagttttaa	gcacctttgt	ttctttgagg	ataccctgt	gtgtactcca	ctcttctgat	3360
gtctttctgg	actcctcgat	ccttgtaaaa	ttgattctgt	ttattggagg	tgaaattcat	3420
tgggtgattc	ctgtgtacaa	cgtaaaagtt	ctgtcattaa	ctgaatagcc	ataaaaagcc	3480
tttaaatctc	cgtaaaagta	caaaaattcg	tcgggcatgt	tgggtgcacac	ctgtagtccc	3540
agctaccgag	gaggctgagg	tgggagaatc	gcttggacct	ggaagggtga	ggttgtaatg	3600
agccaagatt	atgccactgc	actccagcct	gggcaacaga	gtgatactct	gtctcaaaaa	3660
aaaaaaatgt	gtgtgtatat	atatatgtgt	gtatatatat	acacacacat	atatgtatat	3720
atatgcgtat	gtatatatac	acacatatgt	gtatgtgcgt	gtgtacacac	acgtgtgtgt	3780
gcgtgcgtac	acacacacgt	gtgtgcgcgt	gtgtatgtgt	atatatgtgt	gtatatatgt	3840
atatatgtgt	gtatatatgt	atatatgtat	atgtgtatat	atatgtgtat	atatatatga	3900
aatttttcat	aaattctttt	cattatctat	tatcactgaa	attccatcat	accattaaga	3960
tacatgcaga	attgtttctca	ctcataggtg	ggaattgaac	aatgagaaca	catggacaca	4020
ggaaggggaa	catcacacac	cgggtcctgt	tatggggctg	ggggaggggg	gagggatagc	4080
attaggagat	atacctaata	taaatgacga	gttaatgggt	gcagcacacc	aacatggcac	4140
atgtatacat	atgtaacaaa	cctgcacatt	gtgcacatgt	accctaaaac	ttagagtata	4200
attaaaaaaa	aaagatacat	gcaaatttat	gtctgttagg	tattttaccat	atggaaaaac	4260
taaaataatc	aagaaaaggaa	attcagtagg	tggttgacag	tttaaaataca	aatcacaaat	4320
gacatctttt	taaatataac	aagtagctta	tttttaaagg	tgtcacttac	tttgcaaagt	4380
ataaggagaa	ctgttattaa	gaatttacca	ggttggaatg	gctagtgttt	atgggagaga	4440
gttttagcaca	agacggagtg	agacaagatt	gctggggctc	tattttgaat	ccagcagcca	4500
acgctgtatg	gaatagtga	aaagttgcct	ctttctgtgc	ttgttttcta	cttggtatct	4560
ttaagaatgg	gctatttagg	agcaaggagc	ctagcagaaa	gcactctgtca	atcttctaaa	4620
actttaccta	caaaagtttt	actggcttgt	gtcccatcca	gtgtgtttca	aagccagaaa	4680
gtatattggc	cacaagcacc	tgtagggtgc	tgagggtgga	ctgtagtcat	cctgtagtca	4740
tgttttcagt	atgtattgaa	attccttatt	tggacttgat	ttcaaaggta	gaagggcctt	4800
ttacaggtaa	ggaactgaga	ttgagacaca	tcaagagtct	agcctcgagc	ttctgttcag	4860
tgtttttccc	aaaattattg	tttccttctg	gtctgggact	ctagagcaaa	gattgaaaac	4920
tgtggcccaa	agtgtgagcc	aaatccagcc	accatgcgtt	ttttttaaat	caagttttcc	4980
tggaaaacag	ccaaacccat	ttatttggtta	ttgcctatgt	ctgcttccat	gctgcagtgg	5040
cagagttgag	tagttacaac	agagattgca	tggccagcaa	cacctaaaac	atttattagt	5100
tggcccttta	cagaaaacgt	ttgatgctct	ctgccttgca	acattgtgta	cgtgggtggtc	5160
agtgtgcttg	gaatcatagg	tgcaatgtag	gatgcagact	tagaaaacag	tgcccttgct	5220
cccaaggaaat	tgtttgact	ttagatgaca	aggcatgttt	gagacatgtg	aaaggaacaa	5280
taacaagtta	tgtaaagag	gagacaggtt	ctggactgca	ggctatatatt	tcagaccaac	5340
cagaatagtt	acgataatat	cattaacata	aataaaagta	taagtattta	gctacgtaaa	5400
agaaacgatt	tattgcactt	tggattatac	agttcttcat	tcattcattc	aaaaattatt	5460

gccagtctgc	tcatgtgcc	ggcattgttc	tagatgatag	ggcactgcgt	ctctaaatgc	5520
caaatttcgt	atccttgctg	gtggaaggca	atgtcctcct	gctttatgcc	acgacacaaa	5580
ctaagctcct	gctttaacta	tagacagcta	aatcttaaac	gaacactttt	cagtcagttt	5640
agttttctct	taaagtactt	taattccgtt	aaaacctgag	ccaccagatt	tcctgtctgc	5700
ctgtctcttc	cttggcctta	atccaaaact	ctgctgagga	agaagattcg	ttggtacact	5760
gacaattgtt	ttataatcca	ttcatttcat	aacctctcat	ttgctaccca	aaagtgggga	5820
cctaaatctg	tacggattta	cgtgttcaaa	ggccatggcc	tacccaaata	gagaatatct	5880
cctttcttgt	gtttctctca	caacttttgc	tgaagtctct	ccatctttgt	gaacatgaac	5940
ttctcgattt	gtgaggctat	cgctggctaa	ttgggtcatt	aatcctacag	caggcaagac	6000
acagaatttc	ctctcagctc	aagatctctt	cactcccaac	cctcttagaa	cacacttcgc	6060
agcaatcctt	ggagtcttta	aaggtagcct	tttgtgactt	taaaaaacac	ttttactatc	6120
tctcaagggt	acatccttaa	cagaaacaaa	aagattctaa	tcagcgagac	atcaagcttc	6180
ttgcattgct	tatttgtcac	ccaactaaaa	caatgtactt	tcttgatttg	gttttattga	6240
ctggatgaat	tatatatata	caaagattca	attcggaag	cctctgaagt	aagatgaaga	6300
aaaaagtatg	aaactccaga	gaaagcagtt	tgaggcttgt	cctcaggggc	ttcaaggact	6360
gggagaagtc	actgtattct	ggcatcttgc	ttctgtctcc	acttcctccc	acagtgttta	6420
atgctgctgt	gaatttgttt	caaaggagc	ctatagactt	tttttttttt	ttttaattty	6480
gtcacatgag	cctcaggagc	agccttgaca	gctaaaagac	ctcgtaaarrg	rgaagtgtga	6540
agggattgca	tgaaagtgtc	gggggcaagt	ctcagccctc	ggccttttgt	ggaaggtgtg	6600
gggtgtgcag	acacatgtgc	accttcgcac	acatgcactc	gtgcataaat	atctgtgttt	6660
gcaggaaga	aaagataggg	ttgtgggatg	tcccagaag	ccacagggat	tcagtggtt	6720
tagtaccagg	tgaagagcc	gcttcctccc	acactatctc	aggagatgc	ccttctgtag	6780
acctctgtag	ccagtagccc	tcaagagctc	ctggagacag	atggccccga	acagtcctag	6840
ggaagcagtg	tgggcctgtg	gcaaaagctt	ggactgcgaa	gtcagcatga	ttggaatccg	6900
gttcttgact	cccaagcagg	tgcataatgt	ccctgagccc	ttctttcctt	atctgtaata	6960
ttgagaatag	taatacccat	ttctgggccc	ttttgactgt	taatgagaca	acatgtgaat	7020
gcatggcaca	agaaagttaa	ttgctacgtg	tcactgtccc	cccttgccctc	actgctgagc	7080
tgccatcctg	cccatctgag	agggactgtg	tgggagctgy	gggtacagcc	agcacaactg	7140
cctgcagagc	cacgcagggc	actgacaggg	aaggcctgtg	tggggtgccc	ttcaaggcca	7200
cctccgtttt	cttatttctt	tggagattta	cttttgtgct	cctgcttccc	ctccctgaag	7260
ctttgcctgc	tgtccataty	tggaggggat	gaatargatg	agcactgggg	aggggaggag	7320
ccatcactcc	agcaggaata	ttcccagcgg	ctgagtcact	gcatttgatt	ttcagtgatg	7380
acaactgaga	aatcaaagag	ccctaaaaga	ggaggaagtt	tcaggacaat	gttttaaaag	7440
ataaaaaaac	atcaacagca	tggtgtctga	gtggaaaata	atagaagggg	cttgaggaga	7500
ctggaaattc	cagtttgtgt	aagggcrcac	agtgtgttaa	tacagagtcc	tacctcctg	7560
cagtcctctg	atgtgaatc	ccaggctgca	cccacacctg	agcaaagcgg	aggctgggcc	7620
ttattaggtt	ctgactgcgg	gctggatctc	agctgcaggc	tgtgagtttc	ggataccggt	7680
gttttccagc	cttctccaca	ccttatgtaa	tcacagggtga	aaaggtccag	cctcatttgc	7740
agctgtgggt	cttctgcccc	aggaagccag	gaagcgtaga	tttttgtatt	atttgcctcc	7800
acttctccct	cccccagcgt	gccaccgtgc	acatatgttt	tctgttttcc	taagccacgg	7860
caaagcacaa	gcaatttccc	attgtaaaaca	caacctctgcg	tatcaacaca	cacctggctg	7920
cactggattg	accarctttc	tgttcttagg	taaggctgat	ctagtctaga	atagaggagg	7980
aggagggaaa	aaaaaaaaaa	aaaaacaagc	agcagatggc	cccctgaatg	ttgtaaaccg	8040
tgtttctcta	agcaggggtt	ctcaacactc	tcgatatttg	ggccaaataa	taatttgtgg	8100
ggttgcttac	tatattgtaa	gagattcagc	agcatccctg	gcctctaccc	actagatgct	8160
aggagcacc	tgcaccccag	tgtgacaacc	agaaatgcct	ccagatatattg	ccacatgccc	8220
ccagttcaga	accatatttg	taaagcttag	tagcaacttt	ttttttcata	tgctactttg	8280
cgtgttttgt	tgtgaaactg	gaaataaacg	ttaatTTTTA	ggtataaat	ttcaaaaaat	8340
gtaacaggg	cactcagcct	ctcttctggg	aattatgccc	atgacactgt	catttgagg	8400
ccttctttta	aattccactt	gggcagttta	agaacataaa	atgactttct	tagaagctta	8460
cctgaaactt	aaattaacca	caatcattaa	acattcccta	tgtcaataat	ttgactttcc	8520
tactcaaagt	tttttaaggc	atcagttttg	tctagcgtgg	tttttttctt	tagaaaccat	8580
gttggttatg	tgtgaattgc	ccatcttttt	acaatctctg	ctcaataagt	ttatacaatg	8640
agtctctggg	aagagacaga	cgtgggagtg	aaaatatttc	tccttaacca	cagggaaggga	8700
ttttttacaa	tgccttttagc	tgcggatacc	gagggtacct	cacccagcag	gaaggagagg	8760
gaactatact	tgggctaaac	actttcataa	actacttctc	atggaaaaga	aaatccaaat	8820
agtggaaatt	cttttaaaat	atccatgtgc	cttgagatag	aagaaagccc	tttcgtttta	8880
gaaaaatgca	cttaaaaatta	atgaataacct	tgtgatccaa	aaacattttta	tacatatagc	8940

ttcaggtgct	ttgaagtgga	gtgaacttct	atttataaag	tgtgttgccg	tttattatat	9000
agtattatgc	atttacattg	atgatcaaag	aacattgtat	ctgtgcaggc	atgggttccg	9060
aaaaggctga	aaaattccag	gtgagccgtg	gcaacaacct	ctaaaggatc	taggaacctt	9120
aagaggatct	gcctttttatt	taatagaaat	cttagaaaca	aaaataactg	acatggcttg	9180
aatgtcaatt	gtttaaaaaa	aaaaaaaaaa	aggaaaaaaa	atctattgtg	tggtcaggca	9240
gttatttttta	tcatctaggc	ataatttttta	ccaaagaaac	aaaacaatca	ataatgttat	9300
aaaagccact	tatactctga	gcttgaaaca	actgctttat	gccacaaaat	tcctattgct	9360
gtctccgtta	gtgactaatt	caatatgtcc	tgaatgtcaa	cgtatttttta	ttactcagct	9420
aaagttggct	ttgctggatt	aaatgtcatt	taaaatgatc	aattggcagc	ttgtttgggg	9480
ttgttttcac	atztatgaaa	ggaaaagttt	gccggataca	aatgttcttg	aagctgatag	9540
ggaaacgggtg	ttctctggta	agccctgccc	ttccttttgc	catctgataa	gtagataaca	9600
ttctaggtcc	tagttttagt	cctccgaaaa	accaacatgg	cagcccagtg	cagggttaagc	9660
ccttacattg	gagaaatggg	ctgggttcacg	tttcaactgt	ttatgagaag	tagaatgtac	9720
cattacagta	aaagagaagc	aacagaaaca	tgcagtgaag	acgcccattg	ttgtgggttag	9780
agaactgccc	gctttctttt	tgctctacag	taggcttctg	agtggagtgc	cttccgccta	9840
gagtcaagag	ggctgccatg	atgtcaccca	ccttcatatg	ggcaaaatgt	ctttatatga	9900
aactgtaaaa	gacaaccagg	tcgtttctta	attgctgaaa	tttattaaaa	tgaacacact	9960
agaaatcaca	ttcccaatcc	agaggaatcc	aatggcgctg	tcagcctatt	tgcaatggaa	10020
atggttgtaa	acctataggg	agacatagga	ggggctgcac	acaaactact	ttcgttcgtc	10080
ctgatttact	ggcttctttt	ccccctagag	atacagtctc	agtctgtcac	tctatcgccc	10140
aggcttagtg	cagtgggttg	atcatggctc	actgcagccc	caaacccttg	ggctcaagca	10200
attctcccac	ctcagctctc	caactagctg	ggattacagg	catgcaccac	cacgcctgga	10260
taatttttaa	attttttgta	gagatgaggt	ctcgttatgt	tgcttgggct	ggctctgaac	10320
tcccggaact	tcaagcaagt	ctactgcccc	tgcttcccaa	aacaaacatt	gggattataa	10380
ttataagcca	ccacacccaa	ccctaattta	caggcactgt	atgtggtaat	atgtgatttt	10440
gtcagatgtt	ttccagtggg	agagattatg	gaaaattaaa	atgtgtctgc	catttgatag	10500
taggacaaat	acttgaaata	ttaagccaca	gctgagttct	ggccttagtc	cttttggggc	10560
tgtcttgaca	aactgccgta	gactgggtag	ttgggtacga	atagatacgg	attgctccac	10620
agttctgggg	gctggggaga	tcaaggccct	ggcagatgag	gcactctggtg	agggcccact	10680
ttctgggttc	tagacagcac	cttcttgctg	tgtcttcact	tggtggaagg	gtgaggggtc	10740
tctctcaggc	ctctttttaa	agggcactaa	tcccactcac	aggggtgggg	cccccaagac	10800
ctaatacact	cccaaaggta	ccttggtagt	tagttaggat	ttcaacagat	gaatttgggg	10860
aggacatgaa	gattcagacc	acagcagatc	tctattttcc	ctttatagag	aaagtaattc	10920
aagacaagga	gatgcttaca	agggaaaaag	acactttgcc	actttttact	gctttgctta	10980
gaaactagaa	tcatctcctc	tcaaatgcct	gtaaaacgag	ctagattatt	ctcagtctgc	11040
agtaggacac	tgattttctca	aggtacttaa	gatgcttggtg	ttgctcatct	tctccacacc	11100
cccacctcag	cccatccctc	ggcaatacag	aatgcagcca	tggcaagacg	gggtgggcaa	11160
tagaagtggc	tggacagctt	ctggtgttag	agtgggggtc	aaagtccagg	actatgggtg	11220
tgttgtttta	agaaggaggc	cacttgcctc	tttccaaaac	acaatgagtg	acacaccaca	11280
ttaatgttta	aacacagata	atacagaaga	aaggattcca	taagggatac	taaagattta	11340
gggctgctgt	acattttaatg	gtagttcctt	gaaagattaa	gcttctggaa	aatgccacag	11400
ttttctgcca	gtgtcttctg	ctattcaaaag	agaacgctgg	agttcagaaa	agatatactg	11460
agcaggtgta	ctttgttctg	gaaagtccta	agattttata	aacatacacc	cattaacgag	11520
tttctctgag	actagaaatt	gcattgggaa	gtgtgtcata	gcattgggtt	tgggggtcatg	11580
cacagccaag	aatcctgtgt	gtcattcata	agctgtgtcc	tcttgagtaa	tcatcaaacc	11640
ctctcagccc	cagcttctctg	atctataaaa	taggaatagc	aacagcacct	gcctcataag	11700
cggcgtaagg	gtcagatgta	accaggcttg	togaagccac	agcacagtac	ctacaaatag	11760
caccacactta	aataccggtg	ttatttttat	tactttctct	tcctctccgt	tatcactaat	11820
ataataatcc	tgtaaagtaa	gtgctgttat	tcccacttca	taagtgaggc	aacagaacct	11880
cagggaaggtt	aagaagcgtg	tccagggtgg	cccaactgaa	ttcccccttg	taaataatct	11940
cccagagaag	ggtgtatgtt	tctctgcaat	gcagatgtgt	tggctgtaat	atattccaag	12000
tctcaactgg	acactccctc	ttcaaatgtg	ccaggcctag	gccttgccca	aagtaaaaaa	12060
gaaagaacat	tgtagtgcag	gagtcagag	tgcaaatcct	tgtgacctca	ggcaagttat	12120
ttcaacctct	ctgaggatca	gaaataatac	aggtaaagtg	ccgagttcat	acttgtaatt	12180
cagtagtgtg	tcttccatca	ccagccattc	tgacaagtgc	ctataaaaag	tgggcatttc	12240
cagaacctg	cagtgaacac	ctggaaattg	gtgctgtctc	tcatctggag	gccagttaac	12300
ctttaactca	acctagaagg	cacacatctg	tcccagctg	cctctccagg	ttctgctgga	12360
gggcaaccac	acaccttcac	agcacacatc	cagaaagtca	tagaacaagg	ggaaggtgta	12420

151/299

```

catcatgtct tcttcttctt cttttttttt tttttttgag actgagtctc actttgtcac 12480
cgaggctgga gggcagtggt gcgatctcga ctcactgcaa ctccacctc ctgggttcag 12540
gcgattctcc tgcctcagtg tcctgagtag ctgggattac aggcacacgc caccatgcct 12600
ggctaagttt ttgtattttt agtagagacg gggtttcgcc acgttggtca ggctgggtctc 12660
aaactcctgg cctcaagtga tccacctgcc tcagcttccc aaagtgtctg gattacaggc 12720
gtgagccacc acgcccggcc gtgtcttctc ttttaattta ctagcccaca gccaaaaacc 12780
aaggcccaac accatgccta gtccatatta aatcacctaa cacttaataa aatatccatt 12840
gcctgactaa atgttcaaac atcagtctgc aagtggagaa agtgactttt gcactgggtt 12900
cctttctgcc atgatccact atatcaaaac attttttaaa gacctccaaa atgtgataga 12960
atgagaatat ctgtatctct ttttgaaacc atgctagcca cagttcccac agtcagagtc 13020
accaagccac atagtttttt ttttcccacc attttttact cctcactcct ttttgctgtg 13080
ttttagccta ccccagcctt ctcatcttta tccatccatc tcccaccaac accaggataa 13140
ccttttctact ccactatttt ttaccacaca gctctctctg taaccatcag gacctcctt 13200
ccacctttt ttcttccag cctgcattta acacacattc agagcccatt gattcagtta 13260
gaacttgcct cccgtctttc acatgggttc tgcccagggt taagtttggg tcacgaccgt 13320
ggacttctgg gtcactgtat catcatctgt ggaggaggc tgtcgctgg atcatctccg 13380
aggcctccgg cgagtcaaag gtcacacaac aggacctccc tccatctttc tgggcctccg 13440
tttcttcccg gtaaaacaag gaagttagtt agacaatcag tcaaccctaa ctaggcagaa 13500
gcagttgctg gattcttttt tgattcttct ggtagtgcc tcaacaagaa acattttcaa 13560
cagtgttttc ttgccctttt cctctgtag 13589

```

<210> 199

<211> 763

<212> DNA

<213> Homo sapiens

<400> 199

```

gaattcaggg ttttcttttc attttatttt catttggttca tgtgtttgta tttacatata 60
ttgtgcctga atattgtaca tgtatgtgac agttgtgtac tgtagaatca aaaactaatg 120
tctgtgaact gaactcttct tgaacttttt gttgtgtgtg ttattgttgc ttttggagat 180
agggtcttgc tctgtcacc aggtctggact gcagtggcac aatcacagct cactgcagcc 240
ttgagctcct ggtctcaagc aaccctccca cctcagcctc ccaagtagct ggggctgcag 300
gcatatgcta cctgactaat taaaaatttt tttttttttt tgtagagaca gggctctact 360
atttttacta gtttgccggg gccaaagccag tgttgaacta ctggcctcaa gtgatcctcc 420
caccttggcc tccccaaagt gcacccctac aggcatgagc cactgcactc agcctgaact 480
ttcgaaattt attttaaggg cccactttta aatgcttctt ttcagcagct aactttccag 540
cggatgcttc atgtggtgcc agccataaga cgaaaacaag agaagatccc aaagaaaata 600
gaaaaacaaa aaaagaaaaa tttgtcgaat cccagggtgga atctgaatca agtgtactta 660
atgattctcc ctttccagag gatgacagtg aagggtctaca ttccgacagc agagaagaga 720
aacaaaacac taaaagtgca agagagagag cagggcagga cat 763

```

<210> 200

<211> 198

<212> PRT

<213> Homo sapiens

<400> 200

```

Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
  1             5             10             15

Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
          20             25             30

Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
    35             40             45

```

152/299

Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
 50 55 60
 Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
 65 70 75 80
 Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
 85 90 95
 Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg
 100 105 110
 Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
 115 120 125
 Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
 130 135 140
 Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
 145 150 155 160
 Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
 165 170 175
 Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
 180 185 190
 Phe Arg Thr Leu Gly Leu
 195

<210> 201
 <211> 11204
 <212> DNA
 <213> Homo sapiens

<400> 201
 aggttcagag agactgtggg aatatggggg aattagaggc tatctgaggc tcttcaacac 60
 aataacccaa gaagctatatt aaatgctctt taaggatatt acataaatat tactattctc 120
 attgtgcttt tattttgtgt tatcatgatt ataattgaag tgtctactgt tactgcctcc 180
 tgatctttgc tagctatgga gcatggactg ggcttttaga gcagcagccc caaaggaacc 240
 taaacattaa agcagagctg ccctcaatgg tttaacctgt gtgactctgc ctatgacagc 300
 cccaccacc catcttcact ggatccaaat caggagcaag gccgttgggg tacctggtgg 360
 gggtgatgct gtcaggggag gagcccaaaa gggcaagctc aaatttgaat gtgaagggcc 420
 aatgcactgt cagactgaga cagagaacca tcattaattg aagtgaagatt tttctggcct 480
 gagacttgca gggaggcaag aagacactct ggacaccact atggacaggt aaagaggcag 540
 tcttctcgtg ggtgattgca ctggccttcc tctcagagca aatctgagta atgagactgg 600
 tagctatccc tttctctcat gtaactgtct gactgataag atcagcttga tcaatatgca 660
 tatatatatt ttgatctgtc tccttttctt ctattcagat cttatacgct gtcagcccaa 720
 ttctttctgt ttcagacttc tcttgatttc cctcttttcc atgtggcaaa agaagtagtg 780
 cgtacaatgt actgattcgt cctgagattt gtaccatggg tgaaactaat ttatggtaat 840
 aatattaaca tagcaaactt ttagagactc aaatcatgaa aaggtaatag cagtactgta 900
 ctaaaaaagg tagtgctaatt ttctgtaata attttgtaaa tattcaacag taaaacaact 960
 tgaagacaca ctttcctagg gaggcgttac tgaaataatt tagctatagt aagaaaattt 1020
 gtaatttttag aaatgccaa g cattctaaat taattgcttg aaagtcacta tgattgtgtc 1080
 cattataagg agacaaattc attcaagcaa gttatttaaat gttaaaggcc caattgtag 1140
 gcagttaatg gcacttttac tattaactaa tctttccatt tggtcagacg tagcttaact 1200
 tacctcttag gtgtgaattt ggtaaaggtc ctcataatgt ctttatgtgc agtttttgat 1260

aggttattgt catagaactt attctattcc tacatttatg attactatgg atgtatgaga 1320
ataacaccta atccttatac tttacotcaa ttttaactct ttataaagaa cttacattac 1380
agaataaaga ttttttaaaa atatatTTTT ttgtagagac aggggtcttag cccagccgag 1440
gctggtctct aagtcctggc ccaagcgatc ctctgcttg ggcctccta agtgctgaa 1500
ttatagacat gagccatcac atccaatata cagaataaag atttttaatg gaggatttaa 1560
tgttcttcag aaaattttct tgaggtcaga caatgtcaaa tgtctcctca gtttactctg 1620
agattttgaa aacaagtctg agctataggt ccttgtgaag ggtccattgg aaatacttgt 1680
tcaaagtaaa atggaaagca aaggtaaaat cagcagttga aattcagaga aagacagaaa 1740
aggagaaaag atgaaattca acaggacaga agggaaatat attatcatta aggaggacag 1800
tatctgtaga gctcattagt gatggcaaaa tgacttgggtc aggattattt ttaacccgct 1860
tgtttctggg ttgcacggct ggggatgcag ctagggttct gcctcagggg gcacagctgt 1920
ccagagcagc tgtcagcctg caagcctgaa acactccctc ggtaaagtcc ttcctactca 1980
ggacagaaat gacgagaaca gggagctgga aacaggcccc taaccagaga agggaagtaa 2040
tggatcaaca aagtttaacta gcaggtcagg atcacgcaat tcatttcact ctgactggta 2100
acatgtgaca gaaacagtgt aggtcttattg tattttcatg tagagtagga ccaaaaaatc 2160
caccctaaagt cctttatcta tgccacatcc tcttatcta tacttcagg acactttttc 2220
ttccttatga taaggctctc tctctctcca cacacacaca cacacacaca cacacacaca 2280
cacacacaca cacaacacaca cccccgcca accaagggtgc atgtaaaaag atgtagattc 2340
ctctgccttt ctcatctaca cagccagga gggtaagtta atataagagg gatttattgg 2400
taagagatga tgcttaatct gtttaacact gggcctcaaa gagagaattt cttttcttct 2460
gtacttatta agcacctatt atgtgttgag cttatatata caaagggtta ttatatgcta 2520
atatagtaat agtaattggtg gttggtacta tggaattac cataaaaaat attatccttt 2580
taaaataaag ctaattatta ttggtctttt tttagtattc attttatgtt ttttatgttt 2640
ttgatttttt aaaagacaat ctccctgtgt taccaggct ggagtgcagt ggtgcaatca 2700
tagctttctg cagtcttgaa ctctgggt caagcaatcc tcctgccttg gcctcccaa 2760
gtgttgggat acagtcata gccactgcct ctggcctagg atccatttag attaaaatat 2820
gcattttaaa ttttaaaata atatggctaa tttttacctt atgtaatgtg tatactggta 2880
ataaatctag tttgctgcct aaagttaaaa gtgctttcca ataagcttca tgtacgtgag 2940
gggagacatt taaagtgaat cagacagcca ggtgtggtgg ctacgcctg taatcccagc 3000
actctgggag gctgaggtgg gtggtcgt tgagcctgg agttcaagac cagcctgagc 3060
aacatggcaa aacctgttt ctataacaaa aattagccgg gcattggtgg atgtgctgt 3120
gggtccagct actagggggc tgaggcagga gaatctttgg agcccaggag gtcaaggctg 3180
cactgagcag tgcttgccgc actgcactcc agcctgggtg acaggaccag acctgctc 3240
aaaaaaataa gaagaaaaat taaaaataa tggaaacaac tacaaagagc tgttgccta 3300
gatgagctac ttagttaggc tgatattttg gtatttaact tttaaagtca gggctgtgca 3360
cctgcactac attattaaaa tatcaattct caatgtatat ccacacaaag actggtacgt 3420
gaatgttcat agtaocttta ttcacaaaac ccaaagtag agactatcca aatatccatc 3480
aacaagtgaat caaataaaca aaatgtgcta tatccatgca atggaatacc acctgcagt 3540
acaaaggaag aagctacttg gggatgaatc ccaaagtcac gacgctaaat gaaagagtc 3600
gacatgaagg aggagataat gtatgccata cgaaattcta gaaaatgaaa gtaacttata 3660
gtttacagaaa gcaaatcagg gcaggcatag aggtcacac ctgtaatccc agcactttga 3720
gaggccacgt gggaagattg ctagaactca ggagttcaag accagcctgg gcaacacagt 3780
gaaactccat tctccacaaa aatgggaaaa aaagaaagca aatcagtggg tgtcctgtgg 3840
ggaggggaag gactgcaaa agggaagaag ctctgggtgg gtgaggggtg tgattcagg 3900
tctgtatcct gactgtggta gcagtttggg gtgtttacat ccaaaaatat tcgtagaatt 3960
atgcatctta aatgggtgga gtttactgta tgtaaattat acctcaatgt aagaaaaat 4020
aatgtgtaag aaaagtttca attctcttgc cagcaaacgt tattcaaat cctgagccct 4080
ttacttcgca aattctctgc acttctgccc cgtaccatta ggtgacagca ctactccac 4140
aaattggata aatgcatttc tggaaaagac tagggacaaa atccaggcat cacttgtgct 4200
ttcatatcaa ccacgtgtga cagctgtgtg tggctgtctg agctgcaatg gggactcttg 4260
atttctttta ggaaacttgg gttaccagag tatttccaca aatgctattc aaattagtgc 4320
ttatgatatg caagacactg tgctaggagc cagaaaacaa agaggaggag aaatcagtca 4380
ttatgtggga acaacatagc aagatattta gatcattttg actagttaaa aaagcagcag 4440
agtacaaaat cacacatgca atcagtataa tccaaatcat gtaaatatgt gcctgtaga 4500
agactagagg aataaacaca agaactttaa cagtcattgt cattagacac taagtcta 4560
tattattatt agacactatg atatttgaga tttaaaaaat ctttaatat ttaaaattta 4620
gagctcttct atttttccat agtattcaag tttgacaatg atcaagtatt actcttct 4680
tttttttttt tttttttttt tttgagatgg agttttgggtc ttgttgccca tgctggagt 4740

gaatggcatg	accatagctc	actgcaacct	ccacctcctg	ggttcaagca	aagctgtcgc	4800
ctcagcctcc	cggttagatg	ggattacagg	cgcccaccac	cacactcggc	taatgtttgt	4860
atthtttagta	gagatggggg	ttcaccatgt	tgccaggct	ggtctcaaac	tcctgacctc	4920
agaggatcca	cctgcctcag	cctcccaaaag	tgtcgggatt	acagatgtag	gccactgcgc	4980
ccggccaagt	attgctctta	tacattaaaa	aacagggtgtg	agccactgcg	cccagccagg	5040
tattgctctt	atacatataa	aaataggccg	gtgcagtggc	tcacgcctgt	aatcccagca	5100
ctttgggaag	ccaaggcggg	cagaacaccc	gaggtcagga	gtccaaggcc	agcctggcca	5160
agatggtgaa	accccgctct	tattaaaaat	acaaacatta	cctgggcatg	atggtgggcg	5220
cctgtaatcc	cagctactca	ggagggtgag	gcaggaggat	ccgcggagcc	tggcagatct	5280
gcctgagcct	gggaggttga	ggctacagta	agccaagatc	atgccagtat	acttcagcct	5340
gggcgacaaa	gtgagaccgt	aacaaaaaaa	aaaaaattta	aaaaaagaaa	tttagatcaa	5400
gatccaactg	taaaaagtgg	cctaaacacc	acattaaaga	gtttggagtt	tattctgcag	5460
gcagaagaga	accatcaggg	ggtcttcagc	atgggaatgg	catggtgcac	ctggtttttg	5520
tgagatcatg	gtggtgacag	tgtggggaat	gttatttttg	agggactgga	ggcagacaga	5580
ccggttaaaa	ggccagcaca	acagataagg	aggaagaaga	tgagggcttg	gaccgaagca	5640
gagaagagca	aacagggaag	gtacaaattc	aagaaatatt	gggggggtttg	aatcaacaca	5700
tttagatgat	taattaaata	tgaggactga	ggaataagaa	atgagtcaag	gatggttcca	5760
ggctgctagg	ctgcttacct	gaggtggcaa	agtcgggagg	agtggcagtt	taggacaggg	5820
ggcagttgag	gaatattgtt	ttgatcattt	tgagtttgag	gtacaagttg	gacacttagg	5880
taaagactgg	aggggaaatc	tgaatatata	attatgggac	tgaggaacaa	gtttatttta	5940
ttttttgttt	cgttttcttg	ttgaagaaca	aatttaattg	taatcccaag	tcacagcat	6000
ctagaagaca	gtggcaggag	gtgactgtct	tgtggtaag	ggtttggggt	ccttgatgag	6060
tatctctcaa	ttggccttaa	atataagcag	gaaaaggagt	ttatgatgga	ttccaggctc	6120
agcagggctc	aggagggctc	aggcagccag	cagaggaagt	cagagcatct	tctttgggtt	6180
agcccaagta	atgacttcct	taaaaagctg	aaggaaaatc	cagagtgacc	agattataaa	6240
ctgtactctt	gcattttctc	tccctcctct	caccacagc	ctcttgatga	accggaggaa	6300
gtttctttac	caattcaaaa	atgtccgctg	ggctaagggt	cggcgtgaga	cctacctgtg	6360
ctacgtagtg	aagaggcgtg	acagtgtctc	atccttttca	ctggactttg	gttatcttcg	6420
caataaggta	tcaattaaag	tcagctttgc	aagcagttta	atggtcaact	gtgagtgett	6480
ttagagccac	ctgctgatgg	tattacttcc	atcctttttt	ggcattttgtg	tctctatcac	6540
attcctcaaa	tccttttttt	tatttctttt	tccatgtcca	tgcaccata	ttagacatgg	6600
cccaaaatat	gtgatttaat	tcctccccag	taatgctggg	caccctaata	ccactccttc	6660
cttcagtgcc	aagaacaact	gtcctccaaac	tgtttaccag	ctttcctcag	catctgaatt	6720
gcctttgaga	ttaattaagc	taaaagcatt	tttatatggg	agaatattat	cagcttgtcc	6780
aagcaaaaat	tttaaatgtg	aaaaacaaat	tgtgtcttaa	gcatttttga	aaattaagga	6840
agaagaatth	gggaaaaaat	taacgggtgg	tcaattctgt	tttccaaatg	atttcttttc	6900
cctcctactc	acatgggtcg	taggccagtg	aatacattca	acatgggtgat	cccagaaaa	6960
ctcagagaag	cctcggctga	tgatttaatta	aattgatctt	toggctaccc	gagagaatta	7020
catttccaag	agacttcttc	acaaaaatcc	agatgggttt	acataaactt	ctgcccattg	7080
gtattctctc	tctcctaaca	cgctgtgacg	tctgggcttg	gtggaatctc	aggggaagcat	7140
ccgtgggggtg	gaagggtcatc	gtctggctcg	ttgtttgatg	gttatattac	catgcaattt	7200
tctttgccta	catttgtatt	gaatacatcc	caatctcctt	cctattcggg	gacatgacac	7260
attctatttc	agaaggcttt	gatttttatca	agcactttca	tttacttctc	atggcagtg	7320
ctattacttc	tcttacaata	cccactctgtc	tgctttacca	aaatctattt	ccccttttca	7380
gatcctccca	aatggtcctc	ataaaactgtc	ctgcctccac	ctagtgggtcc	aggtatatth	7440
ccacaatgth	acatcaacag	gcacttctag	ccattttcct	tctcaaaagg	tgcaaaaagc	7500
aacttcataa	acacaaatta	aatcttcggg	gaggtagtgt	gatgctgctt	cctcccaact	7560
cagcgcaact	cgtcttcttc	attccacaaa	aacctatagc	cttccttcac	tctgcaggac	7620
tagtgctgcc	aagggttcag	ctctacctac	tgggtgtgctc	ttttgagcaa	gttgcttagc	7680
ctctctgtaa	cacaaggaca	atagctgcaa	gcaccccaa	agatcattgc	aggagacaat	7740
gactaaggct	accagagccg	caataaaaagt	cagtgaattt	tagcgtgggtc	ctctctgtct	7800
ctccagaacg	gctgccacgt	ggaattgtctc	ttcctccgct	acatctcgga	ctgggacctc	7860
gaccctggcc	gctgctaccg	cgtcacctgg	ttcacctcct	ggagccctcg	ctacgactgt	7920
gcccagacatg	tggccgactt	tctgcgaggg	aaccccaacc	tcagtctgag	gatcttcacc	7980
gcgcgcctct	acttctgtga	ggaccgcaag	gctgagcccg	aggggctgcg	gcggctgcac	8040
cgcgccgggg	tgcaaatagc	catcatgacc	ttcaaagggtg	cgaaggggcc	ttccgcgcag	8100
gcgcagtga	gcagcccgca	ttcgggattg	cgatgcggaa	tgaatgagtt	agtggggaag	8160
ctcgagggga	agaagtgggc	ggggattctg	gttcacctct	ggagccgaaa	ttaaagatta	8220

155/299

gaagcagaga	aaagagtga	tggctcagag	acaaggcccc	gaggaaatga	gaaaatgggg	8280
ccagggttgc	ttctttcccc	togatttgga	acctgaactg	tottctaccc	ccatatcccc	8340
gccttttttt	cctttttttt	ttttttgaag	attattttta	ctgctggaat	actttttag	8400
aaaaccacga	aagaactttc	aaagcctggg	aagggtgca	tgaaaattca	gttcgtctct	8460
ccagacagct	tcggcgcatc	cttttggtaa	ggggcttcct	cgctttttta	attttctttc	8520
tttctctaca	gtcttttttg	gagtttcgta	tatttcttat	attttcttat	tgttcaatca	8580
ctctcagttt	tcattctgat	aaaactttat	ttctcctcca	catcagcttt	ttcttctgct	8640
gtttcaccat	tcagagccct	ctgctaaggt	tccttttccc	tcctttttct	ttcttttggt	8700
gtttcacatc	tttaaatttc	tgtctctccc	cagggttgcg	tttcttccct	ggtcagaatt	8760
cttttctcct	tttttttttt	tttttttttt	ttttttaaac	aaacaaacaa	aaaacccaaa	8820
aaaactcttt	cccaattttac	tttcttccaa	catgttacaa	agccatccac	tcagtttaga	8880
agactctccg	gccccaccga	cccccaacct	cgttttgaag	ccattcactc	aatttgcttc	8940
ttcttttctc	tcagagccct	gtatgaggtt	gatgacttac	gagacgcatt	tcgtactttg	9000
ggactttgat	agcaacttcc	aggaatgtca	cacacgatga	aatatctctg	ctgaagacag	9060
tggataaaaa	acagtccttc	aagtcttctc	tgtttttatt	cttcaactct	cactttctta	9120
gagtttacag	aaaaaatatt	tatatacgac	tctttaaaaa	gatctatgtc	ttgaaaatag	9180
agaaggaaca	caggctctggc	cagggacgtg	ctgcaattgg	tgcagttttg	aatgcaacat	9240
tgtcccctac	tgggaataac	agaactgcag	gacctgggag	catcctaaag	tgtcaacgtt	9300
tttctatgac	tttttaggtag	gatgagagca	gaaggtagat	cctaaaaagc	atgggtgagag	9360
gatcaaattg	ttttatatca	acatccttta	ttatttgatt	catttgagtt	aacagtggtg	9420
ttagtgatag	atttttctat	tcttttccct	tgacgtttac	tttcaagtaa	cacaaactct	9480
ttcatcaggc	catgatctat	aggacctcct	aatgagagta	tctgggtgat	tgtgacccca	9540
aaccatctct	ccaaagcatt	aatatccaat	catgcgctgt	atgttttaat	cagcagaagc	9600
atgtttttat	gtttgtacaa	aagaagattg	ttatgggtgg	ggatggaggt	atagaccatg	9660
catggtcacc	ttcaagctac	tttaataaag	gatcttaaaa	tgggcaggag	gactgtgaac	9720
aagacaccct	aataatgggt	tgatgtctga	agtagcaa	cttctggaaa	cgcaaactct	9780
tttaaggaag	tccttaattt	agaaacaccc	acaaacttca	catatcataa	ttagcaaca	9840
attggaagga	agttgcttga	atgttgggga	gaggaatac	tattggctct	cgtgggtctc	9900
ttcatctcag	aaatgccaat	caggccaagg	tttctacat	tttgtatgtg	tgtgatgctt	9960
ctcccaaagg	tatattaact	atataagaga	gttgtagcaa	aacagaatga	taaagctgcg	10020
aaccgtggca	cacgctcata	gttctagctc	cttgggaggt	tgaggaggga	ggatggcttg	10080
aacacagggtg	ttcaaggcca	gcctgggcaa	cataacaaga	tcctgtctct	caaaaaaaaa	10140
aaaaaaaaaa	agaaagagag	agggccgggc	gtggtggctc	acgcctgtaa	tcccagcact	10200
ttgggaggcc	gagccgggcg	gatcacctgt	ggtcaggagt	ttgagaccag	cctggccaac	10260
atggcaaaac	cccgctctga	ctcaaatg	aaaaattagc	caggcgtggt	agcaggcacc	10320
tgtaatocca	gctacttggt	aggctgaggc	aggagaatcg	cttgaaccca	ggaggtggag	10380
gttcagtaa	gctgagatcg	tgcogttgca	ctccagcctg	ggcgacaaga	gcaagactct	10440
gtctcagaaa	aaaaaaaaaa	aaagagagag	agagagaaa	agaacaatat	ttgggagaga	10500
aggatgggga	agcattgcaa	ggaaattgtg	ctttatccaa	caaatgttaa	ggagccaata	10560
agggatccct	atttgcctct	tttgggtgtc	atttgcctct	aacaactgtc	tttgacagtg	10620
agaaaaatat	tcagaataac	catatccctg	tgcggttatt	acctagcaac	ccttgcaatg	10680
aagatgagca	gatccacagg	aaaacttgaa	tgcacaactg	tcttatttta	atcttattgt	10740
acataagttt	gtaaaagagt	taaaaattgt	tacttcatgt	attcatttat	attttatatt	10800
attttgcgtc	taatgatttt	ttattaacat	gatttccctt	tctgatatat	tgaaatggag	10860
tctcaaagct	tcataaattt	ataactttag	aatgatttct	aataacaacg	tatgtaattg	10920
taacattgca	gtaatgggtg	tacgaagcca	tttctcttga	tttttagtaa	acttttatga	10980
cagcaaat	gcttctggct	cactttcaat	cagttaaata	aatgataaat	aattttggaa	11040
gctgtgaaga	taaaatacca	aataaaataa	tataaaagt	atttatatga	agttaaaata	11100
aaaaatcagt	atgatggaat	aaacttgaga	gtccagaagt	tatcccatat	atctgtaatc	11160
aactaat	tcacaagggt	gtaaggacca	ttcaatggag	aaaa		11204

<210> 202

<211> 198

<212> PRT

<213> Homo sapiens

<400> 202

156/299

Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
 1 5 10 15
 Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
 20 25 30
 Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
 35 40 45
 Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
 50 55 60
 Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
 65 70 75 80
 Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
 85 90 95
 Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg
 100 105 110
 Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
 115 120 125
 Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
 130 135 140
 Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
 145 150 155 160
 Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
 165 170 175
 Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
 180 185 190
 Phe Arg Thr Leu Gly Leu
 195

<210> 203

<211> 2791

<212> DNA

<213> Homo sapiens

<400> 203

gaaccatcat taattgaagt gagatttttc tggcctgaga cttgcaggga ggcaagaaga 60
 cactctggac accactatgg acagcctctt gatgaaccgg aggaagtttc tttaaccaatt 120
 caaaaatgtc cgctgggcta agggtcggcg tgagacctac ctgtgctacg tagtgaagag 180
 gcgtgacagt gctacatcct tttcaactgga ctttggttat cttcgcaata agaacggctg 240
 ccacgtggaa ttgctcttcc tccgctacat ctcggaactgg gacctagacc ctggccgctg 300
 ctaccgogtc acctggttca cctcctggag cccctgctac gactgtgccc gacatgtggc 360
 cgactttctg cgaggggaacc ccaacctcag tctgaggatc ttcaccgcgc gcctctactt 420
 ctgtgaggac cgcaaggctg agcccagagg gctgcggcgg ctgcaccgcg ccgggggtgca 480
 aatagccatc atgaccttca aagattatct ttactgctgg aatacttttg tagaaaacca 540
 tgaagaagt ttcaaagcct gggaagggct gcatgaaaat tcagttcgtc tctccagaca 600
 gcttcggcgc atccttttgc cctgtatga ggttgatgac ttacgagacg catttctgtac 660
 tttgggactt tgatagcaac ttccaggaat gtcacacacg atgaaatata tctgctgaag 720

157/299

```

acagtggata aaaaacagtc cttcaagtct tctctgtttt tattcttcaa ctctcacttt 780
cttagagttt acagaaaaaa tttttatata cgactcttta aaaagatcta tgtcttgaaa 840
atagagaagg aacacaggtc tggccaggga cgtgctgcaa ttgggtgcagt tttgaatgca 900
acattgtccc ctactgggaa taacagaact gcaggacctg ggagcatcct aaagtgtcaa 960
cgtttttcta tgacttttag gtaggatgag agcagaaggt agatcctaaa aagcatgggtg 1020
agaggatcaa atgtttttat atcaacatcc tttattattt gattcatttg agttaacagt 1080
ggtgttagtg atagattttt ctattctttt cccttgacgt ttactttcaa gtaacacaaa 1140
ctcttccatc aggccatgat ctataggacc tcctaagtga agtatctggg tgattgtgac 1200
cccaaaccat ctctccaaag cattaatatc caatcatgcg ctgtatgttt taatcagcag 1260
aagcatgttt ttatgtttgt acaaaagaag attgttatgg gtggggatgg aggtatagac 1320
catgcatggg cacccttcaag ctactttaat aaaggatctt aaaatgggca ggaggactgt 1380
gaacaagaca ccctaataat gggttgatgt ctgaagtagc aaatcttctg gaaacgcaaa 1440
ctcttttaag gaagtcacct atttagaaac acccacaacac ttcacatatc ataattagca 1500
aacaattgga aggaagttgc ttgaatgttg gggagaggaa aatctatttg ctctcgtggg 1560
tctcttcatc tcagaaatgc caatcaggtc aagggttgct acattttgta tgtgtgtgat 1620
gcttctccca aagggtatatt aactatataa gagagttgtg acaaaacaga atgataaagc 1680
tgccaaccgt ggcacacgct catagtctta gctgcttggg aggttgagga gggaggatgg 1740
cttgaacaca ggtgttcaag gccagcctgg gcaacataac aagatcctgt ctctcaaaaa 1800
aaaaaaaaaa aaaaagaaag agagaggggc gggcgtgggtg gctcacgcct gtaatcccag 1860
cactttggga ggccgagccg ggcggatcac ctgtggtcag gagtttgaga ccagcctggc 1920
caacatggca aaaccccgtc tgtactcaaa atgcaaaaat tagccaggcg tggtagcagg 1980
cacctgtaat ccagctact tgggaggctg aggcaggaga atcgcttgaa ccaggagggt 2040
ggaggttgca gtaagctgag atcgtgccgt tgcactccag cctgggcgac aagagcaaga 2100
ctctgtctca gaaaaaaaaa aaaaaaagag agagagagag aaagagaaca atatttggga 2160
gagaaggatg gggaagcatt gcaaggaaat tgtgctttat ccaacaaaat gtaaggagcc 2220
aataagggat ccctatattgt ctcttttggg gtctatttgt ccctaacaac tgtctttgac 2280
agtgagaaaa atattcagaa taaccatatc cctgtgccgt tattacctag caacccttgc 2340
aatgaagatg agcagatcca caggaaaact tgaatgcaca actgtcttat tttaatctta 2400
ttgtacataa gtttgtaaaa gagttaaaaa ttgttacttc atgtattcat ttatatctta 2460
tattattttg cgtctaata ttttttatta acatgatttc cttttctgat atattgaaat 2520
ggagtctcaa agcttcataa attttataact ttagaaatga ttctaataac aacgtatgta 2580
attgtaacat tgcagtaatg gtgctacgaa gccatttctc ttgattttta gtaaaactttt 2640
atgacagcaa atttgcttct ggctcacttt caatcagtta aataaatgat aaataatttt 2700
ggaagctgtg aagataaaat accaaataaa ataataataa agtgatttat atgaagttaa 2760
aataaaaaat cagtatgatg gaataaactt g' 2791

```

<210> 204

<211> 198

<212> PRT

<213> Homo sapiens

<400> 204

```

Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
  1              5              10              15

Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
      20              25              30

Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
      35              40              45

Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
      50              55              60

Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
      65              70              75              80

```

158/299

Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
 85 90 95
 Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg
 100 105 110
 Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
 115 120 125
 Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
 130 135 140
 Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
 145 150 155 160
 Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
 165 170 175
 Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
 180 185 190
 Phe Arg Thr Leu Gly Leu
 195

<210> 205

<211> 2791

<212> DNA

<213> Homo sapiens

<400> 205

```

gaaccatcat taattgaagt gagatttttc tggcctgaga cttgcaggga ggcaagaaga 60
cactctggac accactatgg acagcctctt gatgaaccgg aggaagtttc tttaccaatt 120
caaaaatgtc cgctgggcta agggctcggcg tgagacctac ctgtgctacg tagtgaagag 180
gcgtgacagt gctacatcct ttccactgga ctttggttat cttcgcaata agaacggctg 240
ccacgtggaa ttgctcttcc tccgctacat ctcggactgg gacctagacc ctggccgctg 300
ctaccgcgtc acctggttca cctcctggag cccctgctac gactgtgccc gacatgtggc 360
cgactttctg cgagggaacc ccaacctcag tctgaggatc ttcaccgcgc gcctctactt 420
ctgtgaggac cgcaaggctg agcccgaggg gctgcggcgg ctgcaccgcg cgggggtgca 480
aatagccatc atgaccttca aagattattt ttactgctgg aatacttttg tagaaaacca 540
tgaaagaact ttcaaagcct gggaagggct gcatgaaaat tcagttcgtc tctccagaca 600
gcttcggcgc atccttttgc cctgtatga ggttgatgac ttacgagacg catttcgtac 660
tttgggactt tgatagcaac ttccaggaat gtcacacacg atgaaatatc tctgctgaag 720
acagtggata aaaaacagtc cttcaagtct tctctgtttt tattcttcaa ctctcacttt 780
cttagagttt acagaaaaaa tatttatata cgactcttta aaaagatcta tgtcttgaaa 840
atagagaagg aacacaggtc tggccaggga cgtgctgcaa ttggtgcagt tttgaatgca 900
acattgtccc ctactgggaa taacagaact gcaggacctg ggagcatcct aaagtgtcaa 960
cgtttttcta tgacttttag gtaggatgag agcagaaggc agatcctaaa aagcatgggt 1020
agaggatcaa atgtttttat atcaacatcc tttattattt gattcatttg agttaacagt 1080
ggtgttagtg atagattttt ctattctttt cctttgacgt ttactttcaa gtaacacaaa 1140
ctcttccatc aggccatgat ctataggacc tcctaattgag agtatctggg tgattgtgac 1200
cccaaaccat ctctccaaag cattaatatc caatcatgcy ctgtatgttt taatcagcag 1260
aagcatgttt ttatgtttgt acaaaaagaag attgttatgg gtggggatgg aggtatagac 1320
catgcatggt cacttcaag ctactttaat aaaggatcct aaaatgggca ggaggactgt 1380
gaacaagaca ccctaataat gggttgatgt ctgaagtagc aaatcttctg gaaacgcaaa 1440
ctcttttaag gaagtcccta atttagaaac acccacaacac ttcacatatc ataattagca 1500
aacaattgga aggaagtgc ttgaatgttg gggagaggaa aatctatttg ctctcgtggg 1560
tctcttcac tcagaaatgc caatcaggtc aagggttgct acattttgta tgtgtgtgat 1620

```

159/299

```

gtttctccca aaggtatatt aactatataa gagagttgtg acaaaacaga atgataaagc 1680
tgcgaaaccgt ggcacacgct catagttcta gctgcttggg aggttgagga gggaggatgg 1740
cttgaacaca ggtgttcaag gccagcctgg gcaacataac aagatcctgt ctctcaaaaa 1800
aaaaaaaaaa aaaaagaaag agagagggcc gggcgtggtg gctcacgcct gtaatcccag 1860
cactttggga ggccgagccg ggccggtcac ctgtggtcag gagtttgaga ccagcctggc 1920
caacatggca aaaccccgtc tgtactcaaa atgcaaaaat tagccaggcg tggtagcagg 1980
cacctgtaat cccagctact tgggaggctg aggcaggaga atcgcttgaa cccaggaggt 2040
ggaggttgca gtaagctgag atcgtgccgt tgcactccag cctgggcgac aagagcaaga 2100
ctctgtctca gaaaaaaaaa aaaaaaagag agagagagag aaagagaaca atatttggga 2160
gagaaggatg gggaagcatt gcaaggaaat tgtgctttat ccaacaaaat gtaaggagcc 2220
aataagggat ccctatttgt ctcttttggg gtctatttgt ccctaacaac tgtctttgac 2280
agtgagaaaa atattcagaa taaccatata cctgtgcoct tattacctag caacccttgc 2340
aatgaagatg agcagatcca caggaaaact tgaatgcaca actgtcttat tttaattcta 2400
ttgtacataa gtttgtaaaa gagttaaaaa ttgttacttc atgtattcat ttatatatta 2460
tattattttg cgtctaataa ttttttatta acatgatttc cttttctgat atattgaaat 2520
ggagtctcaa agcttcataa atttataact ttagaaatga ttctaataac aacgtatgta 2580
attgtaacat tgcagtaatg gtgctacgaa gccattttctc ttgattttta gtaaactttt 2640
atgacagcaa atttgcttct ggctcacttt caatcagtta aataaatgat aaataatttt 2700
ggaagctgtg aagataaaat accaaataaa ataataataa agtgatttat atgaagttaa 2760
aataaaaaat cagtatgatg gaataaactt g                                     2791

```

<210> 206

<211> 416

<212> PRT

<213> Homo sapiens

<400> 206

```

Pro Asn Ser Asn His Val Ala Ser Gly Ala Gly Glu Ala Ala Ile Glu
 1              5              10              15

Thr Gln Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro
          20              25              30

Pro Pro Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys
          35              40              45

Ser Ser Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly
          50              55              60

Phe Phe Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg
          65              70              75              80

Asp Lys Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr
          85              90              95

Cys Arg Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val
          100             105             110

Arg Asn Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys Pro Glu Cys
          115             120             125

Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys
          130             135             140

Val Arg Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly
          145             150             155             160

```

160/299

Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile
 165 170 175
 Asp Leu Trp Asp Lys Phe Ser Glu Leu Ser Thr Lys Cys Ile Ile Lys
 180 185 190
 Thr Val Glu Phe Ala Lys Gln Leu Pro Gly Phe Thr Thr Leu Thr Ile
 195 200 205
 Ala Asp Gln Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Ile
 210 215 220
 Leu Arg Ile Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe
 225 230 235 240
 Ser Asp Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe
 245 250 255
 Gly Pro Leu Thr Asp Leu Val Phe Ala Phe Ala Asn Gln Leu Leu Pro
 260 265 270
 Leu Glu Met Asp Asp Ala Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu
 275 280 285
 Ile Cys Gly Asp Arg Gln Asp Leu Glu Gln Pro Asp Arg Val Asp Met
 290 295 300
 Leu Gln Glu Pro Leu Leu Glu Ala Leu Lys Val Tyr Val Arg Lys Arg
 305 310 315 320
 Arg Pro Ser Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr
 325 330 335
 Asp Leu Arg Ser Ile Ser Ala Lys Gly Ala Glu Arg Val Ile Thr Leu
 340 345 350
 Lys Met Glu Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu
 355 360 365
 Glu Asn Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly
 370 375 380
 Gly Arg Asp Gly Gly Gly Leu Ala Pro Pro Pro Gly Ser Cys Ser Pro
 385 390 395 400
 Ser Leu Ser Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro
 405 410 415

<210> 207

<211> 1284

<212> DNA

<213> Homo sapiens

<400> 207

cccaacagca accacgtggc cagtggcgcc ggggaggcag ccattgagac ccagagcagc 60
 agttctgaag agatagtgcc cagccctccc tcgccacccc ctctaccccg catctacaag 120
 ccttgctttg tctgtcagga caagtctca ggctaccact atgggggtcag cgctgtgag 180

161/299

```

ggctgcaagg gcttcttccg ccgcagcatc cagaagaaca tgggtgtacac gtgtcaccgg 240
gacaagaact gcatcatcaa caaggtgacc cgaaccgct gccagtactg ccgactgcag 300
aagtgtcttg aagtgggcat gtccaaggag tctgtgagaa acgaccgaaa caagaagaag 360
aaggaggtgc ccaagcccga gtgctctgag agctacacgc tgacgccgga ggtggggggag 420
ctcattgaga aggtgcgcaa agcgcaccag gaaaccttcc ctgccctctg ccagctgggc 480
aaatacacta cgaacaacag ctcagaacaa cgtgtctctc tggacattga cctctgggac 540
aagttcagtg aactctccac caagtgcacg attagactg tggagtctgc caagcagctg 600
ccoggcttca ccacctcac catcgccgac cagatcaccg tcctcaaggc tgcctgcctg 660
gacatcctga tcctgcggat ctgcacgcgg tacacgcccg agcaggacac catgaccttc 720
tcggacgggc tgacctgaa ccggacccag atgcacaacg ctggcttcgg cccctcacc 780
gacctggtct ttgccttcgc caaccagctg ctgcccctgg agatggatga tgcggagacg 840
gggctgctca gcgccatctg cctcatctgc ggagaccgcc aggacctgga gcagccggac 900
cgggtggaca tgctgcagga gccgctgctg gaggcgctaa aggtctacgt gcggaagcgg 960
aggcccagcc gcccacat gttcccacg atgctaata agattactga cctgcgaagc 1020
atcagcgcca agggggtga gcgggtgatc acgctgaaga tggagatccc gggctccatg 1080
ccgctctca tccaggaaat gttggagaac tcagagggcc tggacactct gagcggacag 1140
ccgggggggtg gggggcggga cgggggtggc ctggccccc cgcaggcag ctgtagcccc 1200
agcctcagcc ccagctccaa cagaagcagc ccggccaccg actcccctg accgcccacg 1260
ccacatggac acagccctcg ccct                                     1284

```

<210> 208

<211> 797

<212> PRT

<213> Homo sapiens

<400> 208

```

Met Glu Pro Ala Pro Ala Arg Ser Pro Arg Pro Gln Gln Asp Pro Ala
  1              5              10             15

Arg Pro Gln Glu Pro Thr Met Pro Pro Pro Glu Thr Pro Ser Glu Gly
      20              25             30

Arg Gln Pro Ser Pro Ser Pro Ser Pro Thr Glu Arg Ala Pro Ala Ser
      35              40             45

Glu Glu Glu Phe Gln Phe Leu Arg Cys Gln Gln Cys Gln Ala Glu Ala
      50              55             60

Lys Cys Pro Lys Leu Leu Pro Cys Leu His Thr Leu Cys Ser Gly Cys
      65              70             75             80

Leu Glu Ala Ser Gly Met Gln Cys Pro Ile Cys Gln Ala Pro Trp Pro
      85              90             95

Leu Gly Ala Asp Thr Pro Ala Leu Asp Asn Val Phe Phe Glu Ser Leu
      100             105            110

Gln Arg Arg Leu Ser Val Tyr Arg Gln Ile Val Asp Ala Gln Ala Val
      115            120            125

Cys Thr Arg Cys Lys Glu Ser Ala Asp Phe Trp Cys Phe Glu Cys Glu
      130            135            140

Gln Leu Leu Cys Ala Lys Cys Phe Glu Ala His Gln Trp Phe Leu Lys
      145            150            155            160

His Glu Ala Arg Pro Leu Ala Glu Leu Arg Asn Gln Ser Val Arg Glu

```


162/299

				165					170					175	
Phe	Leu	Asp	Gly	Thr	Arg	Lys	Thr	Asn	Asn	Ile	Phe	Cys	Ser	Asn	Pro
			180					185					190		
Asn	His	Arg	Thr	Pro	Thr	Leu	Thr	Ser	Ile	Tyr	Cys	Arg	Gly	Cys	Ser
		195					200					205			
Lys	Pro	Leu	Cys	Cys	Ser	Cys	Ala	Leu	Leu	Asp	Ser	Ser	His	Ser	Glu
	210					215					220				
Leu	Lys	Cys	Asp	Ile	Ser	Ala	Glu	Ile	Gln	Gln	Arg	Gln	Glu	Glu	Leu
225					230					235					240
Asp	Ala	Met	Thr	Gln	Ala	Leu	Gln	Glu	Gln	Asp	Ser	Ala	Phe	Gly	Ala
				245					250					255	
Val	His	Ala	Gln	Met	His	Ala	Ala	Val	Gly	Gln	Leu	Gly	Arg	Ala	Arg
			260					265					270		
Ala	Glu	Thr	Glu	Glu	Leu	Ile	Arg	Glu	Arg	Val	Arg	Gln	Val	Val	Ala
		275					280					285			
His	Val	Arg	Ala	Gln	Glu	Arg	Glu	Leu	Leu	Glu	Ala	Val	Asp	Ala	Arg
	290					295					300				
Tyr	Gln	Arg	Asp	Tyr	Glu	Glu	Met	Ala	Ser	Arg	Leu	Gly	Arg	Leu	Asp
305					310					315					320
Ala	Val	Leu	Gln	Arg	Ile	Arg	Thr	Gly	Ser	Ala	Leu	Val	Gln	Arg	Met
				325					330					335	
Lys	Cys	Tyr	Ala	Ser	Asp	Gln	Glu	Val	Leu	Asp	Met	His	Gly	Phe	Leu
			340					345					350		
Arg	Gln	Ala	Leu	Cys	Arg	Leu	Arg	Gln	Glu	Glu	Pro	Gln	Ser	Leu	Gln
		355					360					365			
Ala	Ala	Val	Arg	Thr	Asp	Gly	Phe	Asp	Glu	Phe	Lys	Val	Arg	Leu	Gln
		370				375					380				
Asp	Leu	Ser	Ser	Cys	Ile	Thr	Gln	Gly	Lys	Ala	Ile	Glu	Thr	Gln	Ser
385					390					395					400
Ser	Ser	Ser	Glu	Glu	Ile	Val	Pro	Ser	Pro	Pro	Ser	Pro	Pro	Pro	Leu
				405					410					415	
Pro	Arg	Ile	Tyr	Lys	Pro	Cys	Phe	Val	Cys	Gln	Asp	Lys	Ser	Ser	Gly
			420					425					430		
Tyr	His	Tyr	Gly	Val	Ser	Ala	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg
		435					440					445			
Arg	Ser	Ile	Gln	Lys	Asn	Met	Val	Tyr	Thr	Cys	His	Arg	Asp	Lys	Asn
		450				455					460				
Cys	Ile	Ile	Asn	Lys	Val	Thr	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Leu
465					470					475					480

163/299

Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val Arg Asn Asp
 485 490 495
 Arg Asn Lys Lys Lys Lys Glu Val Pro Lys Pro Glu Cys Ser Glu Ser
 500 505 510
 Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys Val Arg Lys
 515 520 525
 Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly Lys Tyr Thr
 530 535 540
 Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile Asp Leu Trp
 545 550 555 560
 Asp Lys Phe Ser Glu Leu Ser Thr Lys Cys Ile Ile Lys Thr Val Glu
 565 570 575
 Phe Ala Lys Gln Leu Pro Gly Phe Thr Thr Leu Thr Ile Ala Asp Gln
 580 585 590
 Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Ile Leu Arg Ile
 595 600 605
 Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe Ser Asp Gly
 610 615 620
 Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe Gly Pro Leu
 625 630 635 640
 Thr Asp Leu Val Phe Ala Phe Ala Asn Gln Leu Leu Pro Leu Glu Met
 645 650 655
 Asp Asp Ala Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu Ile Cys Gly
 660 665 670
 Asp Arg Gln Asp Leu Glu Gln Pro Asp Arg Val Asp Met Leu Gln Glu
 675 680 685
 Pro Leu Leu Glu Ala Leu Lys Val Tyr Val Arg Lys Arg Arg Pro Ser
 690 695 700
 Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr Asp Leu Arg
 705 710 715 720
 Ser Ile Ser Ala Lys Gly Ala Glu Arg Val Ile Thr Leu Lys Met Glu
 725 730 735
 Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu Glu Asn Ser
 740 745 750
 Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly Gly Arg Asp
 755 760 765
 Gly Gly Gly Leu Ala Pro Pro Pro Gly Ser Cys Ser Pro Ser Leu Ser
 770 775 780

164/299

Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro
 785 790 795

<210> 209
 <211> 3036
 <212> DNA
 <213> Homo sapiens

<400> 209
 ctcccccttca gcttctcttc acgcactcca agatctaaac cgagaatcga aactaagctg 60
 ggggtccatgg agcctgcacc cgcccgatct ccgaggcccc agcaggaccc cgcccgccc 120
 caggagccca ccatgcctcc ccccgagacc ccctctgaag gccgccagcc cagccccagc 180
 cccagcccta cagagcgagc ccccgcttcg gaggaggagt tccagtttct gcgctgccag 240
 caatgccagg cggaagccaa gtgcccgaag ctgctgcctt gtctgcacac gctgtgctca 300
 ggatgccttg aggcgtcggg catgcagtgc cccatctgcc aggcgccttg gccctaggt 360
 gcagacacac ccgccctgga taacgtcttt ttcgagagtc tgcagcggcg cctgtcggtg 420
 taccggcaga ttgtggatgc gcaggtgtgt tgcacccgct gcaaagagtc ggccgacttc 480
 tgggtgctttg agtgcgagca gctcctctgc gccaaagtgt tcgaggcaca ccagtggttc 540
 ctcaagcacg agggccggcc cctagcagag ctgcgcaacc agtcggtgcg tgagtctctg 600
 gacggcaccc gcaagaccaa caacatcttc tgctccaacc ccaaccaccg caccctacg 660
 ctgaccagca tctactgccg aggatgttcc aagccgctgt gctgctcgtg cgcgctcctt 720
 gacagcagcc acagtgagct caagtgcgac atcagcgcag agatccagca gcgacaggag 780
 gagctggacg ccatgacgca ggcgtgcag gagcaggata gtgccttttg cgcggttcac 840
 gcgcagatgc acgcggccgt cggccagctg ggcgcgcgc gtgccgagac cgaggagctg 900
 atccgcgagc gcgtgcgcca ggtggtagct cacgtgcggg ctccaggagc cgagctgctg 960
 gaggctgtgg acgcgcggtt ccagcgcgac tacgaggaga tggccagtcg gctgggcccgc 1020
 ctggatgctg tgctgcagcg catccgcacg ggcagcgcgc tgggtgcagag gatgaagtgc 1080
 tacgcctcgg accaggaggt gctggacatg cacggtttcc tgcgccaggc gctctgcgcg 1140
 ctgcgccagg aggagcccca gagcctgcaa gctgcctgac gcaccgatgg ctccgacgag 1200
 ttcaagggtg gcctgcagga cctcagctct tgcatcacc aggggaaagc cattgagacc 1260
 cagagcagca gttctgaaga gatagtgcct agccctccct cgccaccccc tctaccccg 1320
 atctacaagc cttgctttgt ctgtcaggac aagtcctcag gctaccacta tggggtcagc 1380
 gcctgtgagg gctgcaaggc cttcttccgc cgcagcatcc agaagaacat ggtgtacacg 1440
 tgtcaccggg acaagaactg catcatcaac aaggtgacct ggaaccgctg ccagtactgc 1500
 cgactgcaga agtgctttga agtgggcatg tccaaggagt ctgtgagaaa cgaccgaaac 1560
 aagaagaaga aggaggtgcc caagcccag tgccttgaga gctacacgct gacgcggag 1620
 gtgggggagc tcattgagaa ggtgcgcaaa gcgcaccagg aaaccttccc tgccctctgc 1680
 cagctgggca aatacactac gaacaacagc tcagaacaac gtgtctctct ggacattgac 1740
 ctctgggaca agttcagtga actctccacc aagtgcacaa ttaagactgt ggagtctgcc 1800
 aagcagctgc ccggcttcac caccctcacc atcgccgacc agatcaccct cctcaaggct 1860
 gcctgcctgg acatcctgat cctgcggatc tgcacgcggt acacgcccga gcaggacacc 1920
 atgaccttct cggacgggct gaccctgaac cggaccagaa tgcacaacgc tggcttcggc 1980
 cccctcaccg acctggtctt tgcttctgcc aaccagctgc tgccctgga gatggatgat 2040
 gcggagacgg ggctgctcag gcctatctgc ctcatctgcg gagaccgcca ggacctggag 2100
 cagccggacc ggggtggacat gctgcaggag ccgctgctgg aggcgctaaa ggtctacgtg 2160
 cggaagcggg gggccagccg ccccccacatg tcccccaaga tgctaataaa gattactgac 2220
 ctgcgaagca tcagcgccta gggggctgag cgggtgatca cgctgaagat ggagatccc 2280
 ggctccatgc cgcctctcat ccaggaaatg ttggagaact cagagggcct ggacactctg 2340
 agcggacagc cggggggtgg ggggcgggac ggggggtggc tggccccccc gccaggcagc 2400
 ttagcctcca gcctcagccc cagctccaac agaagcagcc cggccacca ctcccgtga 2460
 ccgcccacgc cacatggaca cagccctcgc cctccgcccc ggcttttctc tgcccttcta 2520
 ccgaccatgt gaccccgcac cagccctgcc cccacctgcc ctcccgggca gtactgggga 2580
 ccttccctgg gggacgggga gggaggaggc agcgaactct tggacagagg cctggggcct 2640
 cagtggactg cctgctccca cagcctgggc tgacgtcaga ggcgaggcc aggaactgag 2700
 tgaggccctt ggtcctgggt ctcaggatgg gtctggggg cctcgtgttc atcaagacac 2760
 cctctgccc agtcaccac atcttcatca ccagcaaacg cctcccccac gctcccccac 2820
 cctcagaact cacaagccat tgctccccag ctggggaacc tcaacctccc cctgcctcgc 2880

165/299

gttggtgaca gagggggtgg gacaggggcg ggggggttccc cctgtacata ccctgccata 2940
ccaaccccag gtattaattc tcgctgggtt tgtttttatt ttaatttttt tgttttgatt 3000
tttttaataa gaattttcat tttaagcaaa aaaaaa 3036

<210> 210
<211> 99
<212> PRT
<213> Homo sapiens

<400> 210
Asp Val Ser Asn Thr Thr Thr Ala Gln Lys Arg Lys Cys Ser Gln Thr
1 5 10 15
Gln Cys Pro Arg Lys Val Ile Lys Met Glu Ser Glu Glu Gly Lys Glu
20 25 30
Ala Arg Leu Ala Leu Pro Ala Pro Gly Pro Tyr Ser Thr Pro Leu Arg
35 40 45
Thr Pro Leu Trp Asn Gly Ser Asn His Ser Ile Glu Thr Gln Ser Ser
50 55 60
Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro Pro Pro Leu Pro
65 70 75 80
Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser Gly Tyr
85 90 95

His Tyr Gly

<210> 211
<211> 296
<212> DNA
<213> Homo sapiens

<400> 211
gatgtctcca atacaacgac agcccagaag aggaagtgca gccagaccca gtgccccagg 60
aaggtcatca agatggagtc tgaggagggg aaggaggcaa ggttggctct ccccgccccg 120
ggtccgtact ccaccccgct ccggactccg ctttggaatg gctcaaacca ctccattgag 180
acccagagca gcagttctga agagatagtg cccagccctc cctcgccacc ccctctacc 240
cgcatctaca agccttgctt tgtctgtcag gacaagtcct caggctacca ctatgg 296

<210> 212
<211> 673
<212> PRT
<213> Homo sapiens

<400> 212
Met Asp Leu Thr Lys Met Gly Met Ile Gln Leu Gln Asn Pro Ser His
1 5 10 15
Pro Thr Gly Leu Leu Cys Lys Ala Asn Gln Met Arg Leu Ala Gly Thr
20 25 30
Leu Cys Asp Val Val Ile Met Val Asp Ser Gln Glu Phe His Ala His

166/299

35	40	45
Arg Thr Val Leu Ala Cys Thr Ser Lys Met Phe Glu Ile Leu Phe His		
50	55	60
Arg Asn Ser Gln His Tyr Thr Leu Asp Phe Leu Ser Pro Lys Thr Phe		
65	70	75 80
Gln Gln Ile Leu Glu Tyr Ala Tyr Thr Ala Thr Leu Gln Ala Lys Ala		
	85	90 95
Glu Asp Leu Asp Asp Leu Leu Tyr Ala Ala Glu Ile Leu Glu Ile Glu		
	100	105 110
Tyr Leu Glu Glu Gln Cys Leu Lys Met Leu Glu Thr Ile Gln Ala Ser		
	115	120 125
Asp Asp Asn Asp Thr Glu Ala Thr Met Ala Asp Gly Gly Ala Glu Glu		
	130	135 140
Glu Glu Asp Arg Lys Ala Arg Tyr Leu Lys Asn Ile Phe Ile Ser Lys		
145	150	155 160
His Ser Ser Glu Glu Ser Gly Tyr Ala Ser Val Ala Gly Gln Ser Leu		
	165	170 175
Pro Gly Pro Met Val Asp Gln Ser Pro Ser Val Ser Thr Ser Phe Gly		
	180	185 190
Leu Ser Ala Met Ser Pro Thr Lys Ala Ala Val Asp Ser Leu Met Thr		
	195	200 205
Ile Gly Gln Ser Leu Leu Gln Gly Thr Leu Gln Pro Pro Ala Gly Pro		
	210	215 220
Glu Glu Pro Thr Leu Ala Gly Gly Gly Arg His Pro Gly Val Ala Glu		
225	230	235 240
Val Lys Thr Glu Met Met Gln Val Asp Glu Val Pro Ser Gln Asp Ser		
	245	250 255
Pro Gly Ala Ala Glu Ser Ser Ile Ser Gly Gly Met Gly Asp Lys Val		
	260	265 270
Glu Glu Arg Gly Lys Glu Gly Pro Gly Thr Pro Thr Arg Ser Ser Val		
	275	280 285
Ile Thr Ser Ala Arg Glu Leu His Tyr Gly Arg Glu Glu Ser Ala Glu		
	290	295 300
Gln Val Pro Pro Pro Ala Glu Ala Gly Gln Ala Pro Thr Gly Arg Pro		
305	310	315 320
Glu His Pro Ala Pro Pro Pro Glu Lys His Leu Gly Ile Tyr Ser Val		
	325	330 335
Leu Pro Asn His Lys Ala Asp Ala Val Leu Ser Met Pro Ser Ser Val		
	340	345 350

167/299

Thr Ser Gly Leu His Val Gln Pro Ala Leu Ala Val Ser Met Asp Phe
 355 360 365
 Ser Thr Tyr Gly Gly Leu Leu Pro Gln Gly Phe Ile Gln Arg Glu Leu
 370 375 380
 Phe Ser Lys Leu Gly Glu Leu Ala Val Gly Met Lys Ser Glu Ser Arg
 385 390 395 400
 Thr Ile Gly Glu Gln Cys Ser Val Cys Gly Val Glu Leu Pro Asp Asn
 405 410 415
 Glu Ala Val Glu Gln His Arg Lys Leu His Ser Gly Met Lys Thr Tyr
 420 425 430
 Gly Cys Glu Leu Cys Gly Lys Arg Phe Leu Asp Ser Leu Arg Leu Arg
 435 440 445
 Met His Leu Leu Ala His Ser Ala Gly Ala Lys Ala Phe Val Cys Asp
 450 455 460
 Gln Cys Gly Ala Gln Phe Ser Lys Glu Asp Ala Leu Glu Thr His Arg
 465 470 475 480
 Gln Thr His Thr Gly Thr Asp Met Ala Val Phe Cys Leu Leu Cys Gly
 485 490 495
 Lys Arg Phe Gln Ala Gln Ser Ala Leu Gln Gln His Met Glu Val His
 500 505 510
 Ala Gly Val Arg Ser Tyr Ile Cys Ser Glu Cys Asn Arg Thr Phe Pro
 515 520 525
 Ser His Thr Ala Leu Lys Arg His Leu Arg Ser His Thr Gly Asp His
 530 535 540
 Pro Tyr Glu Cys Glu Phe Cys Gly Ser Cys Phe Arg Asp Glu Ser Thr
 545 550 555 560
 Leu Lys Ser His Lys Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys
 565 570 575
 Asn Gly Cys Asp Lys Lys Phe Ser Leu Lys His Gln Leu Glu Thr His
 580 585 590
 Tyr Arg Val His Thr Gly Glu Lys Pro Phe Glu Cys Lys Leu Cys His
 595 600 605
 Gln Arg Ser Arg Asp Tyr Ser Ala Met Ile Lys His Leu Arg Thr His
 610 615 620
 Asn Gly Ala Ser Pro Tyr Gln Cys Thr Ile Cys Thr Glu Tyr Cys Pro
 625 630 635 640
 Ser Leu Ser Ser Met Gln Lys His Met Lys Gly His Lys Pro Glu Glu
 645 650 655

168/299

Ile Pro Pro Asp Trp Arg Ile Glu Lys Thr Tyr Leu Tyr Leu Cys Tyr
 660 665 670

Val

<210> 213
 <211> 2197
 <212> DNA
 <213> Homo sapiens

<400> 213
 caggaagccc acccagcccc gccacgcaga gcccagaagg aaagaaagcc tcatgcctga 60
 gccgagggga gcaccatgga tctgacaaaa atgggcatga tccagctgca gaaccttagc 120
 caccacacgg ggctactgtg caaggccaac cagatgcggc tggccgggac tttgtgcgat 180
 gtggtcatca tgggtggacag ccaggagttc cacgcccacc ggacggtgct ggctgcacc 240
 agcaagatgt ttgagatcct cttccaccgc aatagtcaac actatacttt ggacttctc 300
 tcgcaaaaga ccttccagca gattctggag tatgcatata cagccacgct gcaagccaag 360
 gcggaggacc tggatgacct gctgtatgcg gccgagatcc tggagatcga gtacctggag 420
 gaacagtgcc tgaagatgct ggagaccatc caggcctcag acgacaatga cacggaggcc 480
 accatggccg atggcggggc cgaggaagaa gaggaccgca aggctcggta cctcaagaac 540
 atcttcatct cgaagcattc cagcgaggag agtgggtatg ccagtgtggc tggacagagc 600
 ctccctgggc ccatggtgga ccagagccct tcagtctcca cttcatttgg tctttcagcc 660
 atgagtccca ccaaggctgc agtggacagt ttgatgacca taggacagtc tctcctgcag 720
 ggaactcttc agccacctgc agggcccagag gagccaactc tggctggggg tgggcggcac 780
 cctgggggtg ctgaggtgaa gacggagatg atgcaggtgg atgaggtgcc cagccaggac 840
 agccctgggg cagccgagtc cagcatctca ggagggatgg gggacaaggt tgaggaaaga 900
 ggcaaaaggg ggcctgggac cccgactcga agcagcgtca tcaccagtgc tagggagcta 960
 cactatgggc gagaggagag tgccgagcag gtgccacccc cagctgaggc tggccaggcc 1020
 cccactggcc gacctgagca cccagcacc cgcctgaga agcatctggg catctactcc 1080
 gtgttgccca accacaaggc tgacgctgta ttgagcatgc cgtcttccgt gacctctggc 1140
 ctccacgtgc agcctgcctt ggctgtctcc atggacttca gcacctatgg ggggctgctg 1200
 ccccagggct tcatccagag ggagctgttc agcaagctgg gggagctggc tgtgggcatg 1260
 aagtcagaga gccggaccat cggagagcag tgcagcgtgt gtggggctga gcttctgat 1320
 aacgaggctg tggagcagca caggaagctg cacagtggga tgaagacgta cgggtgcgag 1380
 ctctgcggga agcggttcct ggatagtttg cggctgagaa tgcacttact ggctcattca 1440
 gcgggtgcca aagcctttgt ctgtgatcag tgcggtgcac agttttcgaa ggaggatgcc 1500
 ctggagacac acaggcagac ccatactggc actgacatgg ccgtcttctg tctgctgtgt 1560
 gggaagcgct tccaggcgca gagcgactg cagcagcaca tggaggtcca cgcgggcgtg 1620
 cgcagctaca tctgcagtga gtgcaaccgc accttccca gccacacggc tctcaaacgc 1680
 cacctgcgct cacatacagg cgaccacccc tacgagtgtg agttctgtgg cagctgcttc 1740
 cgggatgaga gcacactcaa gagccacaaa cgcacccaca cgggtgagaa accctacgag 1800
 tgcaatggct gtgacaagaa gttcagcctc aagcatcagc tggagacgca ctataggggtg 1860
 cacacagggtg agaagccctt tgagtgttaag ctctgccacc agcgtcccg ggactactcg 1920
 gccatgatca agcacctgag aacgcacaac ggcgctcgc cctaccagtg caccatctgc 1980
 acagagtact gccccagcct ctccctccatg cagaagcaca tgaagggcca caagcccagag 2040
 gagatcccg cgcactggag gatagagaag acgtacctct acctgtgcta tgtgtgaagg 2100
 gagggccg cgcgtggag cgagcgggga gccaggaaag aagagttgga gtgagatgaa 2160
 ggaaggacta tgacaaataa aaaaaaaaaa ggaattc 2197

<210> 214
 <211> 673
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Asp Leu Thr Lys Met Gly Met Ile Gln Leu Gln Asn Pro Ser His

169/299

1	5	10	15
Pro Thr Gly Leu Leu Cys Lys Ala Asn Gln Met Arg Leu Ala Gly Thr	20	25	30
Leu Cys Asp Val Val Ile Met Val Asp Ser Gln Glu Phe His Ala His	35	40	45
Arg Thr Val Leu Ala Cys Thr Ser Lys Met Phe Glu Ile Leu Phe His	50	55	60
Arg Asn Ser Gln His Tyr Thr Leu Asp Phe Leu Ser Pro Lys Thr Phe	65	70	75
Gln Gln Ile Leu Glu Tyr Ala Tyr Thr Ala Thr Leu Gln Ala Lys Ala	85	90	95
Glu Asp Leu Asp Asp Leu Leu Tyr Ala Ala Glu Ile Leu Glu Ile Glu	100	105	110
Tyr Leu Glu Glu Gln Cys Leu Lys Met Leu Glu Thr Ile Gln Ala Ser	115	120	125
Asp Asp Asn Asp Thr Glu Ala Thr Met Ala Asp Gly Gly Ala Glu Glu	130	135	140
Glu Glu Asp Arg Lys Ala Arg Tyr Leu Lys Asn Ile Phe Ile Ser Lys	145	150	155
His Ser Ser Glu Glu Ser Gly Tyr Ala Ser Val Ala Gly Gln Ser Leu	165	170	175
Pro Gly Pro Met Val Asp Gln Ser Pro Ser Val Ser Thr Ser Phe Gly	180	185	190
Leu Ser Ala Met Ser Pro Thr Lys Ala Ala Val Asp Ser Leu Met Thr	195	200	205
Ile Gly Gln Ser Leu Leu Gln Gly Thr Leu Gln Pro Pro Ala Gly Pro	210	215	220
Glu Glu Pro Thr Leu Ala Gly Gly Gly Arg His Pro Gly Val Ala Glu	225	230	235
Val Lys Thr Glu Met Met Gln Val Asp Glu Val Pro Ser Gln Asp Ser	245	250	255
Pro Gly Ala Ala Glu Ser Ser Ile Ser Gly Gly Met Gly Asp Lys Val	260	265	270
Glu Glu Arg Gly Lys Glu Gly Pro Gly Thr Pro Thr Arg Ser Ser Val	275	280	285
Ile Thr Ser Ala Arg Glu Leu His Tyr Gly Arg Glu Glu Ser Ala Glu	290	295	300
Gln Val Pro Pro Pro Ala Glu Ala Gly Gln Ala Pro Thr Gly Arg Pro	305	310	315
			320

170/299

Glu His Pro Ala Pro Pro Pro Glu Lys His Leu Gly Ile Tyr Ser Val
 325 330 335
 Leu Pro Asn His Lys Ala Asp Ala Val Leu Ser Met Pro Ser Ser Val
 340 345 350
 Thr Ser Gly Leu His Val Gln Pro Ala Leu Ala Val Ser Met Asp Phe
 355 360 365
 Ser Thr Tyr Gly Gly Leu Leu Pro Gln Gly Phe Ile Gln Arg Glu Leu
 370 375 380
 Phe Ser Lys Leu Gly Glu Leu Ala Val Gly Met Lys Ser Glu Ser Arg
 385 390 395 400
 Thr Ile Gly Glu Gln Cys Ser Val Cys Gly Val Glu Leu Pro Asp Asn
 405 410 415
 Glu Ala Val Glu Gln His Arg Lys Leu His Ser Gly Met Lys Thr Tyr
 420 425 430
 Gly Cys Glu Leu Cys Gly Lys Arg Phe Leu Asp Ser Leu Arg Leu Arg
 435 440 445
 Met His Leu Leu Ala His Ser Ala Gly Ala Lys Ala Phe Val Cys Asp
 450 455 460
 Gln Cys Gly Ala Gln Phe Ser Lys Glu Asp Ala Leu Glu Thr His Arg
 465 470 475 480
 Gln Thr His Thr Gly Thr Asp Met Ala Val Phe Cys Leu Leu Cys Gly
 485 490 495
 Lys Arg Phe Gln Ala Gln Ser Ala Leu Gln Gln His Met Glu Val His
 500 505 510
 Ala Gly Val Arg Ser Tyr Ile Cys Ser Glu Cys Asn Arg Thr Phe Pro
 515 520 525
 Ser His Thr Ala Leu Lys Arg His Leu Arg Ser His Thr Gly Asp His
 530 535 540
 Pro Tyr Glu Cys Glu Phe Cys Gly Ser Cys Phe Arg Asp Glu Ser Thr
 545 550 555 560
 Leu Lys Ser His Lys Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys
 565 570 575
 Asn Gly Cys Asp Lys Lys Phe Ser Leu Lys His Gln Leu Glu Thr His
 580 585 590
 Tyr Arg Val His Thr Gly Glu Lys Pro Phe Glu Cys Lys Leu Cys His
 595 600 605
 Gln Arg Ser Arg Asp Tyr Ser Ala Met Ile Lys His Leu Arg Thr His
 610 615 620

171/299

Asn Gly Ala Ser Pro Tyr Gln Cys Thr Ile Cys Thr Glu Tyr Cys Pro
 625 630 635 640

Ser Leu Ser Ser Met Gln Lys His Met Lys Gly His Lys Pro Glu Glu
 645 650 655

Ile Pro Pro Asp Trp Arg Ile Glu Lys Thr Tyr Leu Tyr Leu Cys Tyr
 660 665 670

Val

<210> 215
 <211> 2197
 <212> DNA
 <213> Homo sapiens

<400> 215
 caggaagccc acccagcccc gccacgcaga gcccagaagg aaagaaagcc tcatgcctga 60
 gccgagggga gcaccatgga tctgacaaaa atgggcatga tccagctgca gaaccctagc 120
 caccccaagg ggctactgtg caaggccaac cagatgcggc tggccgggac tttgtgcgat 180
 gtgggtcatca tgggtggacag ccaggagttc cacgcccacc ggacgggtgct ggccctgcacc 240
 agcaagatgt ttgagatcct cttccaccgc aatagtcaac actatacttt ggacttcttc 300
 tcgccaaaga ctttcagca gattctggag tatgcatata cagccacgct gcaagccaag 360
 gcggaggacc tggatgacct gctgtatgcg gccgagatcc tggagatcga gtacctggag 420
 gaacagtgcc tgaagatgct ggagaccatc caggcctcag acgacaatga cacggaggcc 480
 accatggccg atggcggggc cgaggaagaa gaggaccgca aggctcggta cctcaagaac 540
 atcttcatct cgaagcattc cagcgaggag agtgggtatg ccagtgtggc tggacagagc 600
 ctccctgggc ccatggtgga ccagagccct tcagtctcca cttcatttgg tctttcagcc 660
 atgagtccca ccaaggctgc agtggacagt ttgatgacca taggacagtc tctcctgcag 720
 ggaactcttc agccacctgc agggcccagag gagccaactc tggctggggg tgggcggcac 780
 cctgggggtg ctgaggtgaa gacggagatg atgcaggtgg atgaggtgcc cagccaggac 840
 agccctgggg cagccgagtc cagcatctca ggaggatgg gggacaaggt tgaggaaaga 900
 ggcaaagagg ggcctgggac cccgactcga agcagcgtca tcaccagtgc tagggagcta 960
 cactatgggc gagaggagag tgccgagcag gtgccacccc cagctgaggc tggccaggcc 1020
 cccactggcc gacctgagca cccagcacc cgcctgaga agcatctggg catctactcc 1080
 gtgttgccca accacaaggc tgacgctgta ttgagcatgc cgtcttccgt gacctctggc 1140
 ctccaagtg cgcctgcctt ggctgtctcc atggacttca gcacctatgg ggggctgctg 1200
 cccagggtc tcatccagag ggagctgttc agcaagctgg gggagctggc tgtgggcatg 1260
 aagtcagaga gccggacat cggagagcag tgcagcgtgt gtggggtcga gcttctgat 1320
 aacgaggctg tggagcagca caggaagctg cacagtggga tgaagacgta cgggtgcgag 1380
 ctctgcggga agcggttcct ggatagtttg cggctgagaa tgcacttact ggctcattca 1440
 gcgggtgcca aagcctttgt ctgtgatcag tgcggtgcac agttttcgaa ggaggatgcc 1500
 ctggagacac acaggcagac ccatactggc actgacatgg ccgtcttctg tctgctgtgt 1560
 gggaagcgct tccaggcgca gagcgcaactg cagcagcaca tggaggtcca cgcgggcgtg 1620
 cgcagctaca tctgcagtga gtgcaaccgc accttcccc gccacacggc tctcaaagc 1680
 cacctgcgct cacatacagg cgaccacccc tacgagtgtg agttctgtgg cagctgcttc 1740
 cgggatgaga gcacactcaa gagccacaaa cgcattccca cgggtgagaa accctacgag 1800
 tgcaatggct gtgacaagaa gttcagcctc aagcatcagc tggagacgca ctatagggtg 1860
 cacacagggt agaagccctt tgagtgttaag ctctgccacc agcgtctccg ggactactcg 1920
 gccatgatca agcacctgag aacgcacaaac ggcgcctcgc cctaccagtg caccatctgc 1980
 acagagtact gccccagcct ctctccatg cagaagcaca tgaagggcca caagcccag 2040
 gagatcccg cgcactggag gatagagaag acgtacctct acctgtgcta tgtgtgaagg 2100
 gaggcccgcg gcggtggagc cgagcgggga gccaggaaag aagagttgga gtgagatgaa 2160
 ggaaggacta tgacaaataa aaaaaaaaaa ggaattc 2197

<210> 216

172/299

<211> 29
<212> PRT
<213> Homo sapiens

<400> 216
Arg Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu Glu Met Glu Glu
1 5 10 15
Leu Leu Gln Glu Glu Thr Arg Gln Lys Leu Asn Val Ser
20 25

<210> 217
<211> 89
<212> DNA
<213> Homo sapiens

<400> 217
acgcgaattt gaagatagag acaggtctca tcgggaggaa atggaggagc tgcttcaaga 60
agaaaccgag cagaagctca acgtgtcta 89

<210> 218
<211> 26
<212> PRT
<213> Homo sapiens

<400> 218
Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu Glu Met Glu Phe Lys
1 5 10 15
Arg Ala Lys Ala Asn Leu Asp Lys Asn Lys
20 25

<210> 219
<211> 78
<212> DNA
<213> Homo sapiens

<400> 219
gaatttgaag atagagacag gtctcatcgg gaggaatgg agttcaagag ggccaaggcg 60
aacctagaca agaataag 78

<210> 220
<211> 34
<212> PRT
<213> Homo sapiens

<400> 220
Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu Glu Met Glu Val His
1 5 10 15
Glu Leu Glu Lys Ser Lys Arg Ala Leu Glu Thr Gln Met Glu Glu Met
20 25 30

Lys Thr

173/299

<210> 221
<211> 102
<212> DNA
<213> Homo sapiens

<400> 221
gaatttgaag atagagacag gtctcatcgg gaggaaatgg aggtccatga gctggagaag 60
tccaagcggg ccctggagac ccagatggag gagatgaaga cg 102

<210> 222
<211> 50
<212> PRT
<213> Homo sapiens

<400> 222
Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu Glu Met Glu Asn Glu
1 5 10 15
Val Glu Ser Val Thr Gly Met Leu Asn Glu Ala Glu Gly Lys Ala Ile
20 25 30
Lys Leu Ala Lys Asp Val Ala Ser Leu Ser Ser Gln Leu Gln Asp Thr
35 40 45
Gln Glu
50

<210> 223
<211> 152
<212> DNA
<213> Homo sapiens

<400> 223
gaatttgaag atagagacag gtctcatcgg gaggaaatgg agaatgaagt tgagagcgtc 60
acagggatgc ttaacgaggc cgaggggaag gccattaagc tggccaagga cgtggcgtcc 120
ctcagttccc agctccagga caccaggag tt 152

<210> 224
<211> 1353
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (941)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (1067)
<223> a, c, t, g, other or unknown

<220>

174/299

<221> modified_base

<222> (1077)

<223> a, c, t, g, other or unknown

<400> 224

```
cttggccaac atttctggagg cagtaaagaa agcttataga ataaccacat attagaactt 60
gtgaaggaga aaatatacat atatatatat gtatatatat agtctctcta ttaagtaatt 120
taccataagg ggtttaaata ggaatgtttt ctccaaagtg aatcttgaaa tcttggtgtt 180
tataattgtc aagcctcttt ttttaaaata gatttggtca acaggaagta tttttttcta 240
atTTTTtatt tatagacctt gtcaagcttc ttaattgtta aatattgtta taacaatata 300
tctgggcccgc gcgcggtggc tcaactcctgt aatcccagca ctttgggagg ccagggcggg 360
tgaatcacga ggtcaggaga ttgagacctt cctggctaac acaaagaaac ccatctcta 420
ctaaaaatac aaaaaattag ctgggagagg aggagggcgc ctgtagtccc agctactcgg 480
gaggcggagc ttgcggtgag ccaagatcgc gccactgcac tccagcgact ccgtctcaaa 540
aaaaaaaaaa aaaaaacatc tgagtcggta catggttggt agccgaggag aaaaacatct 600
cttccaaata cgcggatgag agggacagag ctgaggcaga agccaggagg aaggaaacca 660
aggccctgtc cctggctcgg gcccttgaag aggccttgga agccaaagag gaactcgagc 720
ggaccaacaa aatgctcaaa gccgaaatgg aagacctggt cagctccaag gatgacgtgg 780
gcaagaacgt aagtggctct ggggtggttt tctcgtccat gtttcgcctg cccaccctct 840
gtgctattca ccagtccatg cgaggctagc tcctggcctt tttcatagcg aactatcatc 900
ggaaatggaa ggagggtttt ggactggtgc aggggctaaa naggggctga gaatggcagt 960
cgaggatggg tctgagttgg ggggtccgag gataaggctg gggctctgaac tctcaggggt 1020
catcttgagt cccggccatg catcctgtgg gaggccaaag ccacctnccc tgatctncct 1080
gagggtgccgc tcacggtggg tttctcaatc gtcttcatga agttgagcct catagaatgg 1140
ggctgcccgc tctgcccgca ggtccatgag ctggagaagt ccaagcgggc cctggagacc 1200
cagatggagg agatgaagac gcagctggaa gagctggagg acgagctgca agccacggag 1260
gacgccaaac tgccgctgga agtcaacatg caggcgctca agggccagtt cgaaagggat 1320
ctccaagccc gggacgagca gaatgaggag aag                                     1353
```

<210> 225

<211> 744

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (326)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (614)

<223> a, c, t, g, other or unknown

<400> 225

```
gcccggctta aaatttagta tcttttagtg attgctagat ctctttgtca gtgagttaat 60
taatctaatt ggctgatagc agctgaggat gtccccaaga atacttgta gctaagagaa 120
gaaaatggag ggatataatg gataactgtt ttctttgatg ctgttgtaat tcttggtgatt 180
ttcatatatg tgaatacaag acttccacac catgcccttt ctttcggtat ctgtaaaatt 240
tagaagcttt aaaatgtata atgtacattt gttacatttc tgaacctttt tgctcatgct 300
ctttgttccc tgatgtagaa tggtcnattc tgtccgtcaa ggcccaacct gaatgttgct 360
attaaatgtc aggcctttcc tcagtctctg gggctctgaac tgctcagggg tcatcttgag 420
tcccggccat gcatcctgtg ggaggccaaa gccacctccc tgatctcctg aggtgccgct 480
cacggtgggt ttctcaatcg tcttcatgaa gttgagcctc atagaatggg gctgcccgct 540
ctgccggcag gtccatgagc tggagaagtc caagcgggccc ctggagaccc agatggagga 600
gatgaagacg cagntggaag agctggagga cgagctgcaa gccacggagg acgccaaact 660
gcggctggaa gtcaacatgc aggcgctcaa gggccagttc gaaagggatc tccaagcccc 720
```

175/299

ggacgagcag aatgaggaga agag

; 744

<210> 226

<211> 60

<212> DNA

<213> Homo sapiens

<400> 226

tctctgtgcc agtagtgggc atgtagagga ccctaataagg agtattcata ccagcagcag 60

<210> 227

<211> 25

<212> PRT

<213> Homo sapiens

<400> 227

Met	Pro	Arg	Phe	Gly	Phe	Gln	Ile	Gly	Val	Arg	Tyr	Glu	Asn	Lys	Lys
1				5				10					15		

Arg	Glu	Asn	Leu	Ala	Leu	Thr	Leu	Leu
		20				25		

<210> 228

<211> 300

<212> DNA

<213> Homo sapiens

<400> 228

agctctcctt	gcagcccgag	ctgaccctag	gcctccaccc	tggcaggaat	cccaatttgc	60
ctccacttag	tgagcggaag	aatgtgtac	agttgaaact	ccagcagcgc	cggacccggg	120
aagaactggg	gagccaagg	atcatgccgc	ggtttggtt	tcagatagga	gtaggtatg	180
agaacaagaa	gagagaaaac	ttggcgctga	ccctgttata	gtggttatag	tggtgtccct	240
aaagggagga	aatgatttca	gcaaaaactgg	ttgaacagcg	gatgaagata	tggaattcaa	300

<210> 229

<211> 43

<212> PRT

<213> Homo sapiens

<400> 229

Lys	Met	Arg	Lys	Met	Glu	Asp	Asn	Gln	Tyr	Ser	Glu	Ala	Glu	Leu	Ser
1				5				10					15		

Ser	Phe	Ser	Thr	Ser	His	Val	Pro	Glu	Glu	Leu	Lys	Gln	Pro	Leu	His
			20				25					30			

Arg	Lys	Ser	Lys	Ser	Gln	Val	Gln	Ile	Phe	Pro
	35						40			

<210> 230

<211> 916

<212> DNA

<213> Homo sapiens

176/299

<400> 230

```

aaaatgagga aaatggaaga taatcaatat tctgaagctg agctgtcttc ttttagtact 60
tcccatgtgc cagaggaact taagcagccg ttacacagaa agtccaaatc gcaggtagag 120
atcttcccat agtacagcat catgggtaca ttatgcatga aacgtacatt tcctttgatt 180
acaaaaaagc aaatattcta tctttgaaat attttagaat ccaaatgggg tcagatgcct 240
ttctaaaaat gttcataatc ttactgtatt tatgaccaa tccaaaatag ttaagcaaga 300
aagcaattaa tttagctgca ttctgtatag aaattttatg acaagcccca tcctacactt 360
atctttcctt gactttgcaa ttctcttact tttgtacagt tagttcatca tgtttgttta 420
caaatattta tgtattacct cagagtcatt ttccgtgtct atactttttg tcaatgtaat 480
tatattttta gattttttctg aaaagtgaat tctatttttt gtccccttct atgtctagta 540
aattgtagg ttagttaa tagcaagtca tctcatgttg taatttaata gtaaaatgag 600
gatcagaag gaagtgaagt gccaaaggc tacaccaact tactggcaga tttggaaata 660
aaacctgtca atttaaattc aacaaatgaa tgagtgaatg aatgggtactc aaatttatta 720
ggctctacaa cattgtatca gcactatggg aactaaaaat aaatctattt aagggtccat 780
aaatagcaat taaaagagcc tcagtgtttt tgttacaaaa taaaggaagt cgggtactttt 840
ttgtttgaca tccacactca accggattgt tcattcaggt caattaaaaa taaagaaact 900
tcctattacc aaaaaa                                     916

```

<210> 231

<211> 268

<212> PRT

<213> Homo sapiens

<400> 231

```

Met Phe Arg Met Leu Asn Ser Ser Phe Glu Asp Asp Pro Phe Phe Ser
 1             5             10             15

Glu Ser Ile Leu Ala His Arg Glu Asn Met Arg Gln Met Ile Arg Ser
      20             25             30

Phe Ser Glu Pro Phe Gly Arg Asp Leu Leu Ser Ile Ser Asp Gly Arg
      35             40             45

Gly Arg Ala His Asn Arg Arg Gly His Asn Asp Gly Glu Asp Ser Leu
      50             55             60

Thr His Thr Asp Val Ser Ser Phe Gln Thr Met Asp Gln Met Val Ser
      65             70             75             80

Asn Met Arg Asn Tyr Met Gln Lys Leu Glu Arg Asn Phe Gly Gln Leu
      85             90             95

Ser Val Asp Pro Asn Gly His Ser Phe Cys Ser Ser Ser Val Met Thr
      100            105            110

Tyr Ser Lys Ile Gly Asp Glu Pro Pro Lys Val Phe Gln Ala Ser Thr
      115            120            125

Gln Thr Arg Arg Ala Pro Gly Gly Ile Lys Glu Thr Arg Lys Ala Met
      130            135            140

Arg Asp Ser Asp Ser Gly Leu Glu Lys Met Ala Ile Gly His His Ile
      145            150            155            160

His Asp Arg Ala His Val Ile Lys Lys Ser Lys Asn Lys Lys Thr Gly
      165            170            175

```

177/299

Asp Glu Glu Val Asn Gln Glu Phe Ile Asn Met Asn Glu Ser Asp Ala
 180 185 190
 His Ala Phe Asp Glu Glu Trp Gln Ser Glu Val Leu Lys Tyr Lys Pro
 195 200 205
 Gly Arg His Asn Leu Gly Asn Thr Arg Met Arg Ser Val Gly His Glu
 210 215 220
 Asn Pro Gly Ser Arg Glu Leu Lys Arg Arg Glu Lys Pro Gln Gln Ser
 225 230 235 240
 Pro Ala Ile Glu His Gly Arg Arg Ser Asn Val Leu Gly Asp Lys Leu
 245 250 255
 His Ile Lys Gly Ser Ser Val Lys Ser Asn Lys Lys
 260 265

<210> 232
 <211> 1116
 <212> DNA
 <213> Homo sapiens

<400> 232
 gttatgtgtt cccgtccgta ctggaggcta gctcttgtcg cggccgcggc gagttaacat 60
 cgtttttcca atctgtccgc ggctgcccgc acccaagaca gagccagaat gttcaggatg 120
 ctgaacagca gttttgagga tgaccccttc ttctctgagt ccattcttgc acaccgagaa 180
 aatatgagac agatgataag aagtttttct gaaccctttg gaagagactt gctcagtatc 240
 tctgatggta gagggagagc tcataatcgt agaggacata atgatgggtga agattctttg 300
 actcatacag atgtcagctc tttocagacc atggaccaa tgggtgtcaaa tatgagaaac 360
 tatatgcaga aattagaaag aaacttcggt caactttcag tggatccaaa tggacattca 420
 ttttgtttct cctcagttat gacttattcc aaaataggag atgaaccgcc aaagggtttt 480
 caggcctcaa ctcaaactcg tcgagctcca ggaggaataa aggaaaccag gaaagcaatg 540
 agagattctg acagtggact agaaaaaatg gctattggtc atcatatcca tgaccgagct 600
 catgtcatta aaaagtcaaa gaacaagaag actggagatg aagaggtcaa ccaggagtgc 660
 atcaatatga atgaaagcga tgetcatgct tttgatgagg agtggcaaag tgagggtttg 720
 aagtacaaac caggacgaca caatctagga aacactagaa tgagaagtgt tggccatgag 780
 aatcctggct cccgagaact taaaagaagg gagaaacctc aacaaagtcc agccattgaa 840
 catggaagga gatcaaatgt tttgggggac aaactccaca tcaaaggctc atctgtgaaa 900
 agcaacaaaa aataaatagc catgcatttg atttgtttag ttttgattgt ttttaacagtt 960
 agtaatgggtg ctgggtaata agcataagac caatctcttg ctgttaaadc agttctgtcc 1020
 ttggcaactt tcttctgata tctgaatgtt catgaaggct ctagctttat attgtccctc 1080
 ttttaggaat aaaattttga ttttcaacaa aaaaaa 1116

<210> 233
 <211> 268
 <212> PRT
 <213> Homo sapiens

<400> 233
 Met Phe Arg Met Leu Asn Ser Ser Phe Glu Asp Asp Pro Phe Phe Ser
 1 5 10 15
 Glu Ser Ile Leu Ala His Arg Glu Asn Met Arg Gln Met Ile Arg Ser
 20 25 30

178/299

Phe Ser Glu Pro Phe Gly Arg Asp Leu Leu Ser Ile Ser Asp Gly Arg
 35 40 45
 Gly Arg Ala His Asn Arg Arg Gly His Asn Asp Gly Glu Asp Ser Leu
 50 55 60
 Thr His Thr Asp Val Ser Ser Phe Gln Thr Met Asp Gln Met Val Ser
 65 70 75 80
 Asn Met Arg Asn Tyr Met Gln Lys Leu Glu Arg Asn Phe Gly Gln Leu
 85 90 95
 Ser Val Asp Pro Asn Gly His Ser Phe Cys Ser Ser Ser Val Met Thr
 100 105 110
 Tyr Ser Lys Ile Gly Asp Glu Pro Pro Lys Val Phe Gln Ala Ser Thr
 115 120 125
 Gln Thr Arg Arg Ala Pro Gly Gly Ile Lys Glu Thr Arg Lys Ala Met
 130 135 140
 Arg Asp Ser Asp Ser Gly Leu Glu Lys Met Ala Ile Gly His His Ile
 145 150 155 160
 His Asp Arg Ala His Val Ile Lys Lys Ser Lys Asn Lys Lys Thr Gly
 165 170 175
 Asp Glu Glu Val Asn Gln Glu Phe Ile Asn Met Asn Glu Ser Asp Ala
 180 185 190
 His Ala Phe Asp Glu Glu Trp Gln Ser Glu Val Leu Lys Tyr Lys Pro
 195 200 205
 Gly Arg His Asn Leu Gly Asn Thr Arg Met Arg Ser Val Gly His Glu
 210 215 220
 Asn Pro Gly Ser Arg Glu Leu Lys Arg Arg Glu Lys Pro Gln Gln Ser
 225 230 235 240
 Pro Ala Ile Glu His Gly Arg Arg Ser Asn Val Leu Gly Asp Lys Leu
 245 250 255
 His Ile Lys Gly Ser Ser Val Lys Ser Asn Lys Lys
 260 265

<210> 234

<211> 1130

<212> DNA

<213> Homo sapiens

<400> 234

agtgaggcgt cgtccgtact ggaggctagc tcttgctcgcg gccgcggcga gttaacatcg 60
 tttttccaat ctgtccgcgg ctgccaccac ccaagacaga gccagaatgt tcaggatgct 120
 gaacagcagt tttgaggatg accccttctt ctctgagtcc attcttgac accgagaaaa 180
 tatgcgacag atgataagaa gtttttctga accctttgga agagacttgc tcagtatctc 240
 tgatggtaga gggagagctc ataatcgtag aggacataat gatggtgaag attctttgac 300

179/299

```

tcatacagat gtcagctctt tccagacaat ggaccaaagt gtgtcaaata tgagaaacta 360
tatgcagaaa ttagaaagaa acttcggtca actttcagtg gatccaaatg gacattcatt 420
ttgttcttcc tcagttatga cttattccaa aataggagat gaaccgcaa aggtttttca 480
ggcctcaact caaactcgtc gagctccagg aggaataaag gaaaccagga aagcaatgag 540
agattctgac agtggactag aaaaaatggc tattgggtcat catatccatg accgagctca 600
tgtcattaaa aagtcaaaga acaagaagac tggagatgaa gaggtcaacc aggagttcat 660
caatatgaat gaaagtgatg ctcatgcttt tgatgaggag tggcaaagtg aggttttgaa 720
gtacaaacca ggacgacaca atctaggaaa cactagaatg agaagtgttg gccatgagaa 780
tcctgggtcc cgagaactta aaagaaggga gaaacctcaa caaagtccag ccattgaaca 840
tggaaggaga tcaaatgttt tgggggacaa actccacatc aaaggctcat ctgtgaaaag 900
caacaaaaaa taaatagcca tgcatttgat ttgttttagt ttgattgttt taacagttag 960
taatggtgct gggtataaag cataagacca atctcttgct gttaaatcag ttctgtcctt 1020
ggcaactttc ttctgataac tgaatgttca tgaaggctct agctttatat tgtccctctt 1080
ttaggaataa aattttgatt ttcaaaaaaa aaaaaaaaaa aaaaaaaaaa 1130

```

<210> 235

<211> 268

<212> PRT

<213> Homo sapiens

<400> 235

```

Met Phe Arg Met Leu Asn Ser Ser Phe Glu Asp Asp Pro Phe Phe Ser
  1             5             10             15

Glu Ser Ile Leu Ala His Arg Glu Asn Met Arg Gln Met Ile Arg Ser
      20             25             30

Phe Ser Glu Pro Phe Gly Arg Asp Leu Leu Ser Ile Ser Asp Gly Arg
      35             40             45

Gly Arg Ala His Asn Arg Arg Gly His Asn Asp Gly Glu Asp Ser Leu
      50             55             60

Thr His Thr Asp Val Ser Ser Phe Gln Thr Met Asp Gln Met Val Ser
      65             70             75             80

Asn Met Arg Asn Tyr Met Gln Lys Leu Glu Arg Asn Phe Gly Gln Leu
      85             90             95

Ser Val Asp Pro Asn Gly His Ser Phe Cys Ser Ser Ser Val Met Thr
      100            105            110

Tyr Ser Lys Ile Gly Asp Glu Pro Pro Lys Val Phe Gln Ala Ser Thr
      115            120            125

Gln Thr Arg Arg Ala Pro Gly Gly Ile Lys Glu Thr Arg Lys Ala Met
      130            135            140

Arg Asp Ser Asp Ser Gly Leu Glu Lys Met Ala Ile Gly His His Ile
      145            150            155            160

His Asp Arg Ala His Val Ile Lys Lys Ser Lys Asn Lys Lys Thr Gly
      165            170            175

Asp Glu Glu Val Asn Gln Glu Phe Ile Asn Met Asn Glu Ser Asp Ala
      180            185            190

```

180/299

His Ala Phe Asp Glu Glu Trp Gln Ser Glu Val Leu Lys Tyr Lys Pro
 195 200 205

Gly Arg His Asn Leu Gly Asn Thr Arg Met Arg Ser Val Gly His Glu
 210 215 220

Asn Pro Gly Ser Arg Glu Leu Lys Arg Arg Glu Lys Pro Gln Gln Ser
 225 230 235 240

Pro Ala Ile Glu His Gly Arg Arg Ser Asn Val Leu Gly Asp Lys Leu
 245 250 255

His Ile Lys Gly Ser Ser Val Lys Ser Asn Lys Lys
 260 265

<210> 236

<211> 1116

<212> DNA

<213> Homo sapiens

<400> 236

```

gttatgtgtt cccgtccgta ctggaggcta gctcttgtcg cggccgcggc gagttaacat 60
cgtttttcca atctgtccgc ggctgccgcc acccaagaca gagccagaat gttcaggatg 120
ctgaacagca gttttgagga tgacccttc ttctctgagt ccattcttgc acaccgagaa 180
aatatgcgac agatgataag aagtttttct gaaccctttg gaagagactt gctcagtatc 240
tctgatggta gagggagagc tcataatcgt agaggacata atgatggtga agattctttg 300
actcatacag atgtcagctc tttccagacc atggacccaaa tgggtgtcaaa tatgagaaac 360
tatatgcaga aattagaaaag aaacttcggt caactttcag tggatccaaa tggacattca 420
ttttgttctt cctcagttat gacttattcc aaaataggag atgaaccgcc aaaggttttt 480
caggcctcaa ctcaaaactcg tcgagctcca ggaggaataa aggaaaccag gaaagcaatg 540
agagattctg acagtggact agaaaaaatg gctattggtc atcatatcca tgaccgagct 600
catgtcatta aaaagtcaaa gaacaagaag actggagatg aagagggtcaa ccaggagttc 660
atcaatatga atgaaagcga tgctcatgct tttgatgagg agtggcaaaag tgaggttttg 720
aagtacaaac caggacgaca caatctagga aacactagaa tgagaagtgt tggccatgag 780
aatcctggct cccgagaact taaaagaagg gagaaacctc aacaaagtcc agccattgaa 840
catggaagga gatcaaatgt tttgggggac aaactccaca tcaaaggctc atctgtgaaa 900
agcaacaaaa aataaatagc catgcatttg atttgtttag ttttgattgt tttaacagtt 960
agtaatggtg ctgggtaata agcataagac caatctcttg ctgttaaate agttctgtcc 1020
ttggcaactt tcttctgata tctgaatgtt catgaaggtc ctagctttat attgtccctc 1080
ttttaggaat aaaattttga ttttcaacaa aaaaaa 1116

```

<210> 237

<211> 86

<212> PRT

<213> Homo sapiens

<400> 237

Thr Thr Thr Ala Thr Leu Gly Phe Gly Ala Pro Gln Ala Pro Val Val
 1 5 10 15

Asp Arg Glu Lys Gln Pro Ser Glu Gly Ala Phe Ser Glu Asn Asn Ala
 20 25 30

Glu Asn Glu Ser Gly Gly Asp Lys Pro Pro Ile Asp Pro Asn Asn Pro
 35 40 45

181/299

Ala Ala Asn Trp Leu His Ala Arg Ser Thr Arg Lys Lys Arg Cys Pro
 50 55 60

Tyr Thr Lys His Gln Thr Leu Glu Leu Glu Lys Glu Phe Leu Phe Asn
 65 70 75 80

Met Tyr Leu Thr Arg Asp
 85

<210> 238

<211> 258

<212> DNA

<213> Homo sapiens

<400> 238

actacgacag ccactttggg ctttggagcc ccccaggccc cagtagttga tagagaaaaa 60
 caaccacagc aaggcgctt ctctgaaaac aatgctgaga atgagagcgg cggagacaag 120
 cccccatcg atcccaataa cccagcagcc aactggcttc acgcgcgctc cactcggaaa 180
 aagcggtgcc cctatacaaa acaccagacc ctggaactgg agaaagagtt tctgttcaac 240
 atgtacctca ccaggac 258

<210> 239

<211> 198

<212> PRT

<213> Homo sapiens

<400> 239

Met Ala Gly Phe Ser Pro Trp Arg Arg Arg Gln Arg Arg Arg Arg Arg
 1 5 10 15

Arg Arg Arg Ala Arg His Ala Ser Arg Ala Ala Pro Glu Leu Val Gly
 20 25 30

Asp Leu Gly Ser Phe Leu Leu Leu Gly Ser Thr Phe Leu Ser Thr Gly
 35 40 45

Thr Thr Leu Pro Phe Ile Thr Ser Val Glu Ile Val Ser Arg Tyr Leu
 50 55 60

Cys Ala Arg Gly Ser Gly Arg Ala Gly His His Gly Pro Gly Arg Ala
 65 70 75 80

Arg Pro Ala Val Ala Thr Ser Ala Phe Pro Ala Gln Glu Pro Arg Val
 85 90 95

Phe Leu Arg Ser Ala Leu Pro Ala Gly Arg Leu Ser Pro Ser Thr Thr
 100 105 110

His Leu His Leu Val Thr Ala Asp Asn Pro Ala Ala Asn Trp Leu His
 115 120 125

Ala Arg Ser Thr Arg Lys Lys Arg Cys Pro Tyr Thr Lys His Gln Thr
 130 135 140

Leu Glu Leu Glu Lys Glu Phe Leu Phe Asn Met Tyr Leu Thr Arg Asp
 145 150 155 160

182/299

Arg Arg Tyr Glu Val Ala Arg Leu Leu Asn Leu Thr Glu Arg Gln Val
 165 170 175

Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Met Lys Lys Ile Asn Lys
 180 185 190

Asp Arg Ala Lys Asp Glu
 195

<210> 240

<211> 597

<212> DNA

<213> Homo sapiens

<400> 240

atggcagggt tctctccttg gcggcgggcg cagcgggcgga ggcggcgggcg gcggcgggcg 60
 aggcacgctt cgcgggcagc accagaactg gtcgggtgatt taggtagtgtt cctgttggtg 120
 ggatccacct ttctctcgac aggcacgaca ctgcccttca ttacttcagt tgaaatcgtc 180
 tccaggtacc tctgcgcgcg ggggtcgggc cgcgcggggc atcacggccc tggtcgtgcc 240
 aggcctgcg tggcaacctc ggctttccct gctcaggagc ctctgtgtctt tctccgcagc 300
 gctttgccag ccggccggct ttccccttcc accacacacc tccacctggt cacagcagat 360
 aaccacgag ccaactggct tcatgcgcgc tccactcgga aaaagcgggtg cccctataca 420
 aaacaccaga ccctggaact ggagaaagag tttctgttca acatgtacct caccagggac 480
 cgcaggtacg aggtggctcg actgctcaac ctcaccgaga ggcaggtcaa gatctggttc 540
 cagaaccgca ggatgaaaat gaagaaaatc aacaaagacc gagcaaaaaga cgagtga 597

<210> 241

<211> 198

<212> PRT

<213> Homo sapiens

<400> 241

Met Ala Gly Phe Ser Pro Trp Arg Arg Arg Gln Arg Arg Arg Arg Arg
 1 5 10 15

Arg Arg Arg Ala Arg His Ala Ser Arg Ala Ala Pro Glu Leu Val Gly
 20 25 30

Asp Leu Gly Ser Phe Leu Leu Leu Gly Ser Thr Phe Leu Ser Thr Gly
 35 40 45

Thr Thr Leu Pro Phe Ile Thr Ser Val Glu Ile Val Ser Arg Tyr Leu
 50 55 60

Cys Ala Arg Gly Ser Gly Arg Ala Gly His His Gly Pro Gly Arg Ala
 65 70 75 80

Arg Pro Ala Val Ala Thr Ser Ala Phe Pro Ala Gln Glu Pro Arg Val
 85 90 95

Phe Leu Arg Ser Ala Leu Pro Ala Gly Arg Leu Ser Pro Ser Thr Thr
 100 105 110

His Leu His Leu Val Thr Ala Asp Asn Pro Ala Ala Asn Trp Leu His
 115 120 125

183/299

Ala Arg Ser Thr Arg Lys Lys Arg Cys Pro Tyr Thr Lys His Gln Thr
 130 135 140

Leu Glu Leu Glu Lys Glu Phe Leu Phe Asn Met Tyr Leu Thr Arg Asp
 145 150 155 160

Arg Arg Tyr Glu Val Ala Arg Leu Leu Asn Leu Thr Glu Arg Gln Val
 165 170 175

Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Met Lys Lys Ile Asn Lys
 180 185 190

Asp Arg Ala Lys Asp Glu
 195

<210> 242
 <211> 268
 <212> PRT
 <213> Homo sapiens

<400> 242
 Met His His Trp Gly Leu Gly Asn Tyr Tyr Val Asp Ser Phe Leu Leu
 1 5 10 15

Gly Ala Asp Ala Ala Asp Glu Leu Ser Val Gly Ala Met Arg Arg Gly
 20 25 30

Pro Trp Pro Pro Pro Arg Gln Ala Ala Thr Leu Ala Glu His Pro Asp
 35 40 45

Phe Ser Pro Cys Ser Phe Gln Ser Lys Ala Thr Val Phe Gly Ala Ser
 50 55 60

Trp Asn Pro Val His Ala Arg Ala Pro Thr Leu Tyr Pro Leu Val Tyr
 65 70 75 80

His His His His His His Pro Tyr Val His Pro Gln Ala Pro Trp Arg
 85 90 95

Arg Gly Ala Asp Gly Arg Tyr Met Arg Ser Cys Trp Ser Pro Thr Pro
 100 105 110

Gly Ala Leu Ser Phe Ala Gly Leu Pro Ser Ser Arg Pro Tyr Gly Ile
 115 120 125

Lys Pro Glu Pro Leu Ser Ala Arg Arg Gly Asp Cys Pro Thr Leu Asp
 130 135 140

Thr His Thr Phe Ser Leu Thr Asp Tyr Ala Cys Gly Ser Pro Pro Val
 145 150 155 160

Asp Arg Glu Lys Gln Pro Ser Glu Gly Ala Phe Ser Glu Asn Asn Ala
 165 170 175

Glu Asn Glu Ser Gly Gly Asp Lys Pro Pro Ile Asp Pro Asn Asn Pro
 180 185 190

184/299

Ala Ala Asn Trp Leu His Ala Arg Ser Thr Arg Lys Lys Arg Cys Pro
 195 200 205

Tyr Thr Lys His Gln Thr Leu Glu Leu Glu Lys Glu Phe Leu Phe Asn
 210 215 220

Met Tyr Leu Thr Arg Asp Arg Arg Tyr Glu Val Ala Arg Leu Leu Asn
 225 230 235 240

Leu Thr Glu Arg Gln Val Lys Ile Trp Phe Gln Asn Arg Arg Met Lys
 245 250 255

Met Lys Lys Ile Asn Lys Asp Arg Ala Lys Asp Glu
 260 265

<210> 243

<211> 6671

<212> DNA

<213> Homo sapiens

<400> 243

```

cgttctcctc tctttctcct ctctctctgg aataccttac tgggcctggt ggtctccctt 60
cttgaccatt tgcggccctt ggggcactct gttgcaactg cgggcgcagg ttcctagggg 120
ctgggctggg ccgggccagg cgcgatggca gggttctctc cttggcggcg gcggcagcgg 180
cggaggcggc ggccggcggc ggcgaggcac gcttcgcggg cagcaccaga actggtcggg 240
gatttaggta gtttctctgt gttgggatcc acctttctct cgacaggcac gacactgccc 300
ttcattactt cagttgaaat cgtctccagg tacctctgcg cgcgggggtc gggccgcgcg 360
gggcatcacg gccctggctg tgccaggcct gcggtggcaa cctcggcttt ccctgctcag 420
gagcctcggtg tctttctcgg cagcgctttg ccagccggcc ggctttcccc ttccaccaca 480
cacctccacc tggtcacagc aggtagggtt aggttggtg ctctctcgcg gacgcccggg 540
gcgtggtagg aattctgggc tttgggcatt caaggtcagg ggcgcccgtc tccatcctga 600
gcctcccact ggaggctgcg cctgcccagg gacctcctgc cattctcttg taaggctgga 660
acacacacac acacacacac acacacacac acacacacac acacacacca gtcccgggtg 720
tgagctcagg aaagaacctc cttccagtgg agactcaggc tggactagga aggatagggc 780
aggctgggat cctggccttg tcacttacct ttctctctgt aagctcggcc gctgctagga 840
gtcgctctct ttttcttctt tcttttccct gtcttccctt cctcttttat ctcttctttc 900
tttttttctt ctttcttttg ctcttctctt ctttcttttc ttccggttggg ctttttttca 960
tcttctgtct ctgccagatt ctatctcacc tccttatctc cttcccaaag catccttggg 1020
gaggggcccc gagctggctt caggagagcc tagggggtct cactttcctc tgcggctcaa 1080
gtagaggttg ggaagtctgc cgaggaaggg ccgcgtggg gcggtgccc agggcggttg 1140
gtttgggcct ggtgtgttac tctgcagaca aggcctcggg tatgatcac accggatggc 1200
ggcagccttg cgtttcttct cctgtogeta acggctgact aggagatctg attaggggac 1260
attcgctgca gctttgtgtg cccatatcga gggcaggagg ccttcgccag cctcactggg 1320
gactggagct gagcccaaca gcctcgtggt agcctggcca ttcgctggga agctcttagc 1380
tggctcttcc ggctgccggg cactagcttg gggtttgacc gcattgaggg agactggcta 1440
gggcaaagct tgactgcttg cttactagtg gcttccatta ggtacaaaat atgttccata 1500
cagcaccttc gtgcagctgg gtgctgagga gaaggggacc cttccaagag ccagtatggt 1560
ttaaatgggc aaaaagaatc ccaaattcca gagccattga tataaacttg agtcatcggt 1620
ccaaattgta gtctacagat gggagccagt ctgaccattt tccctacaga aaacagaaaa 1680
caaactatct ctccctactc ccaacacaca cagttacaga ttctgtccca caaagctgtt 1740
tcctttccct gcctggactg gagggcccagg aactctttcg ttgcacagcc accgacctgc 1800
tgtctgaaag gaccacacac cccattccct tcaactcctc cctgccattt tctggaccag 1860
gcattggatt tatttcagag atcacagttt cagaaatctc agtcgagaag ggccgtttta 1920
aattatactc atttattatt tctttatcga tacgcaatct ctttcacttc gaaaataaaa 1980
gcagacaaaa aagtcagact attctggctc caaacctttg gctgaaggaa gacaatattt 2040
ggttttctga ttttctcctg ctttctaggg accagtaaca tctgcttaac actcaacgcc 2100

```

185/299

tgctaattgt	tcagtaactc	tcttattttt	gggctaaggc	tgttttaaagg	aacagctttt	2160
ttacttaaaa	aatactgaaa	taatcagtg	cttctcaggg	ataaaacgtg	gaaaaggcat	2220
ccagacatgc	ccagcccatt	tgcagacact	taaaattggg	agccagggtt	tcctccaggg	2280
ttaatTTTTT	aaatgaaaa	ctcagaggct	ggcggactgc	gggtatttta	ggacacgggtg	2340
gactgtggtg	ggggtgggca	tgacctagag	gaatttatgg	ggcaaggaaa	aatattaggg	2400
ggagggagat	gaggcggaca	ggacggggcc	atttcggagt	tcattgtgtc	ggccacttcc	2460
ctcttccagg	cgcgggtgca	ggaaggggca	cccagtcgg	atccgcccgc	ttggcagcct	2520
cgtcgttatt	tgggagtc	cgcgggaagt	gtgtcaggg	gtttgagggg	gggattactg	2580
gaactgctgg	tgaggatgaa	ggcaaaagag	agagagagag	atggacgcgc	ccgaggccgc	2640
cagcctcgcc	gccagggaag	tgggctaatt	aaaaacacac	tgttgcaggc	acagtatcca	2700
cacgtgaatt	tgattacccc	tgttctagga	gtcgtgctt	tctgttagga	attgggggca	2760
gggggagttt	ccttccaatt	aacggagtgg	cggcgacctt	ttaatttacc	ccaacgggtg	2820
agaaataaac	ttcccacacg	tgccaggccc	aggaatggga	ctggagtcca	tgccctttta	2880
ccctccccc	ttctaatttc	cagccctggc	cttgagctgt	ggctgcctct	ctttgggtcc	2940
ttgtacctct	ccgcgagtc	tccgggcccc	gtaggtaacc	aagcgaggcc	cggagtagca	3000
gctggaaagg	gaggaaggag	ccctgaaagc	gtcacgcggc	cccgggacag	gccacatcgg	3060
tgccggcctc	ccaggttccg	gagctgcggg	gtctcttagg	cagggctgcc	ttttcccaaa	3120
ccgaacttgc	cttccattca	tgccacttgt	agttttttcc	cagctgggat	tcacggagcg	3180
caaccaggct	tgcagcgctc	atgggttagag	cctctgaggc	tggagcacag	gctgggtcgc	3240
agcccctgcg	cctgggaatc	ctgattgcc	gctgatgaga	aaggcgggct	gggcgcgcgt	3300
gtggctgggg	tgcagggcgc	gggaccgagc	gcgcgcaca	accaaccagg	ccctcaaacc	3360
cttcgcctct	gtggcgctgg	cgtccctcct	ggccagctcc	tccgtggggt	cctcgtagca	3420
aaaggcgaatt	taagggttgc	ccgggcgcgc	ctcgtccag	gcgggtagct	gtggggacct	3480
acaccgcggg	tactccctga	gcggccggctc	cctgcctgga	gtgccctgg	agggccggcg	3540
gcggctccgt	ttgggacgga	tcttgcgttg	aatttgactt	ttcgagggcg	gccgcgggta	3600
aactcgcctc	tcccggggac	cgcagggatt	atttacaggg	agctcgccaa	ccaaacacaa	3660
cagtctaacc	tttccaagtc	ctcgtaaatt	tttacagctg	ggagccacgg	caggcaaacc	3720
aatctgttgg	tcgtttccga	cttcccgcca	gcctgtgtgg	cttctgaaac	aataactcct	3780
tatgaaatat	cataaatata	gattttaaata	cagttagagcg	acaatgcgat	ttggctgctt	3840
ttttatggct	tcaattattg	tctaatttta	tgtgaggggc	tccgttgccc	gcactcgcgc	3900
acggaccocg	gccttcttga	tggcgtgatt	aattgtgata	taaaatagtc	cgcttaagaa	3960
gtgtgtgtat	ggggggggga	gacgggagag	tacagagaca	aggccagatt	tgatctttta	4020
atcgtcgttg	gccacaatta	aaacaaaacc	catcgtagag	cggcacgata	cctttacata	4080
aaaacatatg	gctttttgcta	taaaaattat	gactgcaaaa	caccggacca	ttaatagcgt	4140
gcggagtgat	ttacgcgtta	ttgttctgct	ggacgggcag	ctgacgcgca	cggccaatgg	4200
gcgcgggcgc	cggcaactta	ttaggtgact	gtacttcccc	cccggtgcca	ccagttgtt	4260
acatgaaatc	tgcagtttca	taatttccgt	gggtcggggc	gcgcggggcca	ggcgtggggc	4320
acggtgatgc	accactgggg	cctgggcaac	tactacgtgg	actcgttcc	gctgggcgc	4380
gacgccgcgg	atgagctgag	cgttggcgct	atgcgcgggg	gacctggcc	acctccccgg	4440
caggcgccga	cgttggccga	gcaccccgac	ttcagcccg	gcagcttcca	gtccaaggcg	4500
acggtgtttg	gcgcctcgtg	gaacccagtg	cagcgcggg	cgccaacgct	gtacccgctg	4560
gtgtaccacc	accatcacca	ccacccctac	gtgcaccccc	aggcgccgtg	gcggcgcggc	4620
gcggacggca	ggtacatgcg	ctcctgctgg	agcccaacgc	ccggtgcgct	ctccttcgcg	4680
ggcttgcctt	ccagccggcc	ttatggcatt	aaacctgaac	cgtgtcggc	cagaaggggt	4740
gactgtccca	cgtttgacac	tcacactttc	tccctgactg	actatgcttg	tggttctcct	4800
ccagttgata	gagaaaaaca	accagcgaa	ggcgcttct	ctgaaaaaaa	tgctgagaat	4860
gagagcggcg	gagacaagcc	ccccatcgat	cccagtaagt	gtctctctcc	ttcaaatccc	4920
gcccggcctc	cacgccggct	cccgatctg	ctggcccgcc	aggtttctct	cgagttgggg	4980
ccaggagcca	gaagttgggtg	tttgggacgc	ctcagatagg	gccccagtc	tggagagcag	5040
tgaagagcgg	cccgaggggc	tacggggggg	gagcgcgctg	ctgcagcaag	agggggcggg	5100
agggcacttc	gggacgagcc	aagactggcc	gcccctctcc	ttccctgccc	aggcccagga	5160
ccgagatact	ttgggcccgtt	cttcgaaaag	tccagtgcag	cccagagagc	cttttgtaca	5220
actagattgt	cgtgagggcg	ccagccaggg	acgcgggagc	tgggagctcg	gggagacggg	5280
ccgattcctt	ccacttcttt	ctcggccagt	ggcggcgcta	aatcctgcca	agatgaggct	5340
gcgggcgacc	cgggccacaa	gggtcccat	gacagattat	tcaaataagc	cacagacgtg	5400
atcagcggcc	ttagggggcc	tgacggcttg	ccagctccga	agccttccag	gaagggtaaa	5460
taaggagtgg	ggggcgtaga	gggacagggt	gggaaagaaa	gacgaaggag	tgaacgggac	5520
agaggaatcc	taatcttgct	acagaacaca	aggcagcatg	ctttccctct	gcgtggcaag	5580

186/299

```

gagacctgtt tccaaatttc attctataca gcgttttgag agtgggagga aggagaaggg 5640
ggacaagagg acagagtagg agaaaggaag gtctcggagg ggaagggcga gccaaagttt 5700
tactcgtgac aattttaagt gactgtctgt gcgtctgtct gccagggttc cattgtgtcc 5760
gaggcctgac tgcctttcct aaccagttca gcagagttct gcacttcggc cagagacccc 5820
atgcaggagg ctcatTTGCC cagcgggatg tgcgtcttct gctcctaaac ccagtgtttc 5880
tcttccccgc agataaccca gcagccaact ggcttcatgc gcgctccact cggaaaaagc 5940
ggtgcccta taaaaaacac cagaccctgg aactggagaa agagtttctg ttcaacatgt 6000
acctcaccag ggaccgcagg tacgaggtgg ctcgactgct caacctcacc gagaggcagg 6060
tcaagatctg gttccagaac cgcaggatga aaatgaagaa aatcaacaaa gaccgagcaa 6120
aagacgagtg atgccatttg ggcttattta gaaaaaaggg taagctagag agaaaaagaa 6180
agaactgtcc gtcccccttc cgcttctctc cttttctcac cccacccta gcctccacca 6240
tccccgcaca aagcggctct aaacctcagg ccacatcttt tccaaggcaa acctgttca 6300
ggctggctcg taggcctgcc gctttgatgg aggaggtatt gtaagctttc attttctata 6360
agaaaaagga aaagttgagg gggggcatta gtgctgatat ctgtgtgtgt tagcttgat 6420
atatattttt aaaaatctac ctgttctga cttaaaacaa aaggaaagaa actacctttt 6480
tataatgcac aactgttgat ggtaggctgt atagttttta gtctgtgtag ttaatttaat 6540
ttgcagtttg tgcggcagat tgctctgcca agatacttga acactgtgtt ttattgtgg 6600
aattatgttt tgtgattcaa acttctgtgt actgggtgat gcaccattg tgattgtgga 6660
agatagaatt c 6671

```

<210> 244

<211> 76

<212> PRT

<213> Homo sapiens

<400> 244

```

Arg Pro Met Pro Arg Leu Glu Pro Thr Phe Glu Ile Asp Glu Glu Glu
  1             5             10             15

Glu Glu Glu Asp Glu Asn Glu Leu Phe Pro Arg Glu Tyr Phe Arg Arg
      20             25             30

Leu Ser Ser Gln Asp Val Leu Arg Cys Gln Ser Ser Ser Lys Arg Lys
    35             40             45

Ser Lys Asp Glu Glu Glu Asp Glu Glu Ser Asp Asp Ala Asp Asp Gly
    50             55             60

Asn Asn Trp Glu His Lys Ser Ile Trp Thr Ala Leu
    65             70             75

```

<210> 245

<211> 415

<212> DNA

<213> Homo sapiens

<400> 245

```

gaggccaatg ccaagattag aacccacatt tgagatcgat gaagaagagg aggaagagga 60
tgaaaaatgaa cttttcccta gagaatactt ccgtcgtttg tcttcgcagg atgtactcag 120
gtgtcagtc tcttctaaga ggaagtctaa agatgaagaa gaagatgaag agtcagatga 180
tgctgatgat gggaataact gggaacacaa gtccatttgg acagcccttt agtcaagctg 240
gagggcagcc aatgggagcc actggagtga acccccagtt agccagcaaa cagagcatgg 300
tcaacagttt gccaccttc cctacagata tcaagaatac ttcagtcacc aacgtgccaa 360
atatgtctca gatgcaaaca tcagtgggaa ttgtaccac acaagcaatt gcaac 415

```

187/299

<210> 246

<211> 68

<212> PRT

<213> Homo sapiens

<400> 246

Met Ala Glu Asn Leu Leu Asp Gly Pro Pro Asn Pro Lys Arg Ala Lys
 1 5 10 15

Leu Ser Ser Pro Gly Phe Ser Ala Asn Asp Ser Thr Asp Thr Pro Ile
 20 25 30

Leu Lys Pro Val Ser Leu Leu Arg Lys Arg Asp Val Lys Asn Ser Pro
 35 40 45

Leu Glu Pro Asp Thr Ser Thr Pro Leu Lys Lys Lys Lys Gly Trp Pro
 50 55 60

Lys Gly Lys Ser
 65

<210> 247

<211> 229

<212> DNA

<213> Homo sapiens

<400> 247

gggctgtttt cgcgagcagg tgaaaatggc tgagaacttg ctggacggac cgcccaaccc 60
 caaaagagcc aaactcagct cgcccgggtt ctcggcgaat gacagcacag acactcctat 120
 cttaaagcca gtatctcttt tgcgaaaacg tgatgtgaag aattctcctc ttgagccaga 180
 tacatccaca cttttgaaaa agaaaaaggg atggcccaaa ggcaagagc 229

<210> 248

<211> 376

<212> PRT

<213> Homo sapiens

<400> 248

Arg Pro Met Pro Arg Leu Glu Pro Thr Phe Glu Ile Asp Glu Glu Glu
 1 5 10 15

Glu Glu Glu Asp Glu Asn Glu Leu Phe Pro Arg Glu Tyr Phe Arg Arg
 20 25 30

Leu Ser Ser Gln Asp Val Leu Arg Cys Gln Ser Ser Ser Lys Arg Lys
 35 40 45

Ser Lys Asp Glu Glu Glu Asp Glu Glu Ser Asp Asp Ala Asp Asp Phe
 50 55 60

Gly Ser Leu Phe Asp Leu Glu Asn Asp Leu Pro Asp Glu Leu Ile Pro
 65 70 75 80

Asn Gly Gly Glu Leu Gly Leu Leu Asn Ser Gly Asn Leu Val Pro Asp
 85 90 95

188/299

Ala Ala Ser Lys His Lys Gln Leu Ser Glu Leu Leu Arg Gly Gly Ser
 100 105 110
 Gly Ser Ser Ile Asn Pro Gly Ile Gly Asn Val Ser Ala Ser Ser Pro
 115 120 125
 Val Gln Gln Gly Leu Gly Gly Gln Ala Gln Gly Gln Pro Asn Ser Ala
 130 135 140
 Asn Met Ala Ser Leu Ser Ala Met Gly Lys Ser Pro Leu Ser Gln Gly
 145 150 155 160
 Asp Ser Ser Ala Pro Ser Leu Pro Lys Gln Ala Ala Ser Thr Ser Gly
 165 170 175
 Pro Thr Pro Ala Ala Ser Gln Ala Leu Asn Pro Gln Ala Gln Lys Gln
 180 185 190
 Val Gly Leu Ala Thr Ser Ser Pro Ala Thr Ser Gln Thr Gly Pro Gly
 195 200 205
 Ile Cys Met Asn Ala Asn Phe Asn Gln Thr His Pro Gly Leu Leu Asn
 210 215 220
 Ser Asn Ser Gly His Ser Leu Ile Asn Gln Ala Ser Gln Gly Gln Ala
 225 230 235 240
 Gln Val Met Asn Gly Ser Leu Gly Ala Ala Gly Arg Gly Arg Gly Ala
 245 250 255
 Gly Met Pro Tyr Pro Thr Pro Ala Met Gln Gly Ala Ser Ser Ser Val
 260 265 270
 Leu Ala Glu Thr Leu Thr Gln Val Ser Pro Gln Met Thr Gly His Ala
 275 280 285
 Gly Leu Asn Thr Ala Gln Ala Gly Gly Met Ala Lys Met Gly Ile Thr
 290 295 300
 Gly Asn Thr Ser Pro Phe Gly Gln Pro Phe Ser Gln Ala Gly Gly Gln
 305 310 315 320
 Pro Met Gly Ala Thr Gly Val Asn Pro Gln Leu Ala Ser Lys Gln Ser
 325 330 335
 Met Val Asn Ser Leu Pro Thr Phe Pro Thr Asp Ile Lys Asn Thr Ser
 340 345 350
 Val Thr Asn Val Pro Asn Met Ser Gln Met Gln Thr Ser Val Gly Ile
 355 360 365
 Val Pro Thr Gln Ala Ile Ala Thr
 370 375

<210> 249

<211> 1128

<212> DNA

189/299

<213> Homo sapiens

<400> 249

```

gaggccaatg ccaagattag aacccacatt tgagatcgat gaagaagagg aggaagagga 60
tgaaaatgaa cttttcccta gagaatactt ccgtcgtttg tcttcgcagg atgtactcag 120
gtgtcagtc tcttctaaga ggaagtctaa agatgaagaa gaagatgaag agtcagatga 180
tgctgatgat tttggatcat tgtttgactt ggaaaatgat cttcctgatg agctgatacc 240
caatggagga gaattaggcc ttttaaacag tgggaaacctt gttccagatg ctgcttccaa 300
acataaacia ctgtcggagc ttctacgagg aggcagcggc tctagtatca acccaggaat 360
aggaaatgtg agcgcagca gccccgtgca gcagggcctg ggtggccagg ctcaagggca 420
gccgaacagt gctaacatgg ccagcctcag tgccatgggc aagagccctc tgagccaggg 480
agattcttca gccccagcc tgccataaca ggcagccagc acctctgggc ccaccccgcc 540
tgccctccaa gcactgaatc cgcaagcaca aaagcaagtg gggctggcga ctagcagccc 600
tgccacgtca cagactggac ctggtatctg catgaatgct aactttaacc agaccacccc 660
aggcctctc aatagtaact ctggccatag cttaattaat caggcttcac aagggcaggc 720
gcaagtcatg aatggatctc ttggggctgc tggcagagga aggggagctg gaatgccgta 780
ccctactcca gccatgcagg gcgcctcgag cagcgtgctg gctgagaccc taacgcagg 840
ttccccgcaa atgactggc acgcgggact gaacaccgca caggcaggag gcattggccaa 900
gatgggaata actgggaaca caagtccatt tggacagccc tttagtcaag ctggaggggca 960
gccaatggga gccactggag tgaaccccca gttagccagc aaacagagca tgggtcaacag 1020
tttgcccacc ttccctacag atatcaagaa tacttcagtc accaacgtgc caaatatgtc 1080
tcagatgcaa acatcagtgg gaattgtacc cacacaagca attgcaac 1128

```

<210> 250

<211> 2004

<212> PRT

<213> Homo sapiens

<400> 250

```

Met Val Lys Leu Ala Asn Pro Leu Tyr Thr Glu Trp Ile Leu Glu Ala
  1              5              10              15

Ile Lys Lys Val Lys Lys Gln Lys Gln Arg Pro Ser Glu Glu Arg Ile
      20              25              30

Cys Asn Ala Val Ser Ser Ser His Gly Leu Asp Arg Lys Thr Val Leu
      35              40              45

Glu Gln Leu Glu Leu Ser Val Lys Asp Gly Thr Ile Leu Lys Val Ser
      50              55              60

Asn Lys Gly Leu Asn Ser Tyr Lys Asp Pro Asp Asn Pro Gly Arg Ile
      65              70              75              80

Ala Leu Pro Lys Pro Arg Asn His Gly Lys Leu Asp Asn Lys Gln Asn
      85              90              95

Val Asp Trp Asn Lys Leu Ile Lys Arg Ala Val Glu Gly Leu Ala Glu
      100             105             110

Ser Gly Gly Ser Thr Leu Lys Ser Ile Glu Arg Phe Leu Lys Gly Gln
      115             120             125

Lys Asp Val Ser Ala Leu Phe Gly Gly Ser Ala Ala Ser Gly Phe His
      130             135             140

Gln Gln Leu Arg Leu Ala Ile Lys Arg Ala Ile Gly His Gly Arg Leu

```

190/299

145		150		155		160
Leu Lys Asp Gly Pro Leu Tyr Arg Leu Asn Thr Lys Ala Thr Asn Val						
	165		170		175	
Asp Gly Lys Glu Ser Cys Glu Ser Leu Ser Cys Leu Pro Pro Val Ser						
	180		185		190	
Leu Leu Pro His Glu Lys Asp Lys Pro Val Ala Glu Pro Ile Pro Ile						
	195		200		205	
Cys Ser Phe Cys Leu Gly Thr Lys Glu Gln Asn Arg Glu Lys Lys Pro						
	210		215		220	
Glu Glu Leu Ile Ser Cys Ala Asp Cys Gly Asn Ser Gly His Pro Ser						
	225		230		235	240
Cys Leu Lys Phe Ser Pro Glu Leu Thr Val Arg Val Lys Ala Leu Arg						
	245		250		255	
Trp Gln Cys Ile Glu Cys Lys Thr Cys Ser Ser Cys Arg Asp Gln Gly						
	260		265		270	
Lys Asn Ala Asp Asn Met Leu Phe Cys Asp Ser Cys Asp Arg Gly Phe						
	275		280		285	
His Met Glu Cys Cys Asp Pro Pro Leu Thr Arg Met Pro Lys Gly Met						
	290		295		300	
Trp Ile Cys Gln Ile Cys Arg Pro Arg Lys Lys Gly Arg Lys Leu Leu						
	305		310		315	320
Gln Lys Lys Ala Ala Gln Ile Lys Arg Arg Tyr Thr Asn Pro Ile Gly						
	325		330		335	
Arg Pro Lys Asn Arg Leu Lys Lys Gln Asn Thr Val Ser Lys Gly Pro						
	340		345		350	
Phe Ser Lys Val Arg Thr Gly Pro Gly Arg Gly Arg Lys Arg Lys Ile						
	355		360		365	
Thr Leu Ser Ser Gln Ser Ala Ser Ser Ser Ser Glu Glu Gly Tyr Leu						
	370		375		380	
Glu Arg Ile Asp Gly Leu Asp Phe Cys Arg Asp Ser Asn Val Ser Leu						
	385		390		395	400
Arg Phe Asn Lys Lys Thr Lys Gly Leu Ile Asp Gly Leu Thr Lys Phe						
	405		410		415	
Phe Thr Pro Ser Pro Asp Gly Arg Lys Ala Arg Gly Glu Val Val Asp						
	420		425		430	
Tyr Ser Glu Gln Tyr Arg Ile Arg Lys Arg Gly Asn Arg Lys Ser Ser						
	435		440		445	
Thr Ser Asp Trp Pro Thr Asp Asn Gln Asp Gly Trp Asp Gly Lys Gln						
	450		455		460	

191/299

Glu Asn Glu Glu Arg Leu Phe Gly Ser Gln Glu Ile Met Thr Glu Lys
 465 470 475 480
 Asp Met Glu Leu Phe Arg Asp Ile Gln Glu Gln Ala Leu Gln Lys Val
 485 490 495
 Gly Val Thr Gly Pro Pro Asp Pro Gln Val Arg Cys Pro Ser Val Ile
 500 505 510
 Glu Phe Gly Lys Tyr Glu Ile His Thr Trp Tyr Ser Ser Pro Tyr Pro
 515 520 525
 Gln Glu Tyr Ser Arg Leu Pro Lys Leu Tyr Leu Cys Glu Phe Cys Leu
 530 535 540
 Lys Tyr Met Lys Ser Arg Thr Ile Leu Gln Gln His Met Lys Lys Cys
 545 550 555 560
 Gly Trp Phe His Pro Pro Ala Asn Glu Ile Tyr Arg Lys Asn Asn Ile
 565 570 575
 Ser Val Phe Glu Val Asp Gly Asn Val Ser Thr Ile Tyr Cys Gln Asn
 580 585 590
 Leu Cys Leu Leu Ala Lys Leu Phe Leu Asp His Lys Thr Leu Tyr Tyr
 595 600 605
 Asp Val Glu Pro Phe Leu Phe Tyr Val Leu Thr Gln Asn Asp Val Lys
 610 615 620
 Gly Cys His Leu Val Gly Tyr Phe Ser Lys Glu Lys His Cys Gln Gln
 625 630 635 640
 Lys Tyr Asn Val Ser Cys Ile Met Ile Leu Pro Gln Tyr Gln Arg Lys
 645 650 655
 Gly Tyr Gly Arg Phe Leu Ile Asp Phe Ser Tyr Leu Leu Ser Lys Arg
 660 665 670
 Glu Gly Gln Ala Gly Ser Pro Glu Lys Pro Leu Ser Asp Leu Gly Arg
 675 680 685
 Leu Ser Tyr Met Ala Tyr Trp Lys Ser Val Ile Leu Glu Cys Leu Tyr
 690 695 700
 His Gln Asn Asp Lys Gln Ile Ser Ile Lys Lys Leu Ser Lys Leu Thr
 705 710 715 720
 Gly Ile Cys Pro Gln Asp Ile Thr Ser Thr Leu His His Leu Arg Met
 725 730 735
 Leu Asp Phe Arg Ser Asp Gln Phe Val Ile Ile Arg Arg Glu Lys Leu
 740 745 750
 Ile Gln Asp His Met Ala Lys Leu Gln Leu Asn Leu Arg Pro Val Asp
 755 760 765

192/299

Val Asp Pro Glu Cys Leu Arg Trp Thr Pro Val Ile Val Ser Asn Ser
 770 775 780
 Val Val Ser Glu Glu Glu Glu Glu Glu Ala Glu Glu Gly Glu Asn Glu
 785 790 795 800
 Glu Pro Gln Cys Gln Glu Arg Glu Leu Glu Ile Ser Val Gly Lys Ser
 805 810 815
 Val Ser His Glu Asn Lys Glu Gln Asp Ser Tyr Ser Val Glu Ser Glu
 820 825 830
 Lys Lys Pro Glu Val Met Ala Pro Val Ser Ser Thr Arg Leu Ser Lys
 835 840 845
 Gln Val Leu Pro His Asp Ser Leu Pro Ala Asn Ser Gln Pro Ser Arg
 850 855 860
 Arg Gly Arg Trp Gly Arg Lys Asn Arg Lys Thr Gln Glu Arg Phe Gly
 865 870 875 880
 Asp Lys Asp Ser Lys Leu Leu Leu Glu Glu Thr Ser Ser Ala Pro Gln
 885 890 895
 Glu Gln Tyr Gly Glu Cys Gly Glu Lys Ser Glu Ala Thr Gln Glu Gln
 900 905 910
 Tyr Thr Glu Ser Glu Glu Gln Leu Val Ala Ser Glu Glu Gln Pro Ser
 915 920 925
 Gln Asp Gly Lys Pro Asp Leu Pro Lys Arg Arg Leu Ser Glu Gly Val
 930 935 940
 Glu Pro Trp Arg Gly Gln Leu Lys Lys Ser Pro Glu Ala Leu Lys Cys
 945 950 955 960
 Arg Leu Thr Glu Gly Ser Glu Arg Leu Pro Arg Arg Tyr Ser Glu Gly
 965 970 975
 Asp Arg Ala Val Leu Arg Gly Phe Ser Glu Ser Ser Glu Glu Glu Glu
 980 985 990
 Glu Pro Glu Ser Pro Arg Ser Ser Ser Pro Pro Ile Leu Thr Lys Pro
 995 1000 1005
 Thr Leu Lys Arg Lys Lys Pro Phe Leu His Arg Arg Arg Arg Val Arg
 1010 1015 1020
 Lys Arg Lys His His Asn Ser Ser Val Val Thr Glu Thr Ile Ser Glu
 1025 1030 1035 1040
 Thr Thr Glu Val Leu Asp Glu Pro Phe Glu Asp Ser Asp Ser Glu Arg
 1045 1050 1055
 Pro Met Pro Arg Leu Glu Pro Thr Phe Glu Ile Asp Glu Glu Glu Glu
 1060 1065 1070
 Glu Glu Asp Glu Asn Glu Leu Phe Pro Arg Glu Tyr Phe Arg Arg Leu

193/299

1075	1080	1085
Ser Ser Gln Asp Val Leu Arg Cys Gln Ser Ser Ser Lys Arg Lys Ser 1090 1095 1100		
Lys Asp Glu Glu Glu Asp Glu Glu Ser Asp Asp Ala Asp Asp Thr Pro 1105 1110 1115 1120		
Ile Leu Lys Pro Val Ser Leu Leu Arg Lys Arg Asp Val Lys Asn Ser 1125 1130 1135		
Pro Leu Glu Pro Asp Thr Ser Thr Pro Leu Lys Lys Lys Lys Gly Trp 1140 1145 1150		
Pro Lys Gly Lys Ser Arg Lys Pro Ile His Trp Lys Lys Arg Pro Gly 1155 1160 1165		
Arg Lys Pro Gly Phe Lys Leu Ser Arg Glu Ile Met Pro Val Ser Thr 1170 1175 1180		
Gln Ala Cys Val Ile Glu Pro Ile Val Ser Ile Pro Lys Ala Gly Arg 1185 1190 1195 1200		
Lys Pro Lys Ile Gln Glu Ser Glu Glu Thr Val Glu Pro Lys Glu Asp 1205 1210 1215		
Met Pro Leu Pro Glu Glu Arg Lys Glu Glu Glu Glu Met Gln Ala Glu 1220 1225 1230		
Ala Glu Glu Ala Glu Glu Gly Glu Glu Glu Asp Ala Ala Ser Ser Glu 1235 1240 1245		
Val Pro Ala Ala Ser Pro Ala Asp Ser Ser Asn Ser Pro Glu Thr Glu 1250 1255 1260		
Thr Lys Glu Pro Glu Val Glu Glu Glu Glu Glu Lys Pro Arg Val Ser 1265 1270 1275 1280		
Glu Glu Gln Arg Gln Ser Glu Glu Glu Gln Gln Glu Leu Glu Glu Pro 1285 1290 1295		
Glu Pro Glu Glu Glu Glu Asp Ala Ala Ala Glu Thr Ala Gln Asn Asp 1300 1305 1310		
Asp His Asp Ala Asp Asp Glu Asp Asp Gly His Leu Glu Ser Thr Lys 1315 1320 1325		
Lys Lys Glu Leu Glu Glu Gln Pro Thr Arg Glu Asp Val Lys Glu Glu 1330 1335 1340		
Pro Gly Val Gln Glu Ser Phe Leu Asp Ala Asn Met Gln Lys Ser Arg 1345 1350 1355 1360		
Glu Lys Ile Lys Asp Lys Glu Glu Thr Glu Leu Asp Ser Glu Glu Glu 1365 1370 1375		
Gln Pro Ser His Asp Thr Ser Val Val Ser Glu Gln Met Ala Gly Ser 1380 1385 1390		

194/299

Glu Asp Asp His Glu Glu Asp Ser His Thr Lys Glu Glu Leu Ile Glu
1395 1400 1405

Leu Lys Glu Glu Glu Glu Ile Pro His Ser Glu Leu Asp Leu Glu Thr
1410 1415 1420

Val Gln Ala Val Gln Ser Leu Thr Gln Glu Glu Ser Ser Glu His Glu
1425 1430 1435 1440

Gly Ala Tyr Gln Asp Cys Glu Glu Thr Leu Ala Ala Cys Gln Thr Leu
1445 1450 1455

Gln Ser Tyr Thr Gln Ala Asp Glu Asp Pro Gln Met Ser Met Val Glu
1460 1465 1470

Asp Cys His Ala Ser Glu His Asn Ser Pro Ile Ser Ser Val Gln Ser
1475 1480 1485

His Pro Ser Gln Ser Val Arg Ser Val Ser Ser Pro Asn Val Pro Ala
1490 1495 1500

Leu Glu Ser Gly Tyr Thr Gln Ile Ser Pro Glu Gln Gly Ser Leu Ser
1505 1510 1515 1520

Ala Pro Ser Met Gln Asn Met Glu Thr Ser Pro Met Met Asp Val Pro
1525 1530 1535

Ser Val Ser Asp His Ser Gln Gln Val Val Asp Ser Gly Phe Ser Asp
1540 1545 1550

Leu Gly Ser Ile Glu Ser Thr Thr Glu Asn Tyr Glu Asn Pro Ser Ser
1555 1560 1565

Tyr Asp Ser Thr Met Gly Gly Ser Ile Cys Gly Asn Ser Ser Ser Gln
1570 1575 1580

Ser Ser Cys Ser Tyr Gly Gly Leu Ser Ser Ser Ser Ser Leu Thr Gln
1585 1590 1595 1600

Ser Ser Cys Val Val Thr Gln Gln Met Ala Ser Met Gly Ser Ser Cys
1605 1610 1615

Ser Met Met Gln Gln Ser Ser Val Gln Pro Ala Ala Asn Cys Ser Ile
1620 1625 1630

Lys Ser Pro Gln Ser Cys Val Val Glu Arg Pro Pro Ser Asn Gln Gln
1635 1640 1645

Gln Gln Pro Pro Pro Pro Pro Pro Gln Gln Pro Gln Pro Pro Pro Pro
1650 1655 1660

Gln Pro Gln Pro Ala Pro Gln Pro Pro Pro Pro Gln Gln Gln Pro Gln
1665 1670 1675 1680

Gln Gln Pro Gln Pro Gln Pro Gln Gln Pro Pro Pro Pro Pro Pro Pro
1685 1690 1695

195/299

Gln Gln Gln Pro Pro Leu Ser Gln Cys Ser Met Asn Asn Ser Phe Thr
 1700 1705 1710
 Pro Ala Pro Met Ile Met Glu Ile Pro Glu Ser Gly Ser Thr Gly Asn
 1715 1720 1725
 Ile Ser Ile Tyr Glu Arg Ile Pro Gly Asp Phe Gly Ala Gly Ser Tyr
 1730 1735 1740
 Ser Gln Pro Ser Ala Thr Phe Ser Leu Ala Lys Leu Gln Gln Leu Thr
 1745 1750 1755 1760
 Asn Thr Ile Met Asp Pro His Ala Met Pro Tyr Ser His Ser Pro Ala
 1765 1770 1775
 Val Thr Ser Tyr Ala Thr Ser Val Ser Leu Ser Asn Thr Gly Leu Ala
 1780 1785 1790
 Gln Leu Ala Pro Ser His Pro Leu Ala Gly Thr Pro Gln Ala Gln Ala
 1795 1800 1805
 Thr Met Thr Pro Pro Pro Asn Leu Ala Ser Thr Thr Met Asn Leu Thr
 1810 1815 1820
 Ser Pro Leu Leu Gln Cys Asn Met Ser Ala Thr Asn Ile Gly Ile Pro
 1825 1830 1835 1840
 His Thr Gln Arg Leu Gln Gly Gln Met Pro Val Lys Gly His Ile Ser
 1845 1850 1855
 Ile Arg Ser Lys Ser Ala Pro Leu Pro Ser Ala Ala Ala His Gln Gln
 1860 1865 1870
 Gln Leu Tyr Gly Arg Ser Pro Ser Ala Val Ala Met Gln Ala Gly Pro
 1875 1880 1885
 Arg Ala Leu Ala Val Gln Arg Gly Met Asn Met Gly Val Asn Leu Met
 1890 1895 1900
 Pro Thr Pro Ala Tyr Asn Val Asn Ser Met Asn Met Asn Thr Leu Asn
 1905 1910 1915 1920
 Ala Met Asn Ser Tyr Arg Met Thr Gln Pro Met Met Asn Ser Ser Tyr
 1925 1930 1935
 His Ser Asn Pro Ala Tyr Met Asn Gln Thr Ala Gln Tyr Pro Met Gln
 1940 1945 1950
 Met Gln Met Gly Met Met Gly Ser Gln Ala Tyr Thr Gln Gln Pro Met
 1955 1960 1965
 Gln Pro Asn Pro His Gly Asn Met Met Tyr Thr Gly Pro Ser His His
 1970 1975 1980
 Ser Tyr Met Asn Ala Ala Gly Val Pro Lys Gln Ser Leu Asn Gly Pro
 1985 1990 1995 2000
 Tyr Met Arg Arg

<210> 251
 <211> 7869
 <212> DNA
 <213> Homo sapiens

<400> 251

```

ggcagcaggt ttggggcacc tccgcgggtcc ggccccggggc cccgggatct cggctgtcct 60
tcctccccgc ataagatgca cttttttctg ctctggagcc gggaatgaaa tattcttgag 120
ttcttacaac tttatgacga gacccatgtg tgggtgtatt gagaaattca ttgggaagtt 180
ggaagacatt tcaaacacaa ggttggtttg gtttctatag tacaattggg gtggcattct 240
gttttgtgaa aggaggaagg acttaggcca gaaaactcat atgctatggt taactggttc 300
ccagcctccg agaatcttgt tttccatggt gtaaaactta ctcagcatca ggataaggga 360
taacgactct atggatatac agaatccttc accatggtaa aactcgcaaa cccgctttat 420
actgagtggg ttttgaggc catcaaaaaa gtgaaaaagc agaaacagcg tccttcagaa 480
gaaaggatat gcaatgctgt gtcttcaccc catggcttgg atcgtaaaac tgttttagaa 540
caattggagt tgagtgttaa agatggaaca attttaaaag tctcaaataa aggactcaat 600
tcctataaag atctgataa tcctgggcga atagcacttc ctaagcctcg gaaccatgga 660
aaattggata ataaacaaa tgtggattgg aataaactga taaagcgggc agttgagggc 720
ttggcagagt ctggtggctc aactttgaaa agcattgaac gttttttgaa aggtcagaag 780
gatgtgtctg cattattcgg aggcagtgtc gcctctggct ttcaccagca gttacgattg 840
gctatcaaac gtgccattgg ccacggcaga ctccctaaag atggacctct ttatcggtc 900
aacactaaag caaccaacgt ggatgggaaa gagagtgtg agtctctttc ctgtttacct 960
ccagtgtccc ttcttcaca tgaagaggat aagccggttg ctgaaccaat ccccatctgt 1020
agttttctgtc ttgtacaaa agaacaaaac cgagaaaaga agccagagga actcatctcc 1080
tgtgccgact gtggcaacag tggccatcca tcctgtttta agttttcccc tgaactaacg 1140
gttcgagtga aggccttacg gtggcagtgc atcgagtgt aaacatgcag ctctgtcga 1200
gatcaaggca aaaaatgcga taacatgtct ttttgtgatt catgtgaccg aggttttcac 1260
atggagtgtt gtgatccgc actcaccctg atgccaaaag gcatgtggat atgtcaaata 1320
tgtcgacctt ggaaaaaagg acgaaaactt ctacaaaaga aggcagcaca gataaaacgg 1380
cgctatacta atccaatagg acgtccaaaa aacagggtta agaaaacaaa cacggtatca 1440
aaaggtccct tcagcaaatg tcgaactggc cctggaaggg gtaggaaacg aaaaatcact 1500
ctttccagcc aatcagcatc atcatcatca gaagaaggat atttagagcg gatagatggc 1560
ttggacttct gcagagatag caatgtctcc ttgaggttca acaagaaaac caaagggtc 1620
attgatggcc ttacaaaatt ttttaccctt tccctgatg gccggaaaag tcgggggggaa 1680
gtggtggact actctgagca atatcgaatc agaaagaggg gcaacaggaa atcaagcact 1740
tcagattggc ccacagacaa tcaggatggc tgggatggca aacaagaaaa tgaggagcga 1800
ctttttggga gccaggaat catgactgag aaagatatgg aattatttct tgatatccaa 1860
gaacaagcac tgcagaaagt tggagtgaat ggtccccctg atccacaagt ccgctgtccc 1920
tctgtcattg agtttgggaa gtatgaaatt cacacctggt actcctcccc atatcctcaa 1980
gaatactcaa ggctgcccc attgtatctt tgtgaatttt gtctaaaata tatgaaaagt 2040
agaactatct tgcagcagca catgaagaaa tgtggttggt tccatcctcc tgccaatgag 2100
atttacagaa agaataatat ttctgtcttt gaggttgatg ggaatgtgag taccatttat 2160
tgtcaaaacc tgtgtctttt ggcaaagtgt tttcttgacc acaaaaccct ctattacgat 2220
gtggagccat ttctttttta tgtactaaca cagaatgatg tcaagggtct ccacctgtt 2280
ggctactttt ctaaggaaaa gcactgcaa cagaagtaca atgtttcctg tataatgatt 2340
cttctcaat accagcgtaa gggctatggc aggtttctca tcgatttcag ttatttgta 2400
tcaaagcgtg aaggccaagc agggctctca tatctgatct gggctcgtct 2460
tcctacatgg catattggaa aagtgtataa ttggagtgc tttatcacca aaatgacaag 2520
cagatcagca ttaagaagtt aagcaagttg actggaatct gccctcaaga catcacttcc 2580
acactccacc acctacgaat gctggacttc cgtagtgaac aatttgtgat tatccgccgg 2640
gaaaaactta tccaggatca catggcaaag ctccagctga atttgcgacc tgtatgatga 2700
gatccagaat gtttgcgctg gactccagtc atagtgtcca actctgtggt ctcagaggag 2760
gaagaagagg aggtcagga aggagaaaac gaagagccac agtgccagga aagagaatta 2820
gagatcagtg tgggaaagtc tgtgtctcat gagaacaaag aacaagattc ttattcagta 2880
gaaagtgaag agaaccaga agttatggct ccagtcagtt ctacacgttt gagcaacaa 2940
gtccttcctc atgatagtct tcctgcaaat agccagccat ctcgaggagg ccgctggggg 3000

```

aggaagaaca	gaaaaaccca	ggaacgtttt	ggtgataaag	attctaaact	gctcttgga	3060
gagacgtctt	cagctcctca	ggaacaatat	ggagaatgtg	gggagaaatc	agaagccacc	3120
caggaacaat	acactgaaag	tgaagaacag	ctggtggctt	ctgaggagca	gccaagccag	3180
gacgggaaac	ctgaccttcc	caagagaaga	ctcagtgagg	gggttgagcc	ctggcgagga	3240
cagctcaaga	aaagccctga	ggctctgaag	tgcagattaa	cagaaggaag	tgagaggctg	3300
ccccgtcgct	acagtgaggg	tgacagggct	gtcctcaggg	gcttcagtga	gagcagcgag	3360
gaggaggagg	agccggaaag	ccctcgggtc	agctcgccac	caattctcac	aaagcccacg	3420
ctgaagcgaa	agaaaccatt	tctccaccga	aggaggagag	tccgaaagcg	caaaccaccac	3480
aatagcagtg	tagtcacaga	aactatcttct	gagaccactg	aagtgttaga	tgaacctttt	3540
gaagattctg	actccgagag	gccaatgcc	agattagaac	ccacatttga	gatcgatgaa	3600
gaagaggagg	aagaggatga	aaatgaactt	ttccctagag	aatacttccg	tcgtttgtct	3660
tcgcaggatg	tactcaggtg	tcagtoctct	tctaagagga	agtctaaaga	tgaagaagaa	3720
gatgaagagt	cagatgatgc	tgatgacact	cctatcttaa	agccagtatc	tcttttgcga	3780
aaacgtgatg	tgaagaattc	tcctcttgag	ccagatacat	ccacaccttt	gaaaaagaaa	3840
aagggatggc	ccaaaggcaa	gagccgcaaa	ccaatccact	ggaagaaaag	acctgggtcga	3900
aaaccaggat	ttaagttgag	tcgggaaatc	atgccagttt	ctactcaagc	atgcgtcatt	3960
gagcccatcg	tttccattcc	taaagctgga	cgtaaacc	agatccagga	gagtgaagaa	4020
actgttgagc	caaaagaaga	catgccccta	cccaggagga	ggaaggagga	ggaggagatg	4080
caagcagagg	cagaagaggc	tgaagagggt	gaggaagagg	atgcagccag	cagtgaagtc	4140
ccagcagcct	ctccagcaga	cagcagcaat	agtcctgaga	ccgaaaccaa	ggagcctgag	4200
gtggaggagg	aagaagagaa	gccccgtgtc	ctcagggagc	agaggcagtc	agaggaggag	4260
cagcaggaat	tagaggagcc	agagccagag	gaggaggaaag	atgcagctgc	agagactgcc	4320
cagaatgacg	accacgacgc	tgatgatgag	gatgatggcc	acctggagtc	cacaaagaaa	4380
aaggagctag	aggaacagcc	cacgagggaa	gatgtcaagg	aggagcctgg	tggtcaagag	4440
tcttttttag	atgctaatat	gcagaagagt	agggaaaaga	taaaggataa	agaggaaacc	4500
gagctggatt	ccgaagagga	gcagccttcc	catgacacgt	ccgtgggtgc	agagcagatg	4560
gctgggtctg	aggacgacca	cgaagaagac	tcccacacta	aggaagagtt	aatcgaatta	4620
aaagaggagg	aagagattcc	tcatagttag	ctggatctgg	aaactgtaca	ggcagtgacg	4680
tctttgactc	aagaagaaag	cagttagcat	gagggcgctt	accaggactg	tgaggaaact	4740
cttcggcggt	gtcagaccct	gcagagttac	accaggctg	acgaggacc	tcagatgtcc	4800
atggttgaag	actgtcatgc	gtcagaacat	aatagcccta	tctcctccgt	tcagtctcac	4860
cccagccagt	cagtccgttc	ggtcagcagt	cccaacgtgc	ctgcccctga	gagtggctac	4920
accagatca	gcccagaaca	aggatccctg	tccgcaccct	ctatgcagaa	catggagacc	4980
agccccatga	tggatgtgcc	ttccgtatca	gaccactctc	agcaggtgg	ggacagcgcc	5040
ttcagtgacc	tgggcagcat	tgagagcacc	actgaaaact	atgagaacc	aagcagttac	5100
gactccacga	tggggcgag	catctgtggg	aacagctctt	cccagagcag	ctgctcctac	5160
ggtgggctgt	cgtcctccag	cagcctcacc	cagagcagct	gtgtgggtcac	tcagcagatg	5220
gccagcatgg	gcagcagctg	cagcatgatg	cagcagagca	gcgtccagcc	tgctgccaac	5280
tgacgcatca	agtcaccta	gagctgcgtg	gtggagaggc	ctcccagtaa	ccagcagcag	5340
cagccgccac	caccgcctcc	acagcagcca	cagccgcgc	cgccacaacc	acaaccagca	5400
ccacagcctc	caccacccca	gcagcagccg	caacagcagc	cgcagcctca	gccccagcag	5460
cctccacccc	caccctctcc	ccagcagcag	cccccgctgt	cacagtgtag	tatgaataac	5520
agtttcaccc	cagctcctat	gatcatggag	ataccagaat	ctggaagcac	tgggaacata	5580
agtatctatg	agaggattcc	aggggatttt	ggtgccggca	gctactctca	accatcagcc	5640
accttcagcc	tagccaagct	gcagcagctg	accaacacca	ttatggaccc	tcatgccatg	5700
ccttatagcc	attctcctgc	tgtgacttcc	tatgcaacca	gtgtttctct	gtccaataca	5760
ggactggctc	agctggctcc	atctcatccc	ttagctggga	ctcctcaagc	acaagccacc	5820
atgacgccac	ccccaactt	ggcatccact	accatgaacc	tcacatctcc	tctgcttcag	5880
tgcaacatgt	ctgccacca	cattggcatt	cctcacacgc	agagattgca	agggcaaatg	5940
ccagtgaagg	ggcacatttc	catccgctcc	aagtctgcgc	cactgccctc	tcgggctgct	6000
caccagcagc	agctgtatgg	ccgtagccca	tcggcagttg	ccatgcaggc	tggccctcgc	6060
gcactggctg	ttcagcgtgg	catgaacatg	ggggttaatc	tgatgcctac	tccgcctat	6120
aatgtcaatt	ccatgaatat	gaacaccttg	aatgccatga	acagctatcg	aatgacacag	6180
cccattgatga	acagcagtta	ccatagtaac	cctgcctaca	tgaaccagac	agcacagtat	6240
cctatgcaga	tgacagatggg	aatgatgggg	agccaggcct	atacccagca	gcctatgcag	6300
cctaaccctc	atgggaacat	gatgtacaca	ggccctccc	atcacagcta	catgaacgct	6360
gctggcgtgc	ccaagcagtc	actcaacgga	ccttacatga	gaagatgagc	aagatgaact	6420
tgcaatcaaa	aaottaaata	tatataaata	aaggaaacct	ttatactgac	aaaccagaga	6480

198/299

```

aaaatggacc tttttccagt taaaatattg ctgtagattt agaggaattt ttcttttggtt 6540
tattttatatt tttagaaaac ctgatcttct cttttttttg ggttcatttt gttgtgggtt 6600
ttggtttttct tcacaatctt gaacatttta cagtagaact catctaaaaa tggatttggg 6660
gatgggggaaa catgcacaaa atcttttcat aattaaaaag agccttactt tctttacata 6720
ccacatggac agaatttgtg taaaagtga ttatctttat tttaaaatgt atgtttcccc 6780
tcactgtttg cagctcccaa tgttgtcatt tttaaatgtt atatacatct caaggggtaa 6840
ccagaccctt tctccaaac ccaacctttc atttcctact tcattccagc aggaggcact 6900
taggggagac tcggatgggg acatggagaa caaccgaagc tctttaaact tattattatt 6960
gttaatatatta ttattattat tattaataaa gtgaggcagg aaaatgcttc tcctttttaa 7020
atccccctcca ctctcacac acacacacct ctgtgaaacc tcccccaaga atgtttcttt 7080
atagacggac ttcattgaaa tctttgttgt tcttgaatca agtgtaatat aatttttttc 7140
ttcttttttta aaatattccc actcagcact cagagacaca aaaatactgt aagtctcaat 7200
taacagcaga atctcagaga aaagctgttt gcaatccaaa tccagccttt ggaggaatag 7260
agatgggtcaa ttaacaatca aaaagaggag attaacctct tgttttttta ccacctggtg 7320
aatcagccat aacgcacaca cagccacccc agcctcttgt ttctagtatg tactttgaaa 7380
tgctaactga gggctttgat gcttgagcct ttgactgata aaactcaa at agcagtcccc 7440
agtgttttgc ctcttaggtt ctttctttaa ttgttgggtg atgactgtac attttagtga 7500
tttgaaaaat aactgacaaa ccattgaaac agtttatatt atgttggaag agatggcgca 7560
gatgtgtgtc agaagggaga tcacggtgtg agtttcgtag ctatttaagt gatacatacc 7620
tctagttttt gtatgtcttt tgagatcctg agttcatccc ctgtgaatca gagtgcacaa 7680
gcacctctcc tgtgagtgcc taatgagaag agggacagac cgaccaccag cacagtaggg 7740
cagatctgga cagcagaatg ttataacgca agttcatgtg ttgctcccaa ctccattctc 7800
ttttctctcg tgcaaccagt ttgcccattc tcttcctatt acttgctcca gggataggta 7860
aaaaaaaaa

```

<210> 252

<211> 2442

<212> PRT

<213> Homo sapiens

<400> 252

```

Met Ala Glu Asn Leu Leu Asp Gly Pro Pro Asn Pro Lys Arg Ala Lys
  1                      5                      10                     15

Leu Ser Ser Pro Gly Phe Ser Ala Asn Asp Ser Thr Asp Phe Gly Ser
      20                      25                     30

Leu Phe Asp Leu Glu Asn Asp Leu Pro Asp Glu Leu Ile Pro Asn Gly
      35                      40                     45

Gly Glu Leu Gly Leu Leu Asn Ser Gly Asn Leu Val Pro Asp Ala Ala
      50                      55                     60

Ser Lys His Lys Gln Leu Ser Glu Leu Leu Arg Gly Gly Ser Gly Ser
      65                      70                     75                     80

Ser Ile Asn Pro Gly Ile Gly Asn Val Ser Ala Ser Ser Pro Val Gln
      85                      90                     95

Gln Gly Leu Gly Gly Gln Ala Gln Gly Gln Pro Asn Ser Ala Asn Met
      100                     105                    110

Ala Ser Leu Ser Ala Met Gly Lys Ser Pro Leu Ser Gln Gly Asp Ser
      115                     120                    125

Ser Ala Pro Ser Leu Pro Lys Gln Ala Ala Ser Thr Ser Gly Pro Thr
      130                     135                    140

```

199/299

Pro Ala Ala Ser Gln Ala Leu Asn Pro Gln Ala Gln Lys Gln Val Gly
 145 150 155 160
 Leu Ala Thr Ser Ser Pro Ala Thr Ser Gln Thr Gly Pro Gly Ile Cys
 165 170 175
 Met Asn Ala Asn Phe Asn Gln Thr His Pro Gly Leu Leu Asn Ser Asn
 180 185 190
 Ser Gly His Ser Leu Ile Asn Gln Ala Ser Gln Gly Gln Ala Gln Val
 195 200 205
 Met Asn Gly Ser Leu Gly Ala Ala Gly Arg Gly Arg Gly Ala Gly Met
 210 215 220
 Pro Tyr Pro Thr Pro Ala Met Gln Gly Ala Ser Ser Ser Val Leu Ala
 225 230 235 240
 Glu Thr Leu Thr Gln Val Ser Pro Gln Met Thr Gly His Ala Gly Leu
 245 250 255
 Asn Thr Ala Gln Ala Gly Gly Met Ala Lys Met Gly Ile Thr Gly Asn
 260 265 270
 Thr Ser Pro Phe Gly Gln Pro Phe Ser Gln Ala Gly Gly Gln Pro Met
 275 280 285
 Gly Ala Thr Gly Val Asn Pro Gln Leu Ala Ser Lys Gln Ser Met Val
 290 295 300
 Asn Ser Leu Pro Thr Phe Pro Thr Asp Ile Lys Asn Thr Ser Val Thr
 305 310 315 320
 Asn Val Pro Asn Met Ser Gln Met Gln Thr Ser Val Gly Ile Val Pro
 325 330 335
 Thr Gln Ala Ile Ala Thr Gly Pro Thr Ala Asp Pro Glu Lys Arg Lys
 340 345 350
 Leu Ile Gln Gln Gln Leu Val Leu Leu Leu His Ala His Lys Cys Gln
 355 360 365
 Arg Arg Glu Gln Ala Asn Gly Glu Val Arg Ala Cys Ser Leu Pro His
 370 375 380
 Cys Arg Thr Met Lys Asn Val Leu Asn His Met Thr His Cys Gln Ala
 385 390 395 400
 Gly Lys Ala Cys Gln Val Ala His Cys Ala Ser Ser Arg Gln Ile Ile
 405 410 415
 Ser His Trp Lys Asn Cys Thr Arg His Asp Cys Pro Val Cys Leu Pro
 420 425 430
 Leu Lys Asn Ala Ser Asp Lys Arg Asn Gln Gln Thr Ile Leu Gly Ser
 435 440 445

200/299

Pro Ala Ser Gly Ile Gln Asn Thr Ile Gly Ser Val Gly Thr Gly Gln
 450 455 460
 Gln Asn Ala Thr Ser Leu Ser Asn Pro Asn Pro Ile Asp Pro Ser Ser
 465 470 475 480
 Met Gln Arg Ala Tyr Ala Ala Leu Gly Leu Pro Tyr Met Asn Gln Pro
 485 490 495
 Gln Thr Gln Leu Gln Pro Gln Val Pro Gly Gln Gln Pro Ala Gln Pro
 500 505 510
 Gln Thr His Gln Gln Met Arg Thr Leu Asn Pro Leu Gly Asn Asn Pro
 515 520 525
 Met Asn Ile Pro Ala Gly Gly Ile Thr Thr Asp Gln Gln Pro Pro Asn
 530 535 540
 Leu Ile Ser Glu Ser Ala Leu Pro Thr Ser Leu Gly Ala Thr Asn Pro
 545 550 555 560
 Leu Met Asn Asp Gly Ser Asn Ser Gly Asn Ile Gly Thr Leu Ser Thr
 565 570 575
 Ile Pro Thr Ala Ala Pro Pro Ser Ser Thr Gly Val Arg Lys Gly Trp
 580 585 590
 His Glu His Val Thr Gln Asp Leu Arg Ser His Leu Val His Lys Leu
 595 600 605
 Val Gln Ala Ile Phe Pro Thr Pro Asp Pro Ala Ala Leu Lys Asp Arg
 610 615 620
 Arg Met Glu Asn Leu Val Ala Tyr Ala Lys Lys Val Glu Gly Asp Met
 625 630 635 640
 Tyr Glu Ser Ala Asn Ser Arg Asp Glu Tyr Tyr His Leu Leu Ala Glu
 645 650 655
 Lys Ile Tyr Lys Ile Gln Lys Glu Leu Glu Glu Lys Arg Arg Ser Arg
 660 665 670
 Leu His Lys Gln Gly Ile Leu Gly Asn Gln Pro Ala Leu Pro Ala Pro
 675 680 685
 Gly Ala Gln Pro Pro Val Ile Pro Gln Ala Gln Pro Val Arg Pro Pro
 690 695 700
 Asn Gly Pro Leu Ser Leu Pro Val Asn Arg Met Gln Val Ser Gln Gly
 705 710 715 720
 Met Asn Ser Phe Asn Pro Met Ser Leu Gly Asn Val Gln Leu Pro Gln
 725 730 735
 Ala Pro Met Gly Pro Arg Ala Ala Ser Pro Met Asn His Ser Val Gln
 740 745 750
 Met Asn Ser Met Gly Ser Val Pro Gly Met Ala Ile Ser Pro Ser Arg

201/299

755					760					765					
Met	Pro	Gln	Pro	Pro	Asn	Met	Met	Gly	Ala	His	Thr	Asn	Asn	Met	Met
770						775					780				
Ala	Gln	Ala	Pro	Ala	Gln	Ser	Gln	Phe	Leu	Pro	Gln	Asn	Gln	Phe	Pro
785					790					795					800
Ser	Ser	Ser	Gly	Ala	Met	Ser	Val	Gly	Met	Gly	Gln	Pro	Pro	Ala	Gln
				805					810					815	
Thr	Gly	Val	Ser	Gln	Gly	Gln	Val	Pro	Gly	Ala	Ala	Leu	Pro	Asn	Pro
			820					825					830		
Leu	Asn	Met	Leu	Gly	Pro	Gln	Ala	Ser	Gln	Leu	Pro	Cys	Pro	Pro	Val
		835					840					845			
Thr	Gln	Ser	Pro	Leu	His	Pro	Thr	Pro	Pro	Pro	Ala	Ser	Thr	Ala	Ala
		850				855					860				
Gly	Met	Pro	Ser	Leu	Gln	His	Thr	Thr	Pro	Pro	Gly	Met	Thr	Pro	Pro
865					870					875					880
Gln	Pro	Ala	Ala	Pro	Thr	Gln	Pro	Ser	Thr	Pro	Val	Ser	Ser	Ser	Gly
				885					890					895	
Gln	Thr	Pro	Thr	Pro	Thr	Pro	Gly	Ser	Val	Pro	Ser	Ala	Thr	Gln	Thr
			900					905					910		
Gln	Ser	Thr	Pro	Thr	Val	Gln	Ala	Ala	Ala	Gln	Ala	Gln	Val	Thr	Pro
		915					920					925			
Gln	Pro	Gln	Thr	Pro	Val	Gln	Pro	Pro	Ser	Val	Ala	Thr	Pro	Gln	Ser
		930					935				940				
Ser	Gln	Gln	Gln	Pro	Thr	Pro	Val	His	Ala	Gln	Pro	Pro	Gly	Thr	Pro
945					950					955					960
Leu	Ser	Gln	Ala	Ala	Ala	Ser	Ile	Asp	Asn	Arg	Val	Pro	Thr	Pro	Ser
			965						970					975	
Ser	Val	Ala	Ser	Ala	Glu	Thr	Asn	Ser	Gln	Gln	Pro	Gly	Pro	Asp	Val
			980					985					990		
Pro	Val	Leu	Glu	Met	Lys	Thr	Glu	Thr	Gln	Ala	Glu	Asp	Thr	Glu	Pro
		995				1000						1005			
Asp	Pro	Gly	Glu	Ser	Lys	Gly	Glu	Pro	Arg	Ser	Glu	Met	Met	Glu	Glu
1010						1015					1020				
Asp	Leu	Gln	Gly	Ala	Ser	Gln	Val	Lys	Glu	Glu	Thr	Asp	Ile	Ala	Glu
1025					1030					1035					1040
Gln	Lys	Ser	Glu	Pro	Met	Glu	Val	Asp	Glu	Lys	Lys	Pro	Glu	Val	Lys
			1045						1050					1055	
Val	Glu	Val	Lys	Glu	Glu	Glu	Glu	Ser	Ser	Ser	Asn	Gly	Thr	Ala	Ser
			1060					1065					1070		

202/299

Gln Ser Thr Ser Pro Ser Gln Pro Arg Lys Lys Ile Phe Lys Pro Glu
 1075 1080 1085
 Glu Leu Arg Gln Ala Leu Met Pro Thr Leu Glu Ala Leu Tyr Arg Gln
 1090 1095 1100
 Asp Pro Glu Ser Leu Pro Phe Arg Gln Pro Val Asp Pro Gln Leu Leu
 1105 1110 1115 1120
 Gly Ile Pro Asp Tyr Phe Asp Ile Val Lys Asn Pro Met Asp Leu Ser
 1125 1130 1135
 Thr Ile Lys Arg Lys Leu Asp Thr Gly Gln Tyr Gln Glu Pro Trp Gln
 1140 1145 1150
 Tyr Val Asp Asp Val Trp Leu Met Phe Asn Asn Ala Trp Leu Tyr Asn
 1155 1160 1165
 Arg Lys Thr Ser Arg Val Tyr Lys Phe Cys Ser Lys Leu Ala Glu Val
 1170 1175 1180
 Phe Glu Gln Glu Ile Asp Pro Val Met Gln Ser Leu Gly Tyr Cys Cys
 1185 1190 1195 1200
 Gly Arg Lys Tyr Glu Phe Ser Pro Gln Thr Leu Cys Cys Tyr Gly Lys
 1205 1210 1215
 Gln Leu Cys Thr Ile Pro Arg Asp Ala Ala Tyr Tyr Ser Tyr Gln Asn
 1220 1225 1230
 Arg Tyr His Phe Cys Glu Lys Cys Phe Thr Glu Ile Gln Gly Glu Asn
 1235 1240 1245
 Val Thr Leu Gly Asp Asp Pro Ser Gln Pro Gln Thr Thr Ile Ser Lys
 1250 1255 1260
 Asp Gln Phe Glu Lys Lys Lys Asn Asp Thr Leu Asp Pro Glu Pro Phe
 1265 1270 1275 1280
 Val Asp Cys Lys Glu Cys Gly Arg Lys Met His Gln Ile Cys Val Leu
 1285 1290 1295
 His Tyr Asp Ile Ile Trp Pro Ser Gly Phe Val Cys Asp Asn Cys Leu
 1300 1305 1310
 Lys Lys Thr Gly Arg Pro Arg Lys Glu Asn Lys Phe Ser Ala Lys Arg
 1315 1320 1325
 Leu Gln Thr Thr Arg Leu Gly Asn His Leu Glu Asp Arg Val Asn Lys
 1330 1335 1340
 Phe Leu Arg Arg Gln Asn His Pro Glu Ala Gly Glu Val Phe Val Arg
 1345 1350 1355 1360
 Val Val Ala Ser Ser Asp Lys Thr Val Glu Val Lys Pro Gly Met Lys
 1365 1370 1375

203/299

Ser Arg Phe Val Asp Ser Gly Glu Met Ser Glu Ser Phe Pro Tyr Arg
 1380 1385 1390
 Thr Lys Ala Leu Phe Ala Phe Glu Glu Ile Asp Gly Val Asp Val Cys
 1395 1400 1405
 Phe Phe Gly Met His Val Gln Glu Tyr Gly Ser Asp Cys Pro Pro Pro
 1410 1415 1420
 Asn Thr Arg Arg Val Tyr Ile Ser Tyr Leu Asp Ser Ile His Phe Phe
 1425 1430 1435 1440
 Arg Pro Arg Cys Leu Arg Thr Ala Val Tyr His Glu Ile Leu Ile Gly
 1445 1450 1455
 Tyr Leu Glu Tyr Val Lys Lys Leu Gly Tyr Val Thr Gly His Ile Trp
 1460 1465 1470
 Ala Cys Pro Pro Ser Glu Gly Asp Asp Tyr Ile Phe His Cys His Pro
 1475 1480 1485
 Pro Asp Gln Lys Ile Pro Lys Pro Lys Arg Leu Gln Glu Trp Tyr Lys
 1490 1495 1500
 Lys Met Leu Asp Lys Ala Phe Ala Glu Arg Ile Ile His Asp Tyr Lys
 1505 1510 1515 1520
 Asp Ile Phe Lys Gln Ala Thr Glu Asp Arg Leu Thr Ser Ala Lys Glu
 1525 1530 1535
 Leu Pro Tyr Phe Glu Gly Asp Phe Trp Pro Asn Val Leu Glu Glu Ser
 1540 1545 1550
 Ile Lys Glu Leu Glu Gln Glu Glu Glu Glu Arg Lys Lys Glu Glu Ser
 1555 1560 1565
 Thr Ala Ala Ser Glu Thr Thr Glu Gly Ser Gln Gly Asp Ser Lys Asn
 1570 1575 1580
 Ala Lys Lys Lys Asn Asn Lys Lys Thr Asn Lys Asn Lys Ser Ser Ile
 1585 1590 1595 1600
 Ser Arg Ala Asn Lys Lys Lys Pro Ser Met Pro Asn Val Ser Asn Asp
 1605 1610 1615
 Leu Ser Gln Lys Leu Tyr Ala Thr Met Glu Lys His Lys Glu Val Phe
 1620 1625 1630
 Phe Val Ile His Leu His Ala Gly Pro Val Ile Asn Thr Leu Pro Pro
 1635 1640 1645
 Ile Val Asp Pro Asp Pro Leu Leu Ser Cys Asp Leu Met Asp Gly Arg
 1650 1655 1660
 Asp Ala Phe Leu Thr Leu Ala Arg Asp Lys His Trp Glu Phe Ser Ser
 1665 1670 1675 1680
 Leu Arg Arg Ser Lys Trp Ser Thr Leu Cys Met Leu Val Glu Leu His

204/299

1685	1690	1695
Thr Gln Gly Gln Asp Arg Phe Val Tyr Thr Cys Asn Glu Cys Lys His 1700	1705	1710
His Val Glu Thr Arg Trp His Cys Thr Val Cys Glu Asp Tyr Asp Leu 1715	1720	1725
Cys Ile Asn Cys Tyr Asn Thr Lys Ser His Ala His Lys Met Val Lys 1730	1735	1740
Trp Gly Leu Gly Leu Asp Asp Glu Gly Ser Ser Gln Gly Glu Pro Gln 1745	1750	1755
Ser Lys Ser Pro Gln Glu Ser Arg Arg Leu Ser Ile Gln Arg Cys Ile 1765	1770	1775
Gln Ser Leu Val His Ala Cys Gln Cys Arg Asn Ala Asn Cys Ser Leu 1780	1785	1790
Pro Ser Cys Gln Lys Met Lys Arg Val Val Gln His Thr Lys Gly Cys 1795	1800	1805
Lys Arg Lys Thr Asn Gly Gly Cys Pro Val Cys Lys Gln Leu Ile Ala 1810	1815	1820
Leu Cys Cys Tyr His Ala Lys His Cys Gln Glu Asn Lys Cys Pro Val 1825	1830	1835
Pro Phe Cys Leu Asn Ile Lys His Lys Leu Arg Gln Gln Gln Ile Gln 1845	1850	1855
His Arg Leu Gln Gln Ala Gln Leu Met Arg Arg Arg Met Ala Thr Met 1860	1865	1870
Asn Thr Arg Asn Val Pro Gln Gln Ser Leu Pro Ser Pro Thr Ser Ala 1875	1880	1885
Pro Pro Gly Thr Pro Thr Gln Gln Pro Ser Thr Pro Gln Thr Pro Gln 1890	1895	1900
Pro Pro Ala Gln Pro Gln Pro Ser Pro Val Ser Met Ser Pro Ala Gly 1905	1910	1915
Phe Pro Ser Val Ala Arg Thr Gln Pro Pro Thr Thr Val Ser Thr Gly 1925	1930	1935
Lys Pro Thr Ser Gln Val Pro Ala Pro Pro Pro Pro Ala Gln Pro Pro 1940	1945	1950
Pro Ala Ala Val Glu Ala Ala Arg Gln Ile Glu Arg Glu Ala Gln Gln 1955	1960	1965
Gln Gln His Leu Tyr Arg Val Asn Ile Asn Asn Ser Met Pro Pro Gly 1970	1975	1980
Arg Thr Gly Met Gly Thr Pro Gly Ser Gln Met Ala Pro Val Ser Leu 1985	1990	1995
		2000

205/299

[illegible]

206/299

Ile Gly Ser Pro Gly Gln Pro Asn Pro Met Ser Pro Gln Gln His Met
2305 2310 2315 2320

Leu Ser Gly Gln Pro Gln Ala Ser His Leu Pro Gly Gln Gln Ile Ala
2325 2330 2335

Thr Ser Leu Ser Asn Gln Val Arg Ser Pro Ala Pro Val Gln Ser Pro
2340 2345 2350

Arg Pro Gln Ser Gln Pro Pro His Ser Ser Pro Ser Pro Arg Ile Gln
2355 2360 2365

Pro Gln Pro Ser Pro His His Val Ser Pro Gln Thr Gly Ser Pro His
2370 2375 2380

Pro Gly Leu Ala Val Thr Met Ala Ser Ser Ile Asp Gln Gly His Leu
2385 2390 2395 2400

Gly Asn Pro Glu Gln Ser Ala Met Leu Pro Gln Leu Asn Thr Pro Ser
2405 2410 2415

Arg Ser Ala Leu Ser Ser Glu Leu Ser Leu Val Gly Asp Thr Thr Gly
2420 2425 2430

Asp Thr Leu Glu Lys Phe Val Glu Gly Leu
2435 2440

<210> 253

<211> 8147

<212> DNA

<213> Homo sapiens

<400> 253

tccgaattcc ttttttttaa ttgaggaatc aacagccgcc atcttgtcgc ggacccgacc 60
ggggcttcga gcgcgatcta ctcgcccccg ccggtcccgg gccccacaac cggccgcgca 120
ccccgctccg cccggccggc ccgctccgcc cggccctcgg cggccgcccc ggccggccccg 180
ctcgctcttc ggctcggcct cccggagccc ggccggcggc ggccggcggc cggccggcggc 240
ggccggcggaa cgggggggtgg gggggccgcg gcggcggcgg cgaccccgct cggcgcatg 300
ttttctctca cggcgccggc ggccggcggc gcggggccgg gagcggagcc cggagcccc 360
tcgtcgtcgg gccgcgagcg aattcattaa gtggggcggc gggggggagc gaggcggcgg 420
cggcgccggc accatgttct cggggactgc ctgagccgcc cggccggggc ccgtcgtctgc 480
cagccggggc cggggggggc gccggggccg cggggcgccc ccaccgagg gtgtcgcgct 540
cgggagggcg gcaggggatg agggggccgc ggccggcggc ggccggcggc gccggggggc 600
ggcggtgagc gctgcggggc gctgttgctg tggctgagat ttggccgccc cctccccac 660
cgggcttgcg ccctccctct ccctcggcgc ccgcccgcgc cgtcgcggc gcccgcgctc 720
gtcctctccc ctgcagccg gcagggcccc cgacccccgt cggggccctc gccggcccg 780
ccgcccgtgc cgggggctgt tttcgcgagc aggtgaaaat ggctgagaac ttgctggacg 840
gaccgccccaa ccccaaaaaga gccaaaactca gctcgcccg tttctcggc aatgacagca 900
cagatttttg atcattgttt gacttggaaa atgatcttcc tgatgagctg ataccata 960
gaggagaatt aggcctttta aacagtggga acctgttcc agatgctgct tccaaacata 1020
aacaactgtc ggagcttcta cgaggaggca gcggctctag tatcaacca ggaataggaa 1080
atgtgagcgc cagcagcccc gtgcagcagg gcctgggtgg ccaggctcaa gggcagccga 1140
acagtgtctaa catggccagc ctacgtgcca tgggcaagag ccctctgagc caggagatt 1200
cttcagcccc cagcctgcct aaacaggcag ccagcacctc tggggccacc cccgctgcct 1260
cccaagcact gaatccgcaa gcacaaaagc aagtggggct ggcgactagc agccctgcca 1320
cgtcacagac tggacctggc atctgcatga atgctaactt taaccagacc caccagggc 1380
tcctcaatag taactctggc catagcttaa ttaatcaggc ttcacaaggc caggcgcaag 1440

207/299

tcataaatgg	atctcttggg	gctgctggca	gaggaagggg	agctggaatg	ccgtacccta	1500
ctccagccat	gcagggcgcc	tcgagcagcg	tgtctggctga	gaccctaacg	cagggtttccc	1560
cgcaaatgac	tggtcacgcg	ggactgaaca	ccgcacaggg	aggaggcatg	gccaagatgg	1620
gaataactgg	gaacacaagt	ccatttggac	agccctttag	tcaagctgga	gggcagccaa	1680
tgggagccac	tggagtgaac	ccccagttag	ccagcaaaaca	gagcatggtc	aacagtttgc	1740
ccaccttccc	tacagatatc	aagaataact	cagtcaccaa	cgtgccaaat	atgtctcaga	1800
tgc aaacatc	agtgggaatt	gtacccacac	aagcaattgc	aacaggcccc	actgcagatc	1860
ctgaaaaacg	caaactgata	cagcagcagc	tggttctact	gcttcctgct	cataagtgtc	1920
agagacgaga	gcaagcaaac	ggagagggtc	gggcctgctc	gctcccgcct	tgtcgaacca	1980
tgaaaaacgt	tttgaatcac	atgacgcatt	gtcaggctgg	gaaagcctgc	caagttgccc	2040
attgtgcac	ttcacgacaa	atcatctctc	attggaagaa	ctgcacacga	catgactgtc	2100
ctgttttgct	ccctttgaaa	aatgccagtg	acaagcgaaa	ccaacaaacc	atcctggggg	2160
ctccagctag	tgaattcaa	aacacaattg	gttctgttgg	cacagggcaa	cagaatgcca	2220
cttctttaag	taaccacaat	cccatagacc	ccagctccat	gcagcgagcc	tatgctgctc	2280
tcggactccc	ctacatgaac	cagccccaga	cgcagctgca	gcctcagggt	cctggccagc	2340
aaccagcaca	gcctcaaacc	caccagcaga	tgaggactct	caacccccct	ggaaataatc	2400
caatgaacat	tccagcagga	ggaataacaa	cagatcagca	gccccaaac	ttgatttcag	2460
aatcagctct	tccgacttcc	ctggggggcca	caaaccocact	gatgaacgat	ggctccaact	2520
ctggtaacat	tggaaacctc	agcactatac	caacagcagc	tcctccttct	agcaaccgtg	2580
taaggaaagg	ctggcacgaa	catgtcactc	aggacctgcg	gagccatcta	gtgcataaac	2640
tcgtccaagc	catcttccca	acacctgatc	ccgcagctct	aaaggatcgc	cgcagtgaaa	2700
acctggttag	ctatgttag	aaagtggaa	gggacatgta	cgagtctgcc	aacagcaggg	2760
atgaatatta	tcacttatta	gcagagaaaa	tctacaagat	acaaaaagaa	ctagaagaaa	2820
aacggagggtc	gcgtttacat	aaacaaggca	tcttggggaa	ccagccagcc	ttaccagccc	2880
cgggggctca	gccccctgtg	attccacagg	cacaacctgt	gagacctcca	aatggacccc	2940
tgtccctgcc	agtgaatcgc	atgcaagttt	ctcaagggat	gaattcattt	aaccccatgt	3000
ccttggggaa	cgtccagttg	ccacaagcac	ccatgggacc	tcgtgcagcc	tccccaatga	3060
accactctgt	ccagatgaac	agcatgggct	cagtgccagg	gatggccatt	tctccttccc	3120
gaatgcctca	gcctccgaac	atgatgggtg	cacacaccaa	caacatgatg	gcccaggcgc	3180
ccgctcagag	ccagtttctg	ccacagaacc	agttcccgtc	atccagcggg	gcgatgagtg	3240
tgggcatggg	gcagccgcca	gccccaaacag	gcgtgtcaca	gggacagggt	cctgggtgctg	3300
ctcttccata	ccctctcaac	atgctggggc	ctcaggccag	ccagctacct	tgcctccag	3360
tgacacagtc	accactgcac	ccaacaccgc	ctcctgcttc	cacggctgct	ggcatgccat	3420
ctctccagca	cacgacacca	cctgggatga	ctcctcccca	gccagcagct	cccactcagc	3480
catcaactcc	tgtgtcgtct	tccgggcaga	ctcccacccc	gactcctggc	tcagtgccca	3540
gtgtacacca	aaccacagag	acccctacag	tccaggcagc	agcccaggcc	cagggtgaccc	3600
cgcagcctca	aacccagtt	cagcccccg	ctgtggctac	ccctcagtc	tcgcagcaac	3660
agccgacgcc	tgtgcacgcc	cagcctcctg	gcacacccgt	ttcccaggca	gcagccagca	3720
ttgataacctg	agtccttacc	ccctcctcgg	tggccagcgc	agaaaccaat	tcccagcagc	3780
caggacagca	cgtacctgtg	ctggaaatga	agacggagac	ccaagcagag	gacactgagc	3840
ccgatcctgg	tgaatccaaa	ggggagccca	ggtctgagat	gatggaggag	gatttgcaag	3900
gagcttccca	agttaaagaa	gaaacagaca	tagcagagca	gaaatcagaa	ccaatggaag	3960
tggatgaaaa	gaaacctgaa	gtgaaagtag	aagttaaaga	ggaagaagag	agtagcagta	4020
acggcacagc	ctctcagtc	acatctcctt	cgcagccgcg	caaaaaaatc	tttaaaccag	4080
aggagttacg	ccaggccctc	atgccaaacc	tagaagcact	gtatcgacag	gacccagagt	4140
cattaccttt	ccggcagcct	gtagatcccc	agctcctcgg	aattccagac	tattttgaca	4200
tcgtaaagaa	tcccatggac	ctctccacca	tcaagcggaa	gctggacaca	gggcaatacc	4260
aagagccctg	gcagtacgtg	gacgacgtct	ggctcatggt	caacaatgcc	tggctctata	4320
atcgcaagac	atcccagatc	tataagtttt	gcagtaagct	tgcagagggt	tttgagcagg	4380
aaattgaccc	tgtcatgcag	tcccttggat	attgctgtgg	acgcaagtat	gagttttccc	4440
cacagacttt	gtgctgctat	gggaagcagc	tgtgtaccat	tcctcgcat	gctgcctact	4500
acagctatca	gaataggtat	catttctgtg	agaagtgttt	cacagagatc	cagggcgaga	4560
atgtgaccct	gggtgacgac	ccttcacagc	cccagacgac	aatttcaaag	gatcagtttg	4620
aaaagaagaa	aaatgatacc	ttagaaccgc	aacctttcgt	tgattgcaag	gagtgtggcc	4680
ggaagatgca	tcagatttgc	gttctgcact	atgacatcat	ttggccttca	ggttttgtgt	4740
gcgacaactg	cttgaagaaa	actggcagac	ctcgaaaaga	aaacaaattc	agtgtctaga	4800
ggctgcagac	cacaagactg	ggaaaccact	tggaaagacc	agtgaacaaa	tttttgccgc	4860
gccagaatca	ccctgaagcc	ggggagggtt	ttgtccgagt	ggtggccagc	tcagacaaga	4920

208/299

cggtggaggt	caagccccggg	atgaagtcaac	ggtttgtgga	ttctggggaa	atgtctgaat	4980
ctttcccata	togaacccaaa	gctctgtttg	cttttgagga	aattgacggc	gtggatgtct	5040
gcttttttgg	aatgcacgtc	caagaatacg	gctctgattg	ccccctcca	aacacgaggc	5100
gtgtgtacat	ttcttatctg	gatagtattc	atttcttccg	gccacgttgc	ctccgcacag	5160
ccgtttacca	tgagatcctt	attggatatt	tagagtatgt	gaagaaatta	gggtatgtga	5220
cagggcacat	ctgggcctgt	cctccaagtg	aaggagatga	ttacatcttc	cattgccacc	5280
cacctgatca	aaaaataccc	aagccaaaac	gactgcagga	gtggtacaaa	aagatgctgg	5340
acaaggcgtt	tgcagagcgg	atcatccatg	actacaagga	tattttcaaa	caagcaactg	5400
aagacaggct	caccagtgcc	aaggaactgc	cctattttga	aggtgatttc	tggcccaatg	5460
tgttagaaga	gagcattaag	gaactagaac	aagaagaaga	ggagaggaaa	aaggaagaga	5520
gactgcagc	cagtgaacc	actgagggca	gtcagggcga	cagcaagaat	gccaaagaga	5580
agaacaacaa	gaaaaccaac	aagaacaaaa	gcagcatcag	ccgcgccaac	aagaagaagc	5640
ccagatgcc	caacgtgtcc	aatgacctgt	ccagaagct	gtatgccacc	atggagaagc	5700
acaaggaggt	cttcttcgtg	atccacctgc	acgtggggcc	tgtcatcaac	accctgcccc	5760
ccatcgtcga	ccccgacccc	ctgctcagct	gtgacctcat	ggatggggcg	gacgccttcc	5820
tcacctctgc	cagagacaag	cactgggagt	tctctctctt	gcgcgcctcc	aagtgggtcca	5880
cgctctgcat	gctggtggag	ctgcacaccc	agggccagga	ccgctttgtc	tacacctgca	5940
acgagtgcaa	gcaccacgtg	gagacgcgct	ggcactgcac	tgtgtgcgag	gactacgacc	6000
tctgcatcaa	ctgctataac	acgaagagcc	atgcccataa	gatggtgaag	tgggggctgg	6060
gcctggatga	cgagggcagc	agccaggggc	agccacagtc	aaagagcccc	caggagtcac	6120
gccggctgag	catccagcgc	tgcattccagt	cgctggtgca	cgcgtgccag	tgccgcaacg	6180
ccaactgtct	gctgccatcc	tgccagaaga	tgaagcgggt	ggtgcagcac	accaagggct	6240
gcaaacgcaa	gaccaacggg	ggctgcccgg	tgtgcaagca	gctcatcgcc	ctctgctgct	6300
accacgccaa	gcaactgcaa	gaaaaacaaat	gccccgtgcc	cttctgcctc	aacatcaaac	6360
acaagctccg	ccagcagcag	atccagcacc	gcctgcagca	ggcccagctc	atgcgccggc	6420
ggatggccac	catgaacacc	cgcaacgtgc	ctcagcagag	tctgccttct	cctacctcag	6480
caccgcccgg	gacccccaca	cagcagccca	gcacacccca	gacgcgcgag	ccccctgccc	6540
agcccccaacc	ctcaccctgt	agcatgtcac	cagctggctt	ccccagcgtg	gcccggactc	6600
agccccccac	cacggtgtcc	acagggaagc	ctaccagcca	ggtgcggggc	ccccaccccc	6660
cggcccagcc	ccctctctga	gcggtggaag	cggctcgcca	gatcgagcgt	gaggcccagc	6720
agcagcagca	cctgtaccgg	gtgaacatca	acaacagcat	gcccccagga	cgcacgggca	6780
tggggacccc	ggggagccag	atggcccccg	tgagcctgaa	tgtgccccga	cccaaccagg	6840
tgagcggggc	cgctcatgccc	agcatgcctc	ccgggcagtg	gcagcaggcg	ccccttcccc	6900
agcagcagcc	catgccaggc	ttgccccaggc	ctgtgatatc	catgcaggcc	caggcggccg	6960
tggctggggc	ccggatgccc	agcgtgcagc	cacccaggag	catctcacc	agcgtctgct	7020
aagacctgct	gcggaccctg	aagtgcacca	gctccccctc	gcagcaacag	cagggtgtga	7080
acattctcaa	atcaaacccc	cagctaattg	cagctttcat	caaacagcgc	acagccaaat	7140
acgtggccaa	tcagcccggc	atgcagcccc	agcctggcct	ccagtcccag	ccgggcatgc	7200
aaccccagcc	tggcatgcac	cagcagccca	gcctgcagaa	cctgaatgcc	atgcaggctg	7260
gcgtgcgcgg	gcccgggtgtg	cctccacagc	agcaggcgat	gggaggcctg	aaccccagg	7320
gccaggcctt	gaacatcatg	aacccaggac	acaaccccaa	catggcgagt	atgaatccac	7380
agtaccgaga	aatgttacgg	aggcagctgc	tgcagcagca	gcagcaacag	cagcagcaac	7440
aacagcagca	acagcagcag	cagcaaggga	gtgccggcat	ggctgggggc	atggcggggc	7500
acggccagtt	ccagcagcct	caaggacccg	gaggctaccc	accggccatg	cagcagcagc	7560
agcgcagtga	gcagcatctc	cccctccagg	gcagctccat	gggcccagatg	gcggctcaga	7620
tgggacagct	tggccagatg	gggcagccgg	ggctgggggc	agacagcacc	cccaacatcc	7680
agcaagccct	gcagcagcgg	attctgcagc	aacagcagat	gaagcagcag	attgggtccc	7740
caggccagcc	gaaccccacg	agcccccagc	aacacatgct	ctcaggacag	ccacaggcct	7800
cgcattctcc	tggccagcag	atcgccacgt	cccttagtaa	ccaggtgcgg	tctccagccc	7860
ctgtccagtc	tccacggccc	cagtcccagc	ctccacattc	cagcccgtca	ccacggatac	7920
agccccagcc	ttcgccacac	cacgtctcac	cccagactgg	ttccccccac	ccgggactcg	7980
cagtcacccat	ggccagctcc	atagatcagg	gacacttggg	gaaccccga	cagagtgcac	8040
tgtcccccca	gctgaacacc	cccagcagga	gtgcgctgtc	cagcgaactg	tccctggctg	8100
gggacaccac	gggggacacg	ctagagaagt	ttgtggaggg	cttgtag		8147

<210> 254

<211> 183

209/299

<212> PRT

<213> Homo sapiens

<400> 254

```

Met Ser Glu Thr Pro Ala Gln Cys Ser Ile Lys Gln Glu Arg Ile Ser
  1             5             10             15

Tyr Thr Pro Pro Glu Ser Pro Val Pro Ser Tyr Ala Ser Ser Thr Pro
      20             25             30

Leu His Val Pro Val Pro Arg Ala Leu Arg Met Glu Glu Asp Ser Ile
      35             40             45

Arg Leu Pro Ala His Leu Arg Leu Gln Pro Ile Tyr Trp Ser Arg Asp
      50             55             60

Asp Val Ala Gln Trp Leu Lys Trp Ala Glu Asn Glu Phe Ser Leu Arg
      65             70             75             80

Pro Ile Asp Ser Asn Thr Phe Glu Met Asn Gly Lys Ala Leu Leu Leu
      85             90             95

Leu Thr Lys Glu Asp Phe Arg Tyr Arg Ser Pro His Ser Gly Asp Val
      100            105            110

Leu Tyr Glu Leu Leu Gln His Ile Leu Lys Gln Arg Lys Pro Arg Ile
      115            120            125

Leu Phe Ser Pro Phe Phe His Pro Gly Asn Ser Ile His Thr Gln Pro
      130            135            140

Glu Val Ile Leu His Gln Asn His Glu Glu Glu Ala Leu Gln Arg Pro
      145            150            155            160

Val Ala Ser Asp Phe Glu Pro Gln Gly Leu Ser Glu Ala Ala Arg Trp
      165            170            175

Asn Ser Lys Glu Asn Leu Leu
      180

```

<210> 255

<211> 549

<212> DNA

<213> Homo sapiens

<400> 255

```

atgtctgaga ctcttgctca gtgtagcatt aagcaggaac gaatttcata tacacctcca 60
gagagcccag tgccgagtta cgcttcctcg acgccacttc atgttccagt gcctcgagcg 120
ctcaggatgg aggaagactc gatccgcctg cctgcgcacc tgcgcttgca gccaatttac 180
tggagcaggg atgacgtagc ccagtggctc aagtgggctg aaaatgagtt ttctttaagg 240
ccaattgaca gcaacacggt tgaaatgaat ggcaaagctc tcctgctgct gaccaaagag 300
gactttcgct atcgatctcc tcattcaggt gatgtgctct atgaactcct tcagcatatt 360
ctgaagcaga ggaaacctcg gattcttttt tcaccattct tccacctgga aaactctata 420
cacacacagc cggaggtcat actgcatcag aacctatgaag aagaagccct tcagcggcca 480
gtagcatctg acttttgagcc tcaggggtctg agtgaagccg ctcgttggaa ctccaaggaa 540
aaccttctc

```


210/299

<210> 256
<211> 763
<212> DNA
<213> Homo sapiens

<400> 256
gaattcaggg ttttcttttc attttatttt catttggttca tgtgtttgta tttacatata 60
ttgtgcctga atattgtaca tgtatgtgac agttgtgtac tgtagaatca aaaactaatg 120
tctgtgaact gaactcttct tgaacttttt gttgtgtgtg ttattgttgc ttttggagat 180
agggtcttgc tctgtcaccg aggtctggact gcagtggcac aatcacagct cactgcagcc 240
ttgagctcct ggtctcaagc aaccctccca cctcagcctc ccaagtagct ggggctgcag 300
gcatatgcta cctgactaat taaaaatttt tttttttttt tgtagagaca gggctctact 360
atttttacta gtttgcccg gccaagccag tgttgaacta ctggcctcaa gtgatcctcc 420
caccttggcc tccccaaagt gcatccctac aggcattgagc cactgcactc agcctgaact 480
ttcgaaattt attttaaggg cccactttta aatgcttctt ttcagcagct aactttccag 540
cggatgcttc atgtggtgac agccataaga cgaaaacaag agaagatccc aaagaaaata 600
gaaaaacaaa aaaagaaaaa tttgtcgaat cccaggtgga atctgaatca agtgacttta 660
atgattctcc ctttccagag gatgacagtg aagggttaca ttccgacagc agagaagaga 720
aacaaaacac taaaagtgca agagagagag cagggcagga cat 763

<210> 257
<211> 604
<212> DNA
<213> Homo sapiens

<400> 257
gaattcaggg ttttcttttc attttatttt catttggttca tgtgtttgta tttacatata 60
ttgtgcctga atattgtaca tgtatgtgac agttgtgtac tgtagaatca aaaactaatg 120
tctgtgaact gaactcttct tgaacttttt gttgtgtgtg ttattgttgc ttttggagat 180
agggtcttgc tctgtcaccg aggtctggact gcagtggcac aatcacagct cactgcagcc 240
ttgagctcct ggtctcaaac aaccctccca cctcagcctc ccaagtagct ggggctgcag 300
gcatatgcta cctgactaat taaaaatttt tttttttttt tgtagagaca gggctctact 360
atttttacta gtttgcccg gccaagccag tgttgaacta ctggcctcaa gtgatcctcc 420
caccttggcc tccccaaagt gcatccctac aggcattgagc cactgcactc agcctgaact 480
ttcgaaattt attttaaggg cccactttta aatgcttctt ttcagcagct aactttccag 540
cggatgcttc atgtggtgac agccataacg atacgctttt agaacttgag ctttggagaa 600
gctt 604

<210> 258
<211> 15
<212> PRT
<213> Homo sapiens

<400> 258
Arg Tyr Arg Ser Pro His Ser Ala His Asp Leu Pro Ala Asn Lys
1 5 10 15

<210> 259
<211> 45
<212> DNA
<213> Homo sapiens

<400> 259
cgctatcgat ctctcatttc agcccacgac ctccctgcaa acaag 45

211/299

<210> 260
<211> 15
<212> PRT
<213> Homo sapiens

<400> 260
Ile Arg Leu Pro Ala His Leu Pro His Asp Leu Pro Ala Asn Lys
1 5 10 15

<210> 261
<211> 45
<212> DNA
<213> Homo sapiens

<400> 261
atccgcctgc ctgcgcacct gccccacgac ctccctgcaa acaag 45

<210> 262
<211> 15
<212> PRT
<213> Homo sapiens

<400> 262
Gln Asn Pro Asn Ser Lys Glu Gly Asp Val Leu Tyr Glu Leu Leu
1 5 10 15

<210> 263
<211> 45
<212> DNA
<213> Homo sapiens

<400> 263
cagaacccca acagcaaaga aggtgatgtg ctctatgaac tcctt 45

<210> 264
<211> 15
<212> PRT
<213> Homo sapiens

<400> 264
Gln Asn Pro Asn Ser Lys Glu Gly Leu Gln Pro Ile Tyr Trp Ser
1 5 10 15

<210> 265
<211> 45
<212> DNA
<213> Homo sapiens

<400> 265
cagaacccca acagcaaaga aggcttgcag ccaatttact ggagc 45

212/299

<210> 266

<211> 829

<212> PRT

<213> Homo sapiens

<400> 266

Met Asn Ser Gly Val Ala Met Lys Tyr Gly Asn Asp Ser Ser Ala Glu
 1 5 10 15

Leu Ser Glu Leu His Ser Ala Ala Leu Ala Ser Leu Lys Gly Asp Ile
 20 25 30

Val Glu Leu Asn Lys Arg Leu Gln Gln Thr Glu Arg Glu Arg Asp Leu
 35 40 45

Leu Glu Lys Lys Leu Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met
 50 55 60

Arg Glu His Glu Asp Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu
 65 70 75 80

Arg Ile Thr Glu Leu His Ser Val Ile Ala Glu Leu Asn Lys Lys Ile
 85 90 95

Asp Arg Leu Gln Gly Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu
 100 105 110

Leu Arg Ser Glu Leu Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser
 115 120 125

Arg Ser Met Asp Gln Asp Gln Thr Ser Val Ser Ile Pro Glu Asn Gln
 130 135 140

Ser Thr Met Val Thr Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser
 145 150 155 160

Glu Leu Gln Arg Val Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg
 165 170 175

Lys Lys Ser Ser Cys Ser Leu Ser Val Ala Glu Val Asp Arg His Ile
 180 185 190

Glu Gln Leu Thr Thr Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr
 195 200 205

Val Glu Glu Ile Glu Gly Val Leu Gly Arg Asp Leu Tyr Pro Asn Leu
 210 215 220

Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu Ala Gly Leu Arg Glu
 225 230 235 240

Glu Asn Glu Ser Leu Thr Ala Met Leu Cys Ser Lys Glu Glu Glu Leu
 245 250 255

Asn Arg Thr Lys Ala Thr Met Asn Ala Ile Arg Glu Glu Arg Asp Arg
 260 265 270

213/299

Leu Arg Arg Arg Val Arg Glu Leu Gln Thr Arg Leu Gln Ser Val Gln
 275 280 285
 Ala Thr Gly Pro Ser Ser Pro Gly Arg Leu Thr Ser Thr Asn Arg Pro
 290 295 300
 Ile Asn Pro Ser Thr Gly Glu Leu Ser Thr Ser Ser Ser Ser Asn Asp
 305 310 315 320
 Ile Pro Ile Ala Lys Ile Ala Glu Arg Val Lys Leu Ser Lys Thr Arg
 325 330 335
 Ser Glu Ser Ser Ser Ser Asp Arg Pro Val Leu Gly Ser Glu Ile Ser
 340 345 350
 Ser Ile Gly Val Ser Ser Ser Val Ala Glu His Leu Ala His Ser Leu
 355 360 365
 Gln Asp Cys Ser Asn Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His
 370 375 380
 Gly Ser Ala Ile Ser Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr
 385 390 395 400
 Glu Arg Leu Asn Ser Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu
 405 410 415
 Leu Thr Ile Thr Leu Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser
 420 425 430
 Met Leu Val Gly Lys Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala
 435 440 445
 Leu Gln Tyr Ser Glu Gln Cys Ile Glu Ala Tyr Glu Leu Leu Leu Ala
 450 455 460
 Leu Ala Glu Ser Glu Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala
 465 470 475 480
 Gly Val Gly Ser Ser Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr
 485 490 495
 Gln Met Leu Lys Arg Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala
 500 505 510
 Ala Lys Ala Leu Leu Met Lys Leu Asp Gly Ser Cys Gly Gly Ala Phe
 515 520 525
 Ala Val Ala Gly Cys Ser Val Gln Pro Trp Glu Ser Leu Ser Ser Asn
 530 535 540
 Ser His Thr Ser Thr Thr Ser Ser Thr Ala Ser Ser Cys Asp Thr Glu
 545 550 555 560
 Phe Thr Lys Glu Asp Glu Gln Arg Leu Lys Asp Tyr Ile Gln Gln Leu
 565 570 575
 Lys Asn Asp Arg Ala Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser

214/299

580					585					590						
Ile	His	Ile	Asp	Pro	Leu	Ser	Tyr	Asp	Val	Lys	Pro	Arg	Gly	Asp	Ser	
595					600					605						
Gln	Arg	Leu	Asp	Leu	Glu	Asn	Ala	Val	Leu	Met	Gln	Glu	Leu	Met	Ala	
610					615					620						
Met	Lys	Glu	Glu	Met	Ala	Glu	Leu	Lys	Ala	Gln	Leu	Tyr	Leu	Leu	Glu	
625					630					635					640	
Lys	Glu	Lys	Lys	Ala	Leu	Glu	Leu	Lys	Leu	Ser	Thr	Arg	Glu	Ala	Gln	
645					650					655						
Glu	Gln	Ala	Tyr	Leu	Val	His	Ile	Glu	His	Leu	Lys	Ser	Glu	Val	Glu	
660					665					670						
Glu	Gln	Lys	Glu	Gln	Arg	Met	Arg	Ser	Leu	Ser	Ser	Thr	Ser	Ser	Gly	
675					680					685						
Ser	Lys	Asp	Lys	Pro	Gly	Lys	Glu	Cys	Ala	Asp	Ala	Ala	Ser	Pro	Ala	
690					695					700						
Leu	Ser	Leu	Ala	Glu	Leu	Arg	Thr	Thr	Cys	Ser	Glu	Asn	Glu	Leu	Ala	
705					710					715					720	
Ala	Glu	Phe	Thr	Asn	Ala	Ile	Arg	Arg	Glu	Lys	Lys	Leu	Lys	Ala	Arg	
725					730					735						
Val	Gln	Glu	Leu	Val	Ser	Ala	Leu	Glu	Arg	Leu	Thr	Lys	Ser	Ser	Glu	
740					745					750						
Ile	Arg	His	Gln	Gln	Ser	Ala	Glu	Phe	Val	Asn	Asp	Leu	Lys	Arg	Ala	
755					760					765						
Asn	Ser	Asn	Leu	Val	Ala	Ala	Tyr	Glu	Lys	Ala	Lys	Lys	Lys	His	Gln	
770					775					780						
Asn	Lys	Leu	Lys	Lys	Leu	Glu	Ser	Gln	Met	Met	Ala	Met	Val	Glu	Arg	
785					790					795					800	
His	Glu	Thr	Gln	Val	Arg	Met	Leu	Lys	Gln	Arg	Ile	Ala	Leu	Leu	Glu	
805					810					815						
Glu	Glu	Asn	Ser	Arg	Pro	His	Thr	Asn	Glu	Thr	Ser	Leu				
820					825											

<210> 267

<211> 4181

<212> DNA

<213> Homo sapiens

<400> 267

```

cctcctgcag caatggctcg tccgtgaaac gcgagccacg gctgctcttt ttaagagtgc 60
ctgcatactc cgtttgcgct tcgcaactgt cctgggtgaa aatggctgtc tagactaaaa 120
tgtggcagaa gggaccaagc agtggatatt gagcctgtga agtccaactc ttaagctccg 180
agacctgggg gactgagagc ccagctctga aaagtgcac atgaattccg gagttgccat 240

```

gaaatatgga aacgactcct cggccgagct gagtgcgctc cattcagcag ccctggcctc 300
 actaaaggga gatatagtgg aacttaataa acgtctccag caaacagaga gggaacggga 360
 ccttctggaa aagaaattgg ccaaggcaca gtgcgagcag tcccacctca tgagagagca 420
 tgaggatgtc caggagcgaa cgacgcttcg ctatgaggaa cgcacacag agctccacag 480
 cgtcattgctg gagctcaaca agaagataga cgtctgcaa ggcaccacca tcagggagga 540
 agatgagtac tcagaactgc gatcagaact cagccagagc caacacgagg tcaacgagga 600
 ctctcgaagc atggaccaag accagacctc tgtctctatc cccgaaaacc agtctaccat 660
 ggttactgct gacatggaca actgcagtga cctgaactca gaactgcaga ggtgctgac 720
 agggctggag aatgttgtct gcggcaggaa gaagagcagc tgcagcctct ccgtggccga 780
 ggtggacagg cacattgagc agctcaccac agccagcgag cactgtgacc tggctattaa 840
 gacagtcgag gagattgagg ggtgcttggt cgggacctg tatcccaacc tggctgaaga 900
 gaggtctcgg tgggagaagg agctggctgg gctgaggaa gagaatgaga gcctgactgc 960
 catgctgtgc agcaaagg agaaactgaa cgggactaag gccaccatga atgccatccg 1020
 ggaagagcgg gaccggctcc ggaggcgggt cagagagctt caaactcgac tacagagcgt 1080
 gcaggccaca ggtccctcca gccctggccg cctcacttcc accaaccgcc cgattaaccc 1140
 cagcactggg gagctgagca caagcagcag cagcaatgac attcccatcg ccaagattgc 1200
 tgagaggggtg aagctatcaa agacaagggtc cgaatcgtca tcatctgatc ggccagtcct 1260
 gggctcagaa atcagtagca taggggtatc cagcagtggt gctgaacacc tggccactc 1320
 acttcaggac tgctccaata tccaagagat ttccaaaca ctctactcac acggatctgc 1380
 catctcagaa agcaagatta gagagtttga ggtggaaca gaacggctga atagccggat 1440
 tgagcacctc aaatcccaaa atgacctcct gaccataacc ttggaggaat gtaaaagcaa 1500
 tgctgagagg atgagcatgc tgggggaaa atacgaatcc aatgccacag cgctgaggct 1560
 ggcttgcag tacagcgagc agtgcacga agcctacgaa ctctcctgg cgctggcaga 1620
 gagtgcgagc agcctcatcc tggggcagtt ccgagcggcg ggcgtgggt cctcccctgg 1680
 agaccagtcg ggggatgaaa acatcactca gatgctcaag cgagctcatg actgccggaa 1740
 gacagctgag aacgctgcc aagccctgct catgaagctg gacggcagct gtgggggagc 1800
 ctttgccgtg gccgctgca gcgtgcagcc ctgggagagc ctttctcca acagccacac 1860
 cagcacaacc agctccacag ccagtagttg cgacaccgag ttactaaaag aagacgagca 1920
 gaggctgaag gattatatcc agcagctcaa gaatgacagg gctgcggtca agctgacct 1980
 gctggagctg gaaagcatcc acatcgatcc tctcagctat gacgtcaagc ctcggggaga 2040
 cagccagagg ctggatctgg aaaaacgcagt gcttatgcag gagctcatgg ccatgaagga 2100
 ggagatggcc gagttgaagg ccagctcta cctactggag aaagagaaga aggccttggg 2160
 gctgaagctg agcacgcggg aggccaggga gcaggcctac ctggtgcaca ttgagcacct 2220
 gaagtccgag gtggaggagc agaaggagca gccgatgcga tccctcagct ccaccagcag 2280
 cggcagcaaa gataaacctg gcaaggagtg tgctgatgct gcctccccag ctctgtccct 2340
 agctgaactc aggacaacgt gcagcgagaa tgagctggct gcggagtcca ccaacgccat 2400
 tcgtcgagaa agaagttga aggccagagt tcaagagctg gtgagtgcct tggagagact 2460
 caccaagagc agtgaaatcc gacatcagca atctgcagag ttctggaatg atctaaagcg 2520
 ggccaacagc aaactgggtg ctgcctatga gaaagcaaa aaaaagcatc aaaaacaaat 2580
 gaagaagtta gagtcgcaga tgatggccat ggtggagaga catgagacc aagtgaggat 2640
 gctcaagcaa agaatagtct tgctagagga ggagaactcc aggccacaca ccaatgaac 2700
 ttctgtttaa tcagcactca cgcaccggag ttctgcccat gggaagttaa ctgcagcagg 2760
 ccactgggga cagaagggcc catgtacttg ttgggaggag gaggaaggg aaggctggca 2820
 ggtaggtcgg cacttggaaca atggagtgcc ccaactcaac ccttgggggtg actggccatg 2880
 gtgacattgt ggaactgtatc cagaggtgcc cgctcttccc tctggggccc acaacagcgt 2940
 gtaaacacat gttctgtgccc tgctcagcag agcctcgttt ctgctttcag cactcactct 3000
 ccccctctc ttctgggtctg gcggctgtgc atcagtggga tcccagacat ttgtttctgt 3060
 aagattttcc attgtatcct ctttttggtg catgctgggc tcatcttcta gaatctcgtt 3120
 tctctctttt cctcctgctt catgggaaaa cagacctgtg tgtgcctcca gcatttaaaa 3180
 ggactgctga tttgtttact acagcaaggc tttggtttcc aagtccggg tctcaacttt 3240
 aagatagagg cggccataag aggtgatctc tgggagttat aggtcatggg aagagcgtag 3300
 acaggtgtta cttacagtcc cagatacact aaagttacaa acagaccacc accaggactg 3360
 tgctgaaca attttgtatt gagagaataa aaacttcctt caatcttcat tttggaggca 3420
 gggctgggaa gggagcgctc tcttgattct gggatttctc cctctcagtg gagccttatt 3480
 aatatccaag acttagagct gggaaatctt ttgatacctg tagtggaact aaaattctgt 3540
 cagggggttc ttcaagagct gagaaacatt atatgcactt cccgcccag ggcactacat 3600
 aattgctgtt ctgctgaatc aaatctcttc cactatgggtg catttgtagc tctggacctg 3660
 tctctaccta aggacaagac actgaggaga tactgaacat tttgcaaaac ttatcacgcc 3720

216/299

```

tacttaagag tgctgtgtaa cccccagttc aagacttagc tcctgttgtc atgacgggga 3780
cagagtggag gaatggtagt taaggcttct tttttgccc cagatacatg gtgatgggta 3840
gcataatggg cttaaaagggt taaatttcaa gcaaaatgct tacagggcta ggcagtacca 3900
aagtaactga attatttcag gaaggctctc aatcttaaaa caaattcatt attctttttc 3960
agttttacct cttctctctc agttctacac tgatacactt gaaggaccat ttactgtttt 4020
tttctgtagc accagagaat ccatccaaag ttccctatga aaaatgtgtt ccattgccat 4080
agctgactac aaattaaagt tgaggagggt tctgcataga gtctttatgt ccataagcta 4140
cgggtagggt tatttttcaga gcatgatata aattccacag g 4181

```

<210> 268
 <211> 1172
 <212> DNA
 <213> Homo sapiens

<400> 268

```

gtgagacatg tctgagactc ctgctcagtg tagcattaag agtttgctcct ctcaacttctg 60
gagaagatgc agacacagga gatcctgagg atactgcgac tgcctgagct aggtgacttg 120
ggacagtttt tccgcagcct ctgggccacc accctcgaca gtggcggggc acggcgatct 180
gtgattgggt ctggccctca gctacttacc cactactatg atgatgcccg gaccatgtac 240
cagtggttcc gccgtgggct tagcatctca gggaaatgggc cctgtcttgg tttcaggaag 300
cctaagcagc cttaccagtg gctgtctac caggaggtgg ccgacagggc tgaatttctg 360
gggtccggac ttctccagca caattgtaaa gcatgcaactg atcagtttat tgggtgtttt 420
gcacaaaatc ggccagagtg gatcattgtg gagctggcct gctacacata ttccatggtg 480
gtggtccgcg tctatgacac cctgggccct ggggctatcc gctacatcat caatacagcg 540
gacatcagca ccgtgattgt ggacaaacct cagaaggctg tgcttctgct agagcatgtg 600
gagaggaagg agactccagg cctcaagctg atcatcctca tggacccatt cgaagaagcc 660
ctgaaagaga gagggcagaa gtgcgggggtg gtcattaaagt ccatgcaggc cgtggaggac 720
tgtggccaag agaatcacca ggctcctgtg ccccgagc ctgatgacct ctccattgtg 780
tgtttcacaa ggggcacgac agggaaacca aaaggtgcga tgcacacca tgggaacgtg 840
gtggctgatt tctcaggett tctgaaagtg acagagagtc agtgggctcc cacttggtgcg 900
gatgtgcaca tttctatatt gccttttagca cacatgtttg agcgaatggg gcagtctgtc 960
gtctattgcc acggagggcg tgttggtctt ttccaggagg atatccgcct tctctcagat 1020
gacatgaggg ctctatgccc caccatcttc cctgtggtcc cactgactgt gaaccggatg 1080
tacgacaaga tcttcagcca ggcaaacaca ccattaaagc gctggctcct ggagtttgca 1140
gcaaagcgta agcaagccga gaagccgaat tc 1172

```

<210> 269
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 269

```

Asn His Ile Met Val Ser Val Ser Pro Pro Glu Glu His Ala Met Pro
  1             5             10             15

Ile Gly Arg Ile Ala Asp Val Gln His Ile Lys Arg Arg Asp Ile Val
      20             25             30

Leu Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala
      35             40             45

Glu Cys Tyr Asn Leu Ser Pro Thr Lys Asp Lys Met Leu Val Ala Val
      50             55             60

Lys Ala Leu Lys Asp Pro Thr Leu Ala Ala Arg Lys Asp Phe Gln Arg
      65             70             75             80

```

217/299

Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile Val Lys Phe
 85 90 95
 Tyr Gly Val Cys Gly Asp Gly Asp Pro Leu Ile Met Val Phe Glu Tyr
 100 105 110
 Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg Ala His Gly Pro Asp
 115 120 125
 Ala Met Ile Leu Val Asp Gly Gln Pro Arg Gln Ala Lys Gly Glu Leu
 130 135 140
 Gly Leu Ser Gln Met Leu His Ile Ala Ser Gln Ile Ala Ser Gly Met
 145 150 155 160
 Val Tyr Leu Ala Ser Gln His Phe Val His Arg Asp Leu Ala Thr Arg
 165 170 175
 Asn Cys Leu Val Gly Ala Asn Leu Leu Val Lys Ile Gly Asp Phe Gly
 180 185 190
 Met Ser Arg Asp Val Tyr Ser Thr Asp Tyr Tyr Arg Val Gly Gly His
 195 200 205
 Thr Met Leu Pro Ile Arg Trp Met Pro Pro Glu Ser Ile Met Tyr Arg
 210 215 220
 Lys Phe Thr Thr Glu Ser Asp Val Trp Ser Phe Gly Val Ile Leu Trp
 225 230 235 240
 Glu Ile Phe Thr Tyr Gly Lys Gln Pro Trp Phe Gln Leu Ser Asn Thr
 245 250 255
 Glu Val Ile Glu Cys Ile Thr Gln Gly Arg Val Leu Glu Arg Pro Arg
 260 265 270
 Val Cys Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp Gln Arg
 275 280 285
 Glu Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile Leu His
 290 295 300
 Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly
 305 310 315

<210> 270

<211> 980

<212> DNA

<213> Homo sapiens

<400> 270

aaccacatca tgggtctctgt ctccccgcct gaagagcacg ccatgcccat tgggagaata 60
 gcagatgtgc agcacattaa gaggagagac atcgtgctga agcgagaact gggtagaggga 120
 gcctttggaa aggtcttctt ggcgagtgct tacaacctca gcccgaccaa ggacaagatg 180
 cttgtggctg tgaaggccct gaaggatccc accctggctg cccggaagga ttccagagg 240
 gaggccgagc tgctcaccaa cctgcagcat gagcacattg tcaagttcta tggagtgtgc 300

218/299

```

ggcgatgggg accccctcat catggtcttt gaatacatga agcatggaga cctgaataag 360
ttcctcaggg cccatggggc agatgcaatg atccttgttg atggacagcc acgccaggcc 420
aagggtgagc tggggctctc ccaaagtctc cacattgcca gtcagatcgc ctcggttatg 480
gtgtacctgg cctcccagca ctttgtgcac cgagacctgg ccaccaggaa ctgcctggtt 540
ggagcgaatc tgctagttaa gattggggac ttgggcatgt ccagagatgt ctacagcacg 600
gattattaca ggggtgggag acacaccatg ctccccattc gctggatgcc tcctgaaagc 660
atcatgtacc ggaagttcac tacagagagt gatgtatgga gcttcggggg gatcctctgg 720
gagatcttca cctatggaaa gcagccatgg ttccaactct caaacacgga ggtcattgag 780
tgcattaccc aaggtcgtgt tttggagcgg ccccgagtct gcccacaaaga ggtgtacgat 840
gtcatgctgg ggtgctggca gagggaacca cagcagcggg tgaacatcaa ggagatctac 900
aaaatcctcc atgctttggg gaaggccacc ccaatctacc tggacattct tggctagtgg 960
tggctggtgg tcatgaattc                                     980

```

<210> 271

<211> 408

<212> PRT

<213> Homo sapiens

<400> 271

```

Glu Asn Asn His Gln Glu Ser Tyr Pro Leu Ser Val Ser Pro Met Glu
 1              5              10              15

Asn Asn His Cys Pro Ala Ser Ser Glu Ser His Pro Lys Pro Ser Ser
      20              25              30

Pro Arg Gln Glu Ser Thr Arg Val Ile Gln Leu Met Pro Ser Pro Ile
      35              40              45

Met His Pro Leu Ile Leu Asn Pro Arg His Ser Val Asp Phe Lys Gln
      50              55              60

Ser Arg Leu Ser Glu Asp Gly Leu His Arg Glu Gly Lys Pro Ile Asn
      65              70              75              80

Leu Ser His Arg Glu Asp Leu Ala Tyr Met Asn His Ile Met Val Ser
      85              90              95

Val Ser Pro Pro Glu Glu His Ala Met Pro Ile Gly Arg Ile Ala Asp
      100              105              110

Val Gln His Ile Lys Arg Arg Asp Ile Val Leu Lys Arg Glu Leu Gly
      115              120              125

Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu Ser
      130              135              140

Pro Thr Lys Asp Lys Met Leu Val Ala Val Lys Ala Leu Lys Asp Pro
      145              150              155              160

Thr Leu Ala Ala Arg Lys Asp Phe Gln Arg Glu Ala Glu Leu Leu Thr
      165              170              175

Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Gly Asp
      180              185              190

Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp Leu
      195              200              205

```

219/299

Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Met Ile Leu Val Asp
 210 215 220
 Gly Gln Pro Arg Gln Ala Lys Gly Glu Leu Gly Leu Ser Gln Met Leu
 225 230 235 240
 His Ile Ala Ser Gln Ile Ala Ser Gly Met Val Tyr Leu Ala Ser Gln
 245 250 255
 His Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Ala
 260 265 270
 Asn Leu Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr
 275 280 285
 Ser Thr Asp Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg
 290 295 300
 Trp Met Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser
 305 310 315 320
 Asp Val Trp Ser Phe Gly Val Ile Leu Trp Glu Ile Phe Thr Tyr Gly
 325 330 335
 Lys Gln Pro Trp Phe Gln Leu Ser Asn Thr Glu Val Ile Glu Cys Ile
 340 345 350
 Thr Gln Gly Arg Val Leu Glu Arg Pro Arg Val Cys Pro Lys Glu Val
 355 360 365
 Tyr Asp Val Met Leu Gly Cys Trp Gln Arg Glu Pro Gln Gln Arg Leu
 370 375 380
 Asn Ile Lys Glu Ile Tyr Lys Ile Leu His Ala Leu Gly Lys Ala Thr
 385 390 395 400
 Pro Ile Tyr Leu Asp Ile Leu Gly
 405

<210> 272

<211> 1403

<212> DNA

<213> Homo sapiens

<400> 272

gagaacaacc accaggagtc ctaccctctg tcagtgtctc ccatggagaa taatcactgc 60
 ccagcgtect ccgagtccca cccgaagcca tccagccccc ggcaggagag cacacgcgtg 120
 atccagctga tgcccagccc catcatgcac cctctgatcc tgaacccccg gcactccgtg 180
 gatttcaaac agtccaggct ctccgaggac gggctgcata gggaaggga gcccatacaac 240
 ctctctcatc gggaagacct ggcttacatg aaccacatca tggctctctgt ctccccgcct 300
 gaagagcacg ccatgccccat tgggagaata gcagatgtgc agcacattaa gaggagagac 360
 atcgtgctga agcgagaact gggtgaggga gccttttgaa aggtcttcct ggccgagtgc 420
 tacaacctca gcccgaacaa ggacaagatg cttgtggctg tgaaggccct gaaggatccc 480
 accctggctg cccggaagga tttccagagg gaggccgagc tgctcaccaa cctgcagcat 540
 gaggacattg tcaagttcta tggagtgtgc ggcgatgggg accccctcat catggtcttt 600
 gaatacatga agcatggaga cctgaataag ttcctcaggg cccatggggc agatgcaatg 660

220/299

```

atccttgtgg atggacagcc acgccaggcc aagggtgagc tggggctctc ccaaagtctc 720
cacattgcca gtcagatgcg ctcggttatg gtgtacctgg cctcccagca ctttgtgcac 780
cgagacctgg ccaccaggaa ctgcctggtt ggagcgaatc tgctagttaa gattggggac 840
ttcggcatgt ccagagatgt ctacagcacg gattattaca ggggtgggag acacaccatg 900
ctccccattc gctggatgcc tcctgaaagc atcatgtacc ggaagttcac tacagagagt 960
gatgtatgga gcttcggggt gatcctctgg gagatcttca cctatggaaa gcagccatgg 1020
ttccaactct caaacacgga ggtcattgag tgcattaccc aaggtcgtgt tttggagcgg 1080
ccccgagtct gcccacaaaga ggtgtacgat gtcagtctgg ggtgctggca gagggaaacca 1140
cagcagcggg tgaacatcaa ggagatctac aaaatcctcc atgctttggg gaaggccacc 1200
ccaatctacc tggacattct tggctagtgg tggctgggtg tcatgaattc atactctgtt 1260
gcctcctctc tccttgctc acatctccct tccacctcac aactccttcc atccttgact 1320
gaagcgaaca tcttcatata aactcaagtg cctgctacac atacaacact gaaaaaagga 1380
aaaaaaaaga aaaaaaaaaa aaa                                     1403

```

<210> 273

<211> 536

<212> PRT

<213> Homo sapiens

<400> 273

```

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
  1              5              10              15

```

```

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
          20              25              30

```

```

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
      35              40              45

```

```

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
      50              55              60

```

```

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
      65              70              75              80

```

```

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
          85              90              95

```

```

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
      100              105              110

```

```

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
      115              120              125

```

```

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
      130              135              140

```

```

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
      145              150              155              160

```

```

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
          165              170              175

```

```

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
      180              185              190

```

```

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg

```

221/299

195					200					205					
Lys	Leu	Asp	Ser	Gly	Gly	Phe	Tyr	Ile	Thr	Ser	Arg	Thr	Gln	Phe	Asn
210					215					220					
Ser	Leu	Gln	Gln	Leu	Val	Ala	Tyr	Tyr	Ser	Lys	His	Ala	Asp	Gly	Leu
225					230					235					240
Cys	His	Arg	Leu	Thr	Thr	Val	Cys	Pro	Thr	Ser	Lys	Pro	Gln	Thr	Gln
				245					250					255	
Gly	Leu	Ala	Lys	Asp	Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Arg	Leu
			260					265					270		
Glu	Val	Lys	Leu	Gly	Gln	Gly	Cys	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr
		275					280					285			
Trp	Asn	Gly	Thr	Thr	Arg	Val	Ala	Ile	Lys	Thr	Leu	Lys	Pro	Gly	Thr
	290					295					300				
Met	Ser	Pro	Glu	Ala	Phe	Leu	Gln	Glu	Ala	Gln	Val	Met	Lys	Lys	Leu
305					310					315					320
Arg	His	Glu	Lys	Leu	Val	Gln	Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro
				325					330					335	
Ile	Tyr	Ile	Val	Thr	Glu	Tyr	Met	Ser	Lys	Gly	Ser	Leu	Leu	Asp	Phe
			340					345					350		
Leu	Lys	Gly	Glu	Thr	Gly	Lys	Tyr	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp
		355					360					365			
Met	Ala	Ala	Gln	Ile	Ala	Ser	Gly	Met	Ala	Tyr	Val	Glu	Arg	Met	Asn
	370					375					380				
Tyr	Val	His	Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Asn
385					390					395					400
Leu	Val	Cys	Lys	Val	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Ile	Glu	Asp
				405					410					415	
Asn	Glu	Tyr	Thr	Ala	Arg	Gln	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr
			420					425					430		
Ala	Pro	Glu	Ala	Ala	Leu	Tyr	Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val
		435					440					445			
Trp	Ser	Phe	Gly	Ile	Leu	Leu	Thr	Glu	Leu	Thr	Thr	Lys	Gly	Arg	Val
	450					455						460			
Pro	Tyr	Pro	Gly	Met	Val	Asn	Arg	Glu	Val	Leu	Asp	Gln	Val	Glu	Arg
465						470					475				480
Gly	Tyr	Arg	Met	Pro	Cys	Pro	Pro	Glu	Cys	Pro	Glu	Ser	Leu	His	Asp
				485					490					495	
Leu	Met	Cys	Gln	Cys	Trp	Arg	Lys	Glu	Pro	Glu	Glu	Arg	Pro	Thr	Phe
			500					505						510	

222/299

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu
530 535

<210> 274
<211> 1611
<212> DNA
<213> Homo sapiens

<400> 274
atgggtagca acaagagcaa gccaaggat gccagccagc ggccgcgcag cctggagccc 60
gccgagaacg tgcacggcgc tggcgggggc gctttccccc cctcgcagac cccagcaag 120
ccagcctcgg ccgacggcca ccgcggcccc agcgcggcct tcgccccgcg ggccgcgcag 180
cccaagctgt tcggaggctt caactcctcg gacaccgtca cctccccgca gagggcgggc 240
ccgctggccg gtggagtgac cacctttgtg gccctctatg actatgagtc taggacggag 300
acagacctgt cttcaagaa aggcgagcgg ctccagattg tcaacaacac agaggagac 360
tggttgctgg cccactcgct cagcacagga cagacaggct acatccccag caactacgtg 420
gcgccctccg actccatcca ggctgaggag tggatatttg gcaagatcac cagacgggag 480
tcagagcggg tactgctcaa tgcagagaac ccgagagga ccttcctcgt gcgagaaagt 540
gagaccacga aagggtgcta ctgcctctca gtgtctgact tcgacaacgc caagggcctc 600
aacgtgaagc actacaagat ccgcaagctg gacagcggcg gcttctacat cacctccgcg 660
accagttca acagcctgca gcagctggtg gcctactact ccaaacacgc cgatggcctg 720
tgccaccgcc tcaccaccgt gtgccccacg tccaagccgc agactcaggg cctggccaag 780
gatgcctggg agatccctcg ggagtcgctg ccgctggagg tcaagctggg ccagggctgc 840
tttggcgagg tgtggatggg gacctggaac ggtaccacca ggtggccat caaaacctg 900
aagcctggca cgatgtctcc agaggccttc ctgcaggagg cccagggtcat gaagaagctg 960
aggcatgaga agctggtgca gttgtatgct gtggtttcag aggagcccat ttacatcgtc 1020
acggagtaca tgagcaaggg gagtttgctg gactttctca agggggagac aggcaagtac 1080
ctgcggctgc ctgagctggg ggacatggct gctcagatcg cctcaggcat ggcgtacgtg 1140
gagcggatga actacgtcca ccgggacctt cgtgcagcca acatcctggt gggagagaa 1200
ctggtgtgca aagtggccga ctttgggctg gctcggctca ttgaagaaa tgagtacacg 1260
gcgcggcaag gtgccaatt ccccatcaag tggacggctc cagaagctgc cctctatggc 1320
cgcttcacca tcaagtcgga cgtgtggtcc ttccggatcc tgctgactga gctcaccaca 1380
aagggaacgg tgccctaccc tgggatggg aaccgcgagg tgctggacca ggtggagcgg 1440
ggctaccgga tgccctgccc gccggagtgt cccgagtcct tgcacgacct catgtgccag 1500
tgctggcgga aggagcctga ggagcggccc accttcgagt acctgcaggc cttcctggag 1560
gactacttca cgtccaccga gccccagtac cagcccgggg agaacctcta g 1611

<210> 275
<211> 226
<212> PRT
<213> Homo sapiens

<400> 275
Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val Tyr Phe Glu
1 5 10 15
Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala Asp Gly Leu
20 25 30
Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr Val Ala Ala
35 40 45

223/299

Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met Lys Glu Leu
 50 55 60
 Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp Val Met Leu
 65 70 75 80
 Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile Lys Asn Asp
 85 90 95
 Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met Thr Gln Leu
 100 105 110
 Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val Glu Glu Lys
 115 120 125
 Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly Ser Leu Val
 130 135 140
 Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly Asp Cys Leu
 145 150 155 160
 Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr Leu Glu Gly
 165 170 175
 Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Ser
 180 185 190
 Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr Lys Glu Ala
 195 200 205
 Ser Thr Pro Arg Thr Arg Ala Ser Cys Gln Ser Ser Gly Gln Pro Leu
 210 215 220
 Arg Pro
 225

<210> 276
 <211> 2442
 <212> DNA
 <213> Homo sapiens

<400> 276
 tccggggcg ccccggcag ccagcgcgac gttccaaaat cgaacctcag tggcgggcgct 60
 cggaagcgga actctgccc ggccgcgcg gctacattgt gctgcggctc actctagagg 120
 ctccccctcc tcccccgac tccctccctc ccccttcccc cgcctttctt ccctccgcga 180
 ccggggccgt gcgtccgtcc cctgcctct gctggcggt cctcctccc ctctccttgc 240
 acccatacct ctttgtacc caccctctgg gtatccctgc gccctcccc tccccctga 300
 ccgcatggac cgteccgcag gcgctgatg ccgcccgcg gacggtggcc cggaccgcag 360
 tgccccaaga gagctctaag ggtaccaagt gacaggttgg cttaactgag actcggggac 420
 ccaagagctc ctgagaagat gtcagcaata caggccgcct ggccatccgg tacagaatgt 480
 attgccaaagt acaacttcca cggcactgcc gagcaggacc tgcccttctg caaaggagac 540
 gtgctcacca ttgtggccgt caccaaggac cccaactggg acaaagccaa aaacaagggtg 600
 ggccgtgagg gcatcatccc agccaactac gtccagaagc gggagggcgt gaaggcggtg 660
 accaaactca gcctcatgcc gtgagttcca cggcaagatc acacgggagc aggtgagcg 720
 gcttctgtac ccgcccgcga caggcctgtt cctggtgcgg gagagcacca actaccccgg 780
 agactacacg ctgtgcgtga gctgcgacgg caaggtggag cactaccgca tcatgtacca 840
 tgccagcaag ctgagcatcg acgaggaggt gtactttgag aacctcatgc agctggtgga 900

224/299

```

gcactacacc tcagacgcag atggactctg tacgcgcctc attaaaccaa aggtcatgga 960
gggcacagtg gcggccagag atgagttcta ccgcagcggc tgggccctga acatgaagga 1020
gctgaagctg ctgcagacca tcgggaaggg ggagttcgga gacgtgatgc tgggcgatta 1080
ccgaggggaac aaagtgcgag tcaagtgcac taagaacgac gccactgccc aggccttcct 1140
ggctgaagcc tcagtcatga cgcaactgag gcatagcaac ctggtgcagc tcctgggcgt 1200
gatcgtggag gagaagggcg ggctctacat cgtcactgag tacatggcca aggggagcct 1260
tgtggactac ctgcggtcta ggggtcggtc agtgcctggc ggagactgtc tcctcaagtt 1320
ctcgctagat gtctgcgagg coactggaata cctggagggc aacaatttcg tgcactcgaga 1380
cctggctgcc cgcaatgtgc tgggtgtctga ggacaacgtg gccaaaggtca gcgacttttg 1440
tctcaccaag gaggcgcca caccaggagc acgggcaagc tgccagtcaa gtggacagcc 1500
cctgaggccc tgagagagaa gaaattctcc actaagtctg acgtgtggag tttcggaatc 1560
cttctctggg aaatctactc ctttgggcga gtgccttata caagaattcc cctgaaggac 1620
gtcgtccctc ggggtgagaa gggctacaag atggatgccc ccgacggctg ccgcccgcga 1680
gtctatgaag tcatgaagaa ctgctggcac ctggacgccc ccatgcccgc ctcccttccta 1740
cagctccgag agcagcttga gcacatcaaa acccagcagc tgcacctgtg acggtggccc 1800
tccgcctggg tcatgggcct gtggggactg aacctggaag atcatggacc tgggtggccc 1860
gtcactggg ccgagcctg aactgagccc cagcgggctg gcgggccttt ttctgcgtc 1920
ccagcctgca cccctccggc cccgtctctc ttggaccacac ctgtggggcc tggggagccc 1980
actgaggggc caggaggagaa ggaggccacg gagcgggagg cagcgcccca ccacgtcggg 2040
cttccctggc ctcccgccac tcgccttctt agagttttat tcctttcctt ttttgagatt 2100
ttttttccgt gtgtttattt tttattattt ttcaagataa ggagaaagaa agtaccagc 2160
aaatgggcat tttacaagaa gtacgaatct tatttttcct gtccctgccg tgaggggtgg 2220
ggggaccggg cccctctcta gggaccctc gccccagcct cattcccat tctgtgtccc 2280
atgtcccgtg tctcctcggt cggcccggtg ttgcgcttga ccatgttgca ctgtttgcat 2340
gcgcccagag cagacgtctg tcaggggctt ggatttcgtg tgccgctgcc acccgccac 2400
ccgccttgtg agatggaatt gtaataaacc acgcatgag ga 2442

```

<210> 277

<211> 1114

<212> PRT

<213> Homo sapiens

<400> 277

```

Met Ala Lys Ala Thr Ser Gly Ala Ala Gly Leu Arg Leu Leu Leu Leu
 1              5              10              15

Leu Leu Leu Pro Leu Leu Gly Lys Val Ala Leu Gly Leu Tyr Phe Ser
 20              25              30

Arg Asp Ala Tyr Trp Glu Lys Leu Tyr Val Asp Gln Ala Ala Gly Thr
 35              40              45

Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Glu Glu Val Pro
 50              55              60

Ser Phe Arg Leu Gly Gln His Leu Tyr Gly Thr Tyr Arg Thr Arg Leu
 65              70              75              80

His Glu Asn Asn Trp Ile Cys Ile Gln Glu Asp Thr Gly Leu Leu Tyr
 85              90              95

Leu Asn Arg Ser Leu Asp His Ser Ser Trp Glu Lys Leu Ser Val Arg
100              105              110

Asn Arg Gly Phe Pro Leu Leu Thr Val Tyr Leu Lys Val Phe Leu Ser
115              120              125

```

225/299

Pro Thr Ser Leu Arg Glu Gly Glu Cys Gln Trp Pro Gly Cys Ala Arg
 130 135 140
 Val Tyr Phe Ser Phe Phe Asn Thr Ser Phe Pro Ala Cys Ser Ser Leu
 145 150 155 160
 Lys Pro Arg Glu Leu Cys Phe Pro Glu Thr Arg Pro Ser Phe Arg Ile
 165 170 175
 Arg Glu Asn Arg Pro Pro Gly Thr Phe His Gln Phe Arg Leu Leu Pro
 180 185 190
 Val Gln Phe Leu Cys Pro Asn Ile Ser Val Ala Tyr Arg Leu Leu Glu
 195 200 205
 Gly Glu Gly Leu Pro Phe Arg Cys Ala Pro Asp Ser Leu Glu Val Ser
 210 215 220
 Thr Arg Trp Ala Leu Asp Arg Glu Gln Arg Glu Lys Tyr Glu Leu Val
 225 230 235 240
 Ala Val Cys Thr Val His Ala Gly Ala Arg Glu Glu Val Val Met Val
 245 250 255
 Pro Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser Ala Pro Thr Phe
 260 265 270
 Pro Ala Gly Val Asp Thr Ala Ser Ala Val Val Glu Phe Lys Arg Lys
 275 280 285
 Glu Asp Thr Val Val Ala Thr Leu Arg Val Phe Asp Ala Asp Val Val
 290 295 300
 Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser Thr Leu Leu Pro
 305 310 315 320
 Gly Asp Thr Trp Ala Gln Gln Thr Phe Arg Val Glu His Trp Pro Asn
 325 330 335
 Glu Thr Ser Val Gln Ala Asn Gly Ser Phe Val Arg Ala Thr Val His
 340 345 350
 Asp Tyr Arg Leu Val Leu Asn Arg Asn Leu Ser Ile Ser Glu Asn Arg
 355 360 365
 Thr Met Gln Leu Ala Val Leu Val Asn Asp Ser Asp Phe Gln Gly Pro
 370 375 380
 Gly Ala Gly Val Leu Leu Leu His Phe Asn Val Ser Val Leu Pro Val
 385 390 395 400
 Ser Leu His Leu Pro Ser Thr Tyr Ser Leu Ser Val Ser Arg Arg Ala
 405 410 415
 Arg Arg Phe Ala Gln Ile Gly Lys Val Cys Val Glu Asn Cys Gln Ala
 420 425 430
 Phe Ser Gly Ile Asn Val Gln Tyr Lys Leu His Ser Ser Gly Ala Asn

226/299

435	440	445
Cys Ser Thr Leu Gly Val Val Thr Ser Ala Glu Asp Thr Ser Gly Ile		
450	455	460
Leu Phe Val Asn Asp Thr Lys Ala Leu Arg Arg Pro Lys Cys Ala Glu		
465	470	475
Leu His Tyr Met Val Val Ala Thr Asp Gln Gln Thr Ser Arg Gln Ala		
	485	490
		495
Gln Ala Gln Leu Leu Val Thr Val Glu Gly Ser Tyr Val Ala Glu Glu		
	500	505
		510
Ala Gly Cys Pro Leu Ser Cys Ala Val Ser Lys Arg Arg Leu Glu Cys		
	515	520
		525
Glu Glu Cys Gly Gly Leu Gly Ser Pro Thr Gly Arg Cys Glu Trp Arg		
530	535	540
Gln Gly Asp Gly Lys Gly Ile Thr Arg Asn Phe Ser Thr Cys Ser Pro		
545	550	555
		560
Ser Thr Lys Thr Cys Pro Asp Gly His Cys Asp Val Val Glu Thr Gln		
	565	570
		575
Asp Ile Asn Ile Cys Pro Gln Asp Cys Leu Arg Gly Ser Ile Val Gly		
	580	585
		590
Gly His Glu Pro Gly Glu Pro Arg Gly Ile Lys Ala Gly Tyr Gly Thr		
595	600	605
Cys Asn Cys Phe Pro Glu Glu Glu Lys Cys Phe Cys Glu Pro Glu Asp		
610	615	620
Ile Gln Asp Pro Leu Cys Asp Glu Leu Cys Arg Thr Val Ile Ala Ala		
625	630	635
		640
Ala Val Leu Phe Ser Phe Ile Val Ser Val Leu Leu Ser Ala Phe Cys		
	645	650
		655
Ile His Cys Tyr His Lys Phe Ala His Lys Pro Pro Ile Ser Ser Ala		
	660	665
		670
Glu Met Thr Phe Arg Arg Pro Ala Gln Ala Phe Pro Val Ser Tyr Ser		
675	680	685
Ser Ser Gly Ala Arg Arg Pro Ser Leu Asp Ser Met Glu Asn Gln Val		
690	695	700
Ser Val Asp Ala Phe Lys Ile Leu Glu Asp Pro Lys Trp Glu Phe Pro		
705	710	715
		720
Arg Lys Asn Leu Val Leu Gly Lys Thr Leu Gly Glu Gly Glu Phe Gly		
	725	730
		735
Lys Val Val Lys Ala Thr Ala Phe His Leu Lys Gly Arg Ala Gly Tyr		
	740	745
		750

227/299

Thr Thr Val Ala Val Lys Met Leu Lys Glu Asn Ala Ser Pro Ser Glu
 755 760 765
 Leu Arg Asp Leu Leu Ser Glu Phe Asn Val Leu Lys Gln Val Asn His
 770 775 780
 Pro His Val Ile Lys Leu Tyr Gly Ala Cys Ser Gln Asp Gly Pro Leu
 785 790 795 800
 Leu Leu Ile Val Glu Tyr Ala Lys Tyr Gly Ser Leu Arg Gly Phe Leu
 805 810 815
 Arg Glu Ser Arg Lys Val Gly Pro Gly Tyr Leu Gly Ser Gly Gly Ser
 820 825 830
 Arg Asn Ser Ser Ser Leu Asp His Pro Asp Glu Arg Ala Leu Thr Met
 835 840 845
 Gly Asp Leu Ile Ser Phe Ala Trp Gln Ile Ser Gln Gly Met Gln Tyr
 850 855 860
 Leu Ala Glu Met Lys Leu Val His Arg Asp Leu Ala Ala Arg Asn Ile
 865 870 875 880
 Leu Val Ala Glu Gly Arg Lys Met Lys Ile Ser Asp Phe Gly Leu Ser
 885 890 895
 Arg Asp Val Tyr Glu Glu Asp Ser Tyr Val Lys Arg Ser Gln Gly Arg
 900 905 910
 Ile Pro Val Lys Trp Met Ala Ile Glu Ser Leu Phe Asp His Ile Tyr
 915 920 925
 Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile
 930 935 940
 Val Thr Leu Gly Gly Asn Pro Tyr Pro Gly Ile Pro Pro Glu Arg Leu
 945 950 955 960
 Phe Asn Leu Leu Lys Thr Gly His Arg Met Glu Arg Pro Asp Asn Cys
 965 970 975
 Ser Glu Glu Met Tyr Arg Leu Met Leu Gln Cys Trp Lys Gln Glu Pro
 980 985 990
 Asp Lys Arg Pro Val Phe Ala Asp Ile Ser Lys Asp Leu Glu Lys Met
 995 1000 1005
 Met Val Lys Arg Arg Asp Tyr Leu Asp Leu Ala Ala Ser Thr Pro Ser
 1010 1015 1020
 Asp Ser Leu Ile Tyr Asp Asp Gly Leu Ser Glu Glu Glu Thr Pro Leu
 1025 1030 1035 1040
 Val Asp Cys Asn Asn Ala Pro Leu Pro Arg Ala Leu Pro Ser Thr Trp
 1045 1050 1055

228/299

Ile Glu Asn Lys Leu Tyr Gly Met Ser Asp Pro Asn Trp Pro Gly Glu
 1060 1065 1070

Ser Pro Val Pro Leu Thr Arg Ala Asp Gly Thr Asn Thr Gly Phe Pro
 1075 1080 1085

Arg Tyr Pro Asn Asp Ser Val Tyr Ala Asn Trp Met Leu Ser Pro Ser
 1090 1095 1100

Ala Ala Lys Leu Met Asp Thr Phe Asp Ser
 1105 1110

<210> 278

<211> 393

<212> PRT

<213> Homo sapiens

<400> 278

Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
 1 5 10 15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
 20 25 30

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
 35 40 45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
 50 55 60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Thr Pro
 65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
 85 90 95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
 100 105 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
 115 120 125

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
 130 135 140

Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
 145 150 155 160

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
 165 170 175

Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
 180 185 190

His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
 195 200 205

229/299

Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
 210 215 220
 Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
 225 230 235 240
 Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
 245 250 255
 Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
 260 265 270
 Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
 275 280 285
 Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
 290 295 300
 Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
 305 310 315 320
 Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
 325 330 335
 Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
 340 345 350
 Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
 355 360 365
 Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
 370 375 380
 Phe Lys Thr Glu Gly Pro Asp Ser Asp
 385 390

<210> 279

<211> 1303

<212> DNA

<213> Homo sapiens

<400> 279

gtccaggagc aggtagctgc tgggctccgg ggacactttg cgttcgggct gggagcgtgc 60
 tttccacgac ggtgacacgc ttccctggat tggcagccag actgccttcc gggtcactgc 120
 catggaggag ccgcagtcag atcctagcgt cgagccccct ctgagtcagg aaacattttc 180
 agacctatgg aaactacttc ctgaaaacaa cgttctgtcc ccttgccgt cccaagcaat 240
 ggatgatttg atgctgtccc cggacgatat tgaacaatgg ttcactgaag acccaggctc 300
 agatgaagct ccagaaatgc cagaggctgc tccccccgtg gcccctgcac cagcgactcc 360
 tacaccggcg gcccctgcac cagccccctc ctggcccctg tcatcttctg tcccttccca 420
 gaaaacctac cagggcagct acggtttccg tctgggcttc ttgcattctg ggacagccaa 480
 gtctgtgact tgcacgtact cccctgccc ctcaacaagatg ttttgccaac tggccaagac 540
 ctgccctgtg cagctgtggg ttgattccac acccccgcgc ggcacccgcg tccgcgccat 600
 ggccatctac aagcagtcac agcacatgac ggaggttgtg aggcgctgcc cccaccatga 660
 gcgctgctca gatagcgatg gtctggcccc tcctcagcat cttatccgag tggaaggaaa 720
 tttgcgtgtg gagtatttgg atgacagaaa cacttttcga catagtgtgg tgggtgcccta 780
 ttgacgcgct gaggttggct ctgactgtac caccatccac tacaactaca tgtgtaacag 840
 ttcttgcattg ggcggcatga accggaggcc catectcacc atcatcacac tggaagactc 900

230/299

```

cagtggtaat ctactgggac ggaacagctt tgaggtgcgt gtttgtgcct gtcctgggag 960
agaccggcgc acagaggaag agaatctccg caagaaaggg gagcctcacc acgagctgcc 1020
cccagggagc actaagcgag cactgcccac caacaccagc tcctctcccc agccaaagaa 1080
gaaaccactg gatggagaat atttcaccct tcagatccgt gggcgtgagc gcttcgagat 1140
gttcogagag ctgaatgagg ccttggaact caaggatgcc caggctggga aggagccagg 1200
ggggagcagg gctcactcca gccacctgaa gtccaaaaag ggtcagtcta cctcccgcga 1260
taaaaaactc atgttcaaga cagaagggcc tgactcagac tga 1303

```

<210> 280

<211> 448

<212> PRT

<213> Homo sapiens

<400> 280

```

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
  1              5              10              15

```

```

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
      20              25              30

```

```

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
    35              40              45

```

```

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
    50              55              60

```

```

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
    65              70              75              80

```

```

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
      85              90              95

```

```

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
    100              105              110

```

```

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
    115              120              125

```

```

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
    130              135              140

```

```

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
    145              150              155              160

```

```

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
    165              170              175

```

```

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
    180              185              190

```

```

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
    195              200              205

```

```

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
    210              215              220

```

```

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro

```

231/299

225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
 405 410 415
 Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
 420 425 430
 Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
 435 440 445

<210> 281

<211> 2816

<212> DNA

<213> Homo sapiens

<400> 281

```

tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggt gtgccaccct 60
acagtactgc cctgaccctt acatccagcg ttctcgtagaa acccagctca tttctcttgg 120
aaagaaagtt attaccgatc caccatgtcc cagagcacac agacaaatga attcctcagt 180
ccagagggtt tccagcatat ctgggatttt ctggaacagc ctatatgttc agttcagccc 240
attgacttga actttgtgga tgaaccatca gaagatggtg cgacaaacaa gattgagatt 300
agcatggact gtatccgcat gcaggactcg gacctgagtg accccatgtg gccacagtac 360
acgaacctgg ggctcctgaa cagcatggac cagcagattc agaacggctc ctcgtccacc 420
agtccctata acacagacca cgcgcagaac agcgtcacgg cgccctcgcc ctacgcacag 480
cccagctcca ctttcgatgc tctctctcca tcaccgcca tcccctccaa caccgactac 540
ccaggccccg acagtttgcg cgtgtccttc cagcagtcga gcaccgcca gtcggccacc 600

```

232/299

```

tggacgtatt ccactgaact gaagaaactc tactgccaaa ttgcaaagac atgccccatc 660
cagatcaagg tgatgacccc acctcctcag ggagctgtta tccgcgccat gcctgtctac 720
aaaaaagctg agcacgtcac ggaggtggtg aagcgggtgcc ccaaccatga gctgagccgt 780
gaattcaacg agggacagat tgcccctcct agtcatttga ttcgagtaga ggggaacagc 840
catgcccagt atgtagaaga tcccatcaca ggaagacaga gtgtgctggt accttatgag 900
ccaccccgagg ttggcactga attcacgaca gtcttgtaga atttcatgtg taacagcagt 960
tgtgttgagg ggatgaaccg ccgtccaatt ttaatcattg ttactctgga aaccagagat 1020
gggcaagtcc tgggcccagc ctgctttgag gcccggtatc gtgcttgccc aggaagagac 1080
aggaaggcgg atgaagatag catcagaaag cagcaagttt cggacagtac aaagaacggg 1140
gatggtagca agcgcccgtt tcgtcagaac acacatggta tccagatgac atccatcaag 1200
aaacgaagat cccagatga tgaactgtta tacttaccag tgagggggccg tgagacttat 1260
gaaatgctgt tgaagatcaa agagtccctg gaactcatgc agtaccttcc tcagcacaca 1320
attgaaacgt acaggcaaca gcaacagcag cagcaccagc acttacttca gaaacatctc 1380
ctttcagcct gcttcaggaa tgagcttggt gagccccgga gagaaactcc aaaacaatct 1440
gacgtcttct ttagacattc caagccccc aaccgatcag tgtaccata gagccctatc 1500
tctatatatt aagtgtgtgt gttgtatttc catgtgtata tgtgagtgtg tgtgtgtgta 1560
tgtgtgtgcg tgtgtatcta gccctcataa acaggacttg aagacacttt ggctcagaga 1620
ccaactgct caaaggcaca aagccactag tgagagaatc ttttgaaggg actcaaacct 1680
ttacaagaaa ggatgttttc tgcagatttt gtatccttag accggccatt ggtgggtgag 1740
gaaccactgt gttgtctgtg gagctttctg ttgtttcctg ggagggaggg gtcaggtggg 1800
gaaagggggc ttaagatggt tattggaacc ctlttctgtc ttcttctgtt gtttttctaa 1860
aattcacagg gaagcttttg agcaggtctc aaacttaaga tgtcttttta agaaaaggag 1920
aaaaaagttg ttattgtctg tgcataagta agttgtagg gactgagaga ctcagtcaga 1980
cccttttaat gctggtcatg taataatatt gcaagtagta agaaacgaag gtgtcaagtg 2040
tactgctggg cagcgaggtg atcattacca aaagtaatca actttgtggg tggagagttc 2100
tttgtgagaa ctgcatatct ttgtgtcctc cctcatgtg taggtagaac atttcttaat 2160
gctgtgtacc tgcctctgcc actgtatggt ggcatctgtt atgctaaagt ttttcttgta 2220
catgaaaccc tggaagacct actacaaaaa aactgttggt tggcccccat agcaggtgaa 2280
ctcattttgt gcttttaata gaaagacaaa tccaccccag taatattgcc cttacgtagt 2340
tgtttaccat tattcaaagc tcaaaataga atttgaagcc ctctcacaaa atctgtgatt 2400
aatttgctta attagagctt ctatccctca agcctaccta ccataaaacc agccatatta 2460
ctgatactgt tcagtgcatt tagccaggag acttacgttt tgagtaagtg agatccaagc 2520
agacgtgtta aaatcagcac tcctggactg gaaattaaag attgaaaggg tagactactt 2580
ttcttttttt tactcaaaag ttttagagaat ctctgtttct ttccatttta aaaacatatt 2640
ttaagataat agcataaaga ctttaaaaat gttcctccc tccatcttcc cacaccagc 2700
caccagcact gtattttctg tcaccaagac aatgatttct tgttattgag gctgttgctt 2760
ttgtggatgt gtgattttta ttttcaataa acttttgcac cttggtttaa aagaaa 2816

```

<210> 282

<211> 641

<212> PRT

<213> Homo sapiens

<400> 282

```

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
  1              5              10             15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
      20              25             30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
      35              40             45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
      50              55             60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser

```

233/299

65	70	75	80
Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn	85	90	95
Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln	100	105	110
Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser	115	120	125
Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln	130	135	140
Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys	145	150	155
Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val	165	170	175
Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr	180	185	190
Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His	195	200	205
Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His	210	215	220
Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro	225	230	235
Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val	245	250	255
Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser	260	265	270
Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu	275	280	285
Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg	290	295	300
Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile	305	310	315
Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys	325	330	335
Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys	340	345	350
Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly	355	360	365
Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu	370	375	380

234/299

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415

Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430

Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445

Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460

Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480

Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495

His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Gly
 500 505 510

Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525

Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540

Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560

Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575

Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590

Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605

Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe
 610 615 620

Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
 625 630 635 640

Glu

<210> 283

<211> 2270

<212> DNA

<213> Homo sapiens

<400> 283

235/299

```

tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggg gtgccaccct 60
acagtactgc cctgaccctt acatccagcg tttcgtagaa acccagctca tttctcttgg 120
aaagaaagtt attaccgatc caccatgtcc cagagcacac agacaaatga attcctcagt 180
ccagaggttt tccagcatat ctgggatttt ctggaacagc ctatatgttc agttcagccc 240
attgacttga acttttgtga tgaaccatca gaagatgggt cgacaaacaa gattgagatt 300
agcatggact gtatccgcat gcaggactcg gacctgagtg accccatgtg gccacagtac 360
acgaacctgg ggctcctgaa cagcatggac cagcagattc agaacggctc ctcgctccacc 420
agtccctata acacagacca cgcgcagaa agcgtcacgg cgccctcgcc ctacgcacag 480
cccagctcca ccttcgatgc tctctctcca tccccgcca tccctccaa caccgactac 540
ccaggcccg caggtttcga cgtgtccttc cagcagtcga gcaccgcaa gtccggccacc 600
tggacgtatt cactgaact gaagaaactc tactgcaaaa ttgcaaagac atgccccatc 660
cagatcaagg tgatgacccc acctctcag ggagctgtta tccgcgccat gcctgtctac 720
aaaaaacgt agcagctac ggaggtgggt aagcgggtgc ccaacatga gctgagccgt 780
gaattcaacg agggacagat tgccctcct agtcatttga ttcgagtaga ggggaacagc 840
catgcccagt atgtagaaga tcccatcaca ggaagacaga gtgtgctggg accttatgag 900
ccaccccgagg ttggcactga attcacgaca gtcttgtaca atttcatgtg taacagcagt 960
tgtgttgagg ggatgaaccg ccgtccaatt ttaatcattg ttactctgga aaccagagat 1020
gggcaagtc tgggccgacg ctgctttgag gcccgatct gtgcttgccc aggaagagac 1080
aggaaggcgg atgaagatag catcagaaag cagcaagttt cggacagtac aaagaacggg 1140
gatggtacga agcgcgcgtt tcgtcagaac acacatggta tccagatgac atccatcaag 1200
aaacgaagat cccagatga tgaactgtta tacttaccag tgaggggccc tgagacttat 1260
gaaatgtctg tgaagatcaa agagtccctg gaactcatgc agtaccttcc tcagcacaca 1320
attgaaacgt acaggcaaca gcaacagcag cagcaccagc acttacttca gaaacagacc 1380
tcaatacagt ctccatcttc atatggtaac agctccccac ctctgaacaa aatgaacagc 1440
atgaacaagc tgccttctgt gagccagctt atcaaccctc agcagcgcaa cgccctcact 1500
cctacaacca ttcctgatgg catgggagcc aacattccca tgatgggcac ccacatgcca 1560
atggctggag acatgaatgg actcagcccc acccaggcac tccctcccc actctccatg 1620
ccatccacct cccactgcac acccccacct ccgtatccaa cagattgcag cattgtcggg 1680
ttcttagcga ggttgggctg ttcacatgt ctggactatt tcacgaccca ggggctgacc 1740
accatctatc agattgagca ttactccatg gatgatctgg caagtctgaa aatccctgag 1800
caatttcgac atgcatctg gaagggcatc ctggaccacc ggcagctcca cgaattctcc 1860
tcccttctc atctcctgcg gacccaagc agtgccctca cagtcagtgt gggctccagt 1920
gagacccggg gtgagcgtgt tattgatgct gtgcgattca cctccgcca gaccatctct 1980
ttccacccc gagatgagtg gaatgacttc aactttgaca tggatgctcg ccgcaataag 2040
caacagcgca tcaaagagga gggggagtga gcctcaccat gtgagctctt cctatccctc 2100
tcctaactgc cagcccccta aaagcactcc tgcttaatct tcaaagcctt ctccctagct 2160
cctcccttc ctcttgtctg atttcttagg ggaaggagaa gtaagaggct acctcttacc 2220
taacatctga cctggcatct aattctgatt ctggctttaa gccttcaaaa 2270

```

<210> 284

<211> 471

<212> PRT

<213> Homo sapiens

<400> 284

```

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1             5             10            15

```

```

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20             25            30

```

```

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35             40            45

```

```

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50             55            60

```

236/299

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu

237/299

370 375 380

Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
385 390 395 400

Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
405 410 415

Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
420 425 430

Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
435 440 445

Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Arg
450 455 460

Ser Gly Lys Ser Glu Asn Pro
465 470

<210> 285
<211> 2031
<212> DNA
<213> Homo sapiens

<400> 285

tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggt gtgccaccct 60
acagtactgc cctgaccctt acatccagcg tttcgtagaa acccagctca tttctcttgg 120
aaagaaagt attaccgatc caccatgtcc cagagcacac agacaaatga attcctcagt 180
ccagaggttt tccagcatat ctgggatttt ctggaacagc ctatatgttc agttcagccc 240
attgacttga actttgtgga tgaaccatca gaagatggtg cgacaaacaa gattgagatt 300
agcatggact gtatccgcat gcaggactcg gacctgagt accccatgtg gccacagtac 360
acgaacctgg ggctcctgaa cagcatggac cagcagattc agaacggctc ctcgctccacc 420
agtccttata acacagacca cgcgcagaac agcgtcacgg cgccctcgcc ctacgcacag 480
cccagctcca ccttcgatgc tctctctcca tcaccgcca tcccctccaa caccgactac 540
ccaggcccg caggtttcga cgtgtccttc cagcagtcga gcaccgcaa gtcggccacc 600
tggagctatt ccactgaact gaagaaactc tactgcaaaa ttgcaaagac atgccccatc 660
cagatcaagg tgatgacccc acctcctcag ggagctgtta tccgcgccat gcctgtctac 720
aaaaaagctg agcacgtcac ggaggtggtg aagcgggtgc ccaaccatga gctgagccgt 780
gaattcaacg agggacagat tgcccctcct agtcatttga ttcgagtaga ggggaacagc 840
catgcccagt atgtagaaga tcccatcaca ggaagacaga gtgtgctggt accttatgag 900
ccaccccagg ttggcactga attcacgaca gtcttgtaca atttcattgt taacagcagt 960
tgtgttgagg ggatgaaccg cgtccaatt ttaatcattg ttactctgga aaccagagat 1020
gggcaagtcc tgggcccagc ctgcttttag gcccggtct gtgcttgccc aggaagagac 1080
aggaaggcgg atgaagatag catcagaaag cagcaagttt cggacagtac aaagaacggt 1140
gatggtacga agcggccggt tcgtcagaac acacatggt tccagatgac atccatcaag 1200
aaacgaagat cccagatga tgaactgtta tacttaccag tgaggggccc tgagacttat 1260
gaaatgctgt tgaagatcaa agagtccctg gaactcatgc agtaccttcc tcagcacaca 1320
attgaaacgt acaggcaaca gcaacagcag cagcaccagc acttacttca gaaacagacc 1380
tcaatacagt ctocatcttc atatggtaac agctccccc ctctgaacaa aatgaacagc 1440
atgaacaagc tgccttctgt gagccagctt atcaaccctc agcagcgcaa cgccctcact 1500
cctacaacca ttcttgatgg catgggagcc aacagatctg gcaagtctga aaatccctga 1560
gcaatttctga catgcatctt ggaagggcat cctggaccac cggcagctcc acgaattctc 1620
ctccccttct catctcctgc ggacccaag cagtgcctct acagtcagt tgggctccag 1680
tgagacccgg ggtgagcgtg ttattgatgc tgtgcgattc accctccgcc agaccatctc 1740
tttccacccc cgagatgagt ggaatgactt caactttgac atggatgctc gccgcaataa 1800
gcaacagcgc atcaaagagg agggggagtg agcctcacca tgtgagctct tcctatccct 1860

238/299

ctcctaactg ccagccccct aaaagcactc ctgcttaatc ttcaaagcct tctccctagc 1920
 tctccccctt cctcttgtct gatttcttag gggaaggaga agtaagaggc tacctcttac 1980
 ctaacatctg acctggcatc taattctgat tctggcttta agccttcaaa a 2031

<210> 286

<211> 416

<212> PRT

<213> Homo sapiens

<400> 286

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175

Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190

Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220

Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240

Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255

239/299

Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Ile Pro Asp Gly Met Gly Ala Asn Arg Ser Gly Lys Ser Glu Asn Pro
 405 410 415

<210> 287

<400> 287

000

<210> 288

<211> 461

<212> PRT

<213> Homo sapiens

<400> 288

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

240/299

His	Ser	Phe	Asp	Val	Ser	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	85	90	95
Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	100	105	110
Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val	Met	Thr	Pro	Pro	Pro	Gln	Gly	115	120	125
Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	130	135	140
Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His	Glu	Leu	Ser	Arg	Glu	Phe	Asn	145	150	155
Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	165	170	175
Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val	180	185	190
Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val	195	200	205
Leu	Tyr	Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	210	215	220
Arg	Pro	Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	225	230	235
Leu	Gly	Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	245	250	255
Asp	Arg	Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	260	265	270
Ser	Thr	Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	275	280	285
His	Gly	Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	290	295	300
Glu	Leu	Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	305	310	315
Leu	Lys	Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His	325	330	335
Thr	Ile	Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu	340	345	350
Leu	Gln	Lys	Gln	Thr	Ser	Ile	Gln	Ser	Pro	Ser	Ser	Tyr	Gly	Asn	Ser	355	360	365
Ser	Pro	Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn	Lys	Leu	Pro	Ser	Val	370	375	380

241/299

Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400

Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415

Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430

Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445

Tyr Pro Thr Asp Cys Ser Ile Val Gly Ile Trp Gln Val
 450 455 460

<210> 289

<400> 289
 000

<210> 290

<211> 586

<212> PRT

<213> Homo sapiens

<400> 290

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

242/299

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Gly Phe Leu Ala Arg Leu Gly Cys
 450 455 460
 Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr

243/299

465 470 475 480
 Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
 485 490 495
 Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
 500 505 510
 Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser
 515 520 525
 Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
 530 535 540
 Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
 545 550 555 560
 Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn
 565 570 575
 Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
 580 585

<210> 291

<400> 291

000

<210> 292

<211> 393

<212> PRT

<213> Homo sapiens

<400> 292

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly

244/299

115	120	125
Ala Val Ile Arg Ala Met	Pro Val Tyr Lys Lys	Ala Glu His Val Thr
130	135	140
Glu Val Val Lys Arg Cys	Pro Asn His Glu Leu	Ser Arg Glu Phe Asn
145	150	155
Glu Gly Gln Ile Ala Pro	Pro Ser His Leu Ile	Arg Val Glu Gly Asn
165	170	175
Ser His Ala Gln Tyr Val	Glu Asp Pro Ile Thr	Gly Arg Gln Ser Val
180	185	190
Leu Val Pro Tyr Glu Pro	Pro Gln Val Gly Thr	Glu Phe Thr Thr Val
195	200	205
Leu Tyr Asn Phe Met Cys	Asn Ser Ser Cys Val	Gly Gly Met Asn Arg
210	215	220
Arg Pro Ile Leu Ile Ile	Val Thr Leu Glu Thr	Arg Asp Gly Gln Val
225	230	235
Leu Gly Arg Arg Cys Phe	Glu Ala Arg Ile Cys	Ala Cys Pro Gly Arg
245	250	255
Asp Arg Lys Ala Asp Glu	Asp Ser Ile Arg Lys	Gln Gln Val Ser Asp
260	265	270
Ser Thr Lys Asn Gly Asp	Gly Thr Lys Arg Pro	Phe Arg Gln Asn Thr
275	280	285
His Gly Ile Gln Met Thr	Ser Ile Lys Lys Arg	Arg Ser Pro Asp Asp
290	295	300
Glu Leu Leu Tyr Leu Pro	Val Arg Gly Arg Glu	Thr Tyr Glu Met Leu
305	310	315
Leu Lys Ile Lys Glu Ser	Leu Glu Leu Met Gln	Tyr Leu Pro Gln His
325	330	335
Thr Ile Glu Thr Tyr Arg	Gln Gln Gln Gln Gln	His Gln His Leu
340	345	350
Leu Gln Lys His Leu Leu	Ser Ala Cys Phe Arg	Asn Glu Leu Val Glu
355	360	365
Pro Arg Arg Glu Thr Pro	Lys Gln Ser Asp Val	Phe Phe Arg His Ser
370	375	380
Lys Pro Pro Asn Arg Ser	Val Tyr Pro	
385	390	

<210> 293

<400> 293

000

245/299

<210> 294

<211> 471

<212> PRT

<213> Homo sapiens

<400> 294

```

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1             5             10             15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
      20             25             30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
      35             40             45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
      50             55             60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
      65             70             75             80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
      85             90             95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
      100            105            110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
      115            120            125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
      130            135            140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
      145            150            155            160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
      165            170            175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
      180            185            190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
      195            200            205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
      210            215            220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
      225            230            235            240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
      245            250            255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
      260            265            270

```

246/299

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Arg
 450 455 460
 Ser Gly Lys Ser Glu Asn Pro
 465 470

<210> 295

<400> 295

000

<210> 296

<211> 516

<212> PRT

<213> Homo sapiens

<400> 296

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30

247/299

```

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
    35              40              45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
    50              55              60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
    65              70              75              80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
              85              90              95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
    100              105              110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
    115              120              125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
    130              135              140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
    145              150              155              160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
    165              170              175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
    180              185              190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
    195              200              205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
    210              215              220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
    225              230              235              240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
    245              250              255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
    260              265              270

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
    275              280              285

Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
    290              295              300

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
    305              310              315              320

Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
    325              330              335

```

248/299

Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Gly
 500 505 510
 Ile Trp Gln Val
 515

<210> 297

<400> 297

000

<210> 298

<211> 641

<212> PRT

<213> Homo sapiens

<400> 298

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15
 Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30
 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45

249/299

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60
 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly

250/299

355	360	365
Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu		
370	375	380
Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln		
385	390	395 400
Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser		
	405	410 415
Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser		
	420	425 430
Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg		
	435	440 445
Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile		
	450	455 460
Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu		
	465	470 475 480
Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser		
	485	490 495
His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Gly		
	500	505 510
Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr		
	515	520 525
Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp		
	530	535 540
Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys		
	545	550 555 560
Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His		
	565	570 575
Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser		
	580	585 590
Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg		
	595	600 605
Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe		
	610	615 620
Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly		
	625	630 635 640
Glu		

<210> 299

251/299

<400> 299
000

<210> 300
<211> 448
<212> PRT
<213> Homo sapiens

<400> 300

Met	Ser	Gln	Ser	Thr	Gln	Thr	Asn	Glu	Phe	Leu	Ser	Pro	Glu	Val	Phe
1				5					10					15	
Gln	His	Ile	Trp	Asp	Phe	Leu	Glu	Gln	Pro	Ile	Cys	Ser	Val	Gln	Pro
			20					25					30		
Ile	Asp	Leu	Asn	Phe	Val	Asp	Glu	Pro	Ser	Glu	Asp	Gly	Ala	Thr	Asn
		35					40					45			
Lys	Ile	Glu	Ile	Ser	Met	Asp	Cys	Ile	Arg	Met	Gln	Asp	Ser	Asp	Leu
	50					55					60				
Ser	Asp	Pro	Met	Trp	Pro	Gln	Tyr	Thr	Asn	Leu	Gly	Leu	Leu	Asn	Ser
65					70					75					80
Met	Asp	Gln	Gln	Ile	Gln	Asn	Gly	Ser	Ser	Ser	Thr	Ser	Pro	Tyr	Asn
				85					90					95	
Thr	Asp	His	Ala	Gln	Asn	Ser	Val	Thr	Ala	Pro	Ser	Pro	Tyr	Ala	Gln
			100					105					110		
Pro	Ser	Ser	Thr	Phe	Asp	Ala	Leu	Ser	Pro	Ser	Pro	Ala	Ile	Pro	Ser
		115					120					125			
Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	Ser	Phe	Asp	Val	Ser	Phe	Gln	Gln
	130					135					140				
Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys
145					150					155					160
Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val
			165						170					175	
Met	Thr	Pro	Pro	Pro	Gln	Gly	Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr
			180					185					190		
Lys	Lys	Ala	Glu	His	Val	Thr	Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His
		195					200					205			
Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His
	210					215					220				
Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro
225					230					235					240
Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val
				245					250					255	

252/299

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
 405 410 415
 Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
 420 425 430
 Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
 435 440 445

<210> 301

<400> 301
 000

<210> 302

<211> 461

<212> PRT

<213> Homo sapiens

<400> 302

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

253/299

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser

254/299

355	360	365
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val		
370	375	380
Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr		
385	390	395 400
Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met		
405	410	415
Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro		
420	425	430
Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro		
435	440	445
Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val		
450	455	460

<210> 303
 <211> 1386
 <212> DNA
 <213> Homo sapiens

<400> 303
 atgttgtacc tggaaaacaa tgcccagact caatttagtg agccacagta cacgaacctg 60
 gggctcctga acagcatgga ccagcagatt cagaacggct cctcgtccac cagtccctat 120
 aacacagacc acgcgagaa cagcgtcacg gcgcccctgc cctacgcaca gccagctcc 180
 accttcgatg ctctctctcc atcaccgccc atccccctcca acaccgacta cccaggccc 240
 cacagtttctg acgtgtcctt ccagcagtcg agcaccgcca agtcggccac ctggacgtat 300
 tccactgaac tgaagaaact ctactgcaa attgcaaaga catgccccat ccagatcaag 360
 gtgatgaccc cacctcctca gggagctgtt atccgcgcca tgcctgtcta caaaaaagct 420
 gagcacgtca cggaggtggt gaagcgggtg cccaaccatg agctgagccg tgaattcaac 480
 gagggacaga ttgcccctcc tagtcatttg attcgagtag aggggaacag ccatgcccag 540
 tatgtagaag atcccatcac aggaagacag agtgtgtgtg taccttatga gccaccccag 600
 gttggcactg aattcacgac agtcttgtac aatttcatgt gtaacagcag ttgtgttgga 660
 gggatgaacc gccgtccaat tttaatcatt gttactctgg aaaccagaga tgggcaagtc 720
 ctgggcccag cctgctttga ggcccggatc tgtgcttgcc caggaagaga caggaaggcg 780
 gatgaagata gcatcagaaa gcagcaagtt tcggacagta caaagaacgg tgatggtacg 840
 aagcgcctgt ttctgcagaa cacacatggt atccagatga catccatcaa gaaacgaaga 900
 tccccagatg atgaactggt atacttacca gtgaggggccc gtgagactta tgaaatgctg 960
 ttgaagatca aagagtcctt ggaactcatg cagtaccttc ctcagcacac aattgaaacg 1020
 tacaggcaac agcaacagca gcagcaccag cacttacttc agaaacagac ctcaatacag 1080
 tctccatctt catatggtaa cagctcccca cctctgaaca aaatgaacag catgaacaag 1140
 ctgccttctg tgagccagct tatcaacct cagcagcgca acgcccctcac tcctacaacc 1200
 attcctgatg gcatgggagc caacattccc atgatgggca cccacatgcc aatggctgga 1260
 gacatgaatg gactcagccc caccaggca ctccctcccc cactctccat gccatccacc 1320
 tcccactgca cacccccacc tccgtatccc acagattgca gcattgtcag gatctggcaa 1380
 gtctga 1386

<210> 304
 <211> 393
 <212> PRT
 <213> Homo sapiens

255/299

<400> 304

```

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1             5             10             15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
      20             25             30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
      35             40             45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
      50             55             60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
      65             70             75             80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
      85             90             95

Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
      100             105             110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
      115             120             125

Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
      130             135             140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
      145             150             155             160

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
      165             170             175

Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
      180             185             190

Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
      195             200             205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
      210             215             220

Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
      225             230             235             240

Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
      245             250             255

Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
      260             265             270

Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
      275             280             285

His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
      290             295             300

```

256/299

Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys His Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu
 355 360 365
 Pro Arg Arg Glu Thr Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser
 370 375 380
 Lys Pro Pro Asn Arg Ser Val Tyr Pro
 385 390

<210> 305
 <211> 1182
 <212> DNA
 <213> Homo sapiens

<400> 305
 atgttgtagc tggaatacaaa tgcccagact caatttagtg agccacagta cacgaacctg 60
 gggctcctga acagcatgga ccagcagatt cagaacgggt cctcgtccac cagtcacctat 120
 aacacagacc acgcgcagaa cagcgtcacg ggcgcctcgc cctacgcaca gccagctcc 180
 accttcgatg ctctctctcc atcaccgcc atccctcca acaccgacta cccaggcccg 240
 cacagtttcg acgtgtcctt ccagcagtcg agcaccgcca agtcggccac ctggacgtat 300
 tccactgaac tgaagaaact ctactgcaa attgcaaaga catgccccat ccagatcaag 360
 gtgatgacct caccctccta gggagctgtt atccgcgcca tgcctgtcta caaaaaagct 420
 gagcacgtca cggaggtggt gaagcgggtg cccaaccatg agctgagccg tgaattcaac 480
 gagggacaga ttgcccctcc tagtcatttg attcgagtag aggggaacag ccatgcccag 540
 tatgtagaag atcccatcac aggaagacag agtgtgtctg taccttatga gccaccccag 600
 gttggcactg aattcacgac agtcttgtag aatttcattg gtaacagcag ttgtgttgga 660
 gggatgaacc gccgtccaat tttaatcatt gttactctgg aaaccagaga tgggcaagtc 720
 ctgggccgac gctgctttga ggcccggatc tgtgcttgcc caggaagaga caggaaggcg 780
 gatgaagata gcatcagaaa gcagcaagtt tcggacagta caaagaacgg tgatggtacg 840
 aagcgcctgt ttctgcagaa cacacatggt atccagatga catccatcaa gaaacgaaga 900
 tccccagatg atgaactgtt atacttacca gtgaggggcc gtgagactta tgaaatgctg 960
 ttgaagatca aagagtccct ggaactcatg cagtaccttc ctcagcacac aattgaaacg 1020
 tacaggcaac agcaacagca gcagcaccag cacttacttc agaaacatct cctttcagcc 1080
 tgcttcagga atgagcttgt ggagccccgg agagaaactc caaaacaatc tgacgtcttc 1140
 tttagacatt ccaagcccc aaaccgatca gtgtacccat ag 1182

<210> 306
 <211> 586
 <212> PRT
 <213> Homo sapiens

<400> 306
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

257/299

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335

258/299

Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys
 450 455 460
 Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr
 465 470 475 480
 Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
 485 490 495
 Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
 500 505 510
 Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser
 515 520 525
 Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
 530 535 540
 Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
 545 550 555 560
 Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn
 565 570 575
 Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
 580 585

<210> 307

<211> 1761

<212> DNA

<213> Homo sapiens

<400> 307

atgttgtagc tggaatacaa tgcccagact caatttagtg agccacagta cacgaacctg 60
 gggctcctga acagcatgga ccagcagatt cagaacggct cctcgtccac cagtccttat 120
 aacacagacc acgcgcagaa cagcgtcacg gcgcctcgc cctacgcaca gccagctcc 180

259/299

```

accttcgatg ctctctctcc atcaccgcc atcccctcca acaccgacta cccaggcccg 240
cacagtttcg acgtgtcctt ccagcagtcg agcaccgcc aatcgggccac ctggacgtat 300
tccactgaac tgaagaaact ctactgccaa attgcaaaga catgccccat ccagatcaag 360
gtgatgaccc cacctcctca gggagctgtt atccgcgcc tgctgtctta caaaaaagct 420
gagcacgtca cggagggtgt gaagcgtgtc cccaaccatg agctgagccg tgaattcaac 480
gagggacaga ttgcccctcc tagtcatttg attcgagtag aggggaacag ccatgcccag 540
tatgtagaag atcccatcac aggaagacag agtgtgtctg taccttatga gccaccccag 600
gttggcactg aattcacgac agtcttgtac aatttcatgt gtaacagcag ttgtgttgga 660
gggatgaacc gccgtccaat tttaatcatt gttactcttg aaaccagaga tgggcaagtc 720
ctgggcccgc gctgctttga ggcccggatc tgtgcttgcc caggaagaga caggaaggcg 780
gatgaagata gcatcagaaa gcagcaagtt tcggacagta caaagaacgg tgatggtacg 840
aagcgcccgt ttcgtcagaa cacacatggt atccagatga catccatcaa gaaacgaaga 900
tccccagatg atgaactgtt atacttacca gtgagggggc gtgagactta tgaaatgctg 960
ttgaagatca aagagtcctt ggaactcatg cagtaccttc ctgagcacac aattgaaacg 1020
tacaggcaac agcaacagca gcagcaccag cacttacttc agaaacagac ctcaatacag 1080
tctccatctt catatggtaa cagctcccca cctctgaaca aaatgaacag catgaacaag 1140
ctgccttctg tgagccagct tatcaaccct cagcagcgca acgccctcac tcctacaacc 1200
attcctgatg gcatggggag caacattccc atgatgggca cccacatgcc aatggctgga 1260
gacatgaatg gactcagccc caccagcgca ctccctcccc cactctccat gccatccacc 1320
tcccactgca cccccccacc tccgtatccc acagattgca gcattgtcag tttcttagcg 1380
agggttgggt gttcatcatg tctggactat ttcacgaccc aggggctgac caccatctat 1440
cagattgagc attactccat ggatgatctg gcaagtctga aaatccctga gcaatttcga 1500
catgcgatct ggaagggcat cctggaccac cggcagctcc acgaattctc ctccccttct 1560
catctcctgc ggaccccaag cagtgcctct acagtcagtg tgggctccag tgagaccggg 1620
ggtagcgtg ttattgatgc tgtgcgattc accctccgcc agaccatctc tttcccacc 1680
cgagatgagt ggaatgactt caactttgac atggatgctc gccgcaataa gcaacagcgc 1740
atcaaagagg agggggagtg a 1761

```

<210> 308

<211> 516

<212> PRT

<213> Homo sapiens

<400> 308

```

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
  1                      5                      10                      15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
      20                      25                      30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
      35                      40                      45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
      50                      55                      60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
      65                      70                      75                      80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
      85                      90                      95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
      100                      105                      110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
      115                      120                      125

```

260/299

Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	Ser	Phe	Asp	Val	Ser	Phe	Gln	Gln	130	135	140
Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys	145	150	155
Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val	165	170	175
Met	Thr	Pro	Pro	Pro	Gln	Gly	Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr	180	185	190
Lys	Lys	Ala	Glu	His	Val	Thr	Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His	195	200	205
Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His	210	215	220
Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro	225	230	235
Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val	245	250	255
Gly	Thr	Glu	Phe	Thr	Thr	Val	Leu	Tyr	Asn	Phe	Met	Cys	Asn	Ser	Ser	260	265	270
Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Ile	Ile	Val	Thr	Leu	275	280	285
Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg	Cys	Phe	Glu	Ala	Arg	290	295	300
Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala	Asp	Glu	Asp	Ser	Ile	305	310	315
Arg	Lys	Gln	Gln	Val	Ser	Asp	Ser	Thr	Lys	Asn	Gly	Asp	Gly	Thr	Lys	325	330	335
Arg	Pro	Phe	Arg	Gln	Asn	Thr	His	Gly	Ile	Gln	Met	Thr	Ser	Ile	Lys	340	345	350
Lys	Arg	Arg	Ser	Pro	Asp	Asp	Glu	Leu	Leu	Tyr	Leu	Pro	Val	Arg	Gly	355	360	365
Arg	Glu	Thr	Tyr	Glu	Met	Leu	Leu	Lys	Ile	Lys	Glu	Ser	Leu	Glu	Leu	370	375	380
Met	Gln	Tyr	Leu	Pro	Gln	His	Thr	Ile	Glu	Thr	Tyr	Arg	Gln	Gln	Gln	385	390	395
Gln	Gln	Gln	His	Gln	His	Leu	Leu	Gln	Lys	Gln	Thr	Ser	Ile	Gln	Ser	405	410	415
Pro	Ser	Ser	Tyr	Gly	Asn	Ser	Ser	Pro	Pro	Leu	Asn	Lys	Met	Asn	Ser	420	425	430

261/299

Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445

Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460

Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480

Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495

His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Arg
 500 505 510

Ile Trp Gln Val
 515

<210> 309

<211> 1551

<212> DNA

<213> Homo sapiens

<400> 309

```

atgtcccaga gcacacagac aaatgaattc ctccagtcag aggtttttcca gcatatctgg 60
gattttcttg aacagcctat atgttcagtt cagccatttg acttgaactt tgtggatgaa 120
ccatcagaag atggtgcgac aaacaagatt gagattagca tggactgtat ccgcatgcag 180
gactcggacc tgagtgacct catgtggcca cagtacacga acctggggct cctgaacagc 240
atggaccagc agattcagaa cggtctctcg tccaccagtc cctataacac agaccacgcg 300
cagaacagcg tcacggcgcc ctgcgcctac gcacagccca gctccacctt cgatgctctc 360
tctccatcac ccgcatccc ctccaacacc gactaccag gcccgcacag ttctgacgtg 420
tccttccagc agtcgagcac cgccaagtcg gccacctgga cgtattccac tgaactgaag 480
aaactctact gccaaattgc aaagacatgc cccatccaga tcaaggtgat gacccacact 540
cctcagggag ctgttatccg cgccatgcct gtctacaaaa aagctgagca cgtcacggag 600
gtggtgaagc ggtgccccaa ccatgagctg agcgtgaat tcaacgaggg acagattgcc 660
cctcctagtc atttgattcg agtagagggg aacagccatg cccagtatgt agaagatccc 720
atcacaggaa gacagagtgt gctggtacct tatgagccac cccaggttgg cactgaattc 780
acgacagtct tgtacaattt catgtgtaac agcagttgtg ttggagggat gaaccgccgt 840
ccaattttaa tcattgttac tctggaaacc agagatgggc aagtcctggg ccgacgctgc 900
tttgaggccc ggatctgtgc ttgcccagga agagacagga aggcggatga agatagcatc 960
agaaagcagc aagtttcgga cagtacaaag aacggtgatg gtacgaagcg cccgtttcgt 1020
cagaacacac atggtatcca gatgacatcc atcaagaaac gaagatcccc agatgatgaa 1080
ctgttatact taccagttag gggccgtgag acttatgaaa tgctgttgaa gatcaaagag 1140
tccctggaac tcatgcagta ccttcctcag cacacaattg aaacgtacag gcaacagcaa 1200
cagcagcagc accagcactt acttcagaaa cagacctcaa tacagtctcc atcttcatat 1260
ggtaacagct cccacactct gaacaaaatg aacagcatga acaagctgcc ttctgtgagc 1320
cagcttatca accctcagca gcgcaacgcc ctactccta caaccattcc tgatggcatg 1380
ggagccaaca ttcccatgat gggcaccac atgccaatgg ctggagacat gaatggactc 1440
agccccaccc agcccactcc tccccactc tccatgccat ccacctcca ctgcacacc 1500
ccacctccgt atcccacaga ttgcagcatt gtcaggatct ggcaagtctg a 1551

```

<210> 310

<211> 641

<212> PRT

<213> Homo sapiens

262/299

<400> 310

```

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1           5           10           15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
      20           25           30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
      35           40           45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
      50           55           60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
      65           70           75           80

Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
      85           90           95

Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
      100           105           110

Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
      115           120           125

Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
      130           135           140

Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
      145           150           155           160

Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
      165           170           175

Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
      180           185           190

Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
      195           200           205

Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
      210           215           220

Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
      225           230           235           240

Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
      245           250           255

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
      260           265           270

Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
      275           280           285

Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
      290           295           300

```

263/299

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Ser
 500 505 510
 Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp Tyr Phe Thr Thr
 515 520 525
 Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr Ser Met Asp Asp
 530 535 540
 Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His Ala Ile Trp Lys
 545 550 555 560
 Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser Ser Pro Ser His
 565 570 575
 Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser Val Gly Ser Ser
 580 585 590
 Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg Phe Thr Leu Arg
 595 600 605
 Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn Asp Phe Asn Phe

264/299

610 615 620
 Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile Lys Glu Glu Gly
 625 630 635 640

Glu

<210> 311
 <211> 1926
 <212> DNA
 <213> Homo sapiens

<400> 311
 atgtcccaga gcacacagac aaatgaattc ctcagtcacag aggtttttcca gcatatctgg 60
 gatttttctgg aacagcctat atgttcagtt cagccattg acttgaactt tgtggatgaa 120
 ccatcagaag atggtgcgac aaacaagatt gagattagca tggactgtat ccgcatgcag 180
 gactcggacc tgagtgaccc catgtggcca cagtacacga acctggggct cctgaacagc 240
 atggaccagc agattcagaa cggtctcctcg tccaccagtc cctataacac agaccacgcg 300
 cagaacagcg tcacggcgcc ctccacacc gctacccag gccgcacag tttcgacgtg 360
 tctccatcac ccgccatccc ctccaacacc gactacccag gccgcacag tttcgacgtg 420
 tcttccagc agtcgagcac cgccaagtcg gccacctgga cgtattccac tgaactgaag 480
 aaactctact gccaaattgc aaagacatgc cccatccaga tcaaggtgat gacccacact 540
 cctcagggag ctgttatccg cgccatgcct gtctacaaaa aagctgagca cgtcacggag 600
 gtggatgaagc ggtgccccaa ccatgagctg agccgtgaat tcaacgaggg acagattgcc 660
 cctcctagtc atttgattcg agtagagggg aacagccatg cccagtatgt agaagatccc 720
 atcacaggaa gacagagtgt gctgggtacct tatgagccac cccaggttgg cactgaattc 780
 acgacagtct tgtacaattt catgtgtaac agcagttgtg ttggagggat gaaccgccgt 840
 ccaattttta tcatgtttac tctgaaaacc agagatgggc aagtcctggg ccgacgctgc 900
 tttgaggccc ggatctgtgc ttgcccagga agagacagga aggcggatga agatagcatc 960
 agaaagcagc aagtttcgga cagtacaaaag aacggtgatg gtacgaagcg cccgtttcgt 1020
 cagaacacac atggtatcca gatgacatcc atcaagaaac gaagatcccc agatgatgaa 1080
 ctgttatact taccagtgtg gggccgtgag acttatgaaa tgctgttgaa gatcaaagag 1140
 tccctggaac tcatgcagta ccttcctcag cacacaattg aaacgtacag gcaacagcaa 1200
 cagcagcagc accagcactt acttcagaaa cagacctcaa tacagtctcc atcttcatat 1260
 ggtaacagct cccacactct gaacaaaatg aacagcatga acaagctgcc ttctgtgagc 1320
 cagcttatca accctcagca gcgcaacgcc ctcactccta caaccattcc tgatggcatg 1380
 ggagccaaca ttcctatgat gggcaccac atgccaatgg ctggagacat gaatggactc 1440
 agccccacc aggcaactcc tccccactc tccatgcat ccacctcca ctgcacacc 1500
 ccacctccgt atcccacaga ttgcagcatt gtcagtttct tagcgaggtt gggctgttca 1560
 tcatgtctgg actatttcac gacccagggg ctgaccacca tctatcagat tgagcattac 1620
 tccatggatg atctggcaag tctgaaaatc cctgagcaat ttcgacatgc gatctggaag 1680
 ggcactcctg accaccggca gctccacgaa ttctcctccc cttctcatct cctgcccacc 1740
 ccaagcagtg cctctacagt cagtgtgggc tccagtgaga cccgggggtga gcgtgttatt 1800
 gatgctgtgc gattcacctt ccgccagacc atctctttcc caccctgaga tgagtggaa 1860
 gacttcaact ttgacatgga tgctcgccgc aataagcaac agcgcatcaa agaggagggg 1920
 gagtga 1926

<210> 312
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 312
 Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15

265/299

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30
 Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45
 Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60
 Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80
 Met Asp Gln Gln Ile Gln Asn Gly Ser Ser Ser Thr Ser Pro Tyr Asn
 85 90 95
 Thr Asp His Ala Gln Asn Ser Val Thr Ala Pro Ser Pro Tyr Ala Gln
 100 105 110
 Pro Ser Ser Thr Phe Asp Ala Leu Ser Pro Ser Pro Ala Ile Pro Ser
 115 120 125
 Asn Thr Asp Tyr Pro Gly Pro His Ser Phe Asp Val Ser Phe Gln Gln
 130 135 140
 Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Thr Glu Leu Lys
 145 150 155 160
 Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val
 165 170 175
 Met Thr Pro Pro Pro Gln Gly Ala Val Ile Arg Ala Met Pro Val Tyr
 180 185 190
 Lys Lys Ala Glu His Val Thr Glu Val Val Lys Arg Cys Pro Asn His
 195 200 205
 Glu Leu Ser Arg Glu Phe Asn Glu Gly Gln Ile Ala Pro Pro Ser His
 210 215 220
 Leu Ile Arg Val Glu Gly Asn Ser His Ala Gln Tyr Val Glu Asp Pro
 225 230 235 240
 Ile Thr Gly Arg Gln Ser Val Leu Val Pro Tyr Glu Pro Pro Gln Val
 245 250 255
 Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys

266/299

325	330	335
Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys		
340	345	350
Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly		
355	360	365
Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu		
370	375	380
Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln		
385	390	395
Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys		
405	410	415
Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser		
420	425	430
Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro		
435	440	445

<210> 313
 <211> 2816
 <212> DNA
 <213> Homo sapiens

<400> 313
 tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggt gtgccaccct 60
 acagtactgc cctgaccctt acatccagcg tttcgtagaa acccagctca tttctcttgg 120
 aaagaaagtt attaccgatc caccatgtcc cagagcacac agacaaatga attcctcagt 180
 ccagagggtt tccagcatat ctgggatttt ctggaacagc ctatatgttc agttcagccc 240
 attgacttga actttgtgga tgaaccatca gaagatggtg cgacaaacaa gattgagatt 300
 agcatggact gtatccgcat gcaggactcg gacctgagtg accccatgtg gccacagtac 360
 acgaacctgg ggctcctgaa cagcatggac cagcagattc agaacggctc ctctgtccacc 420
 agtccctata acacagacca cgcgcagaac agcgtcacgg cgccctcgcc ctacgcacag 480
 cccagctcca ccttcgatgc tctctctcca tcaccgcca tcccctccaa caccgactac 540
 ccaggcccg caggtttcga cgtgtccttc cagcagtcga gcaccgccaa gtcgggccacc 600
 tggacgtatt ccactgaact gaagaaactc tactgccaaa ttgcaaagac atgccccatc 660
 cagatcaagg tgatgacccc acctcctcag ggagctgtta tccgcgccat gcctgtctac 720
 aaaaaagctg agcacgtcac ggagggtggtg aagcggtgcc ccaaccatga gctgagccgt 780
 gaattcaacg agggacagat tgcccctcct agtcatttga ttcgagtaga ggggaacagc 840
 catgcccagt atgtagaaga tcccatcaca ggaagacaga gtgtgctggt accttatgag 900
 ccaccccgag ttggcactga attcacgaca gtcttgtaca atttcattgt taacagcagt 960
 tgtgttggag ggatgaaccg ccgtccaatt ttaatcattg ttactctgga aaccagagat 1020
 gggcaagtcc tgggcccagc ctgctttgag gcccgatct gtgcttgccc aggaagagac 1080
 aggaaggcgg atgaagatag catcagaaag cagcaagttt cggacagtac aaagaacggt 1140
 gatggtacga agcgcctggt tcgtcagaac acacatggta tccagatgac atccatcaag 1200
 aaacgaagat cccagatga tgaactgtta tacttaccag tgaggggccc tgagacttat 1260
 gaaatgctgt tgaagatcaa agagtccctg gaactcatgc agtaccttcc tcagcacaca 1320
 attgaaacgt acaggcaaca gcaacagcag cagcaccagc acttacttca gaaacatctc 1380
 ctttcagcct gcttcaggaa tgagcttgtg gagccccgga gagaaactcc aaaacaatct 1440
 gacgtcttct ttagacattc caagccccca aaccgatcag tgtaccata gagccctatc 1500
 tctatatttt aagtgtgtgt gttgtatttc catgtgtata tgtgagtgtg tgtgtgtgta 1560
 tgtgtgtgcg tgtgtatcta gccctcataa acaggacttg aagacacttt ggctcagaga 1620
 cccaactgct caaaggcaca aagccactag tgagagaatc ttttgaaggg actcaaacct 1680

267/299

```

ttacaagaaa ggatgttttc tgcagatttt gtatccttag accggccatt ggtgggtgag 1740
gaaccactgt gtttgtctgt gagctttctg ttgtttcctg ggagggaggg gtcaggtggg 1800
gaaaggggca ttaagatggt tattggaacc cttttctgtc ttcttctggt gtttttctaa 1860
aattcacagg gaagcttttg agcaggtctc aaacttaaga tgtcttttta agaaaaggag 1920
aaaaaagttg ttattgtctg tgcataagta agttgtaggt gactgagaga ctcagtcaga 1980
cccttttaat gctggtcatt taataatatt gcaagtagta agaaacgaag gtgtcaagtg 2040
tactgctggg cagcgaggtg atcattacca aaagtaatca actttgtggg tggagagttc 2100
tttgtgagaa cttgcattat ttgtgtcctc cctcatgtg taggtagaac atttcttaat 2160
gctgtgtacc tgcctctgcc actgtatggt ggcactgtgt atgctaaagt ttttcttgta 2220
catgaaaccc tggaagacct actacaaaaa aactgttggt tggcccccat agcaggtgaa 2280
ctcattttgt gcttttaata gaaagacaaa tccacccag taatattgcc cttacgtagt 2340
tgtttacctt tattcaaagc tcaaaataga atttgaagcc ctctcacaaa atctgtgatt 2400
aatttgctta attagagctt ctatccctca agcctaccta ccataaaacc agccatatta 2460
ctgatactgt tcagtgcatt tagccaggag acttacgttt tgagtaagtg agatccaagc 2520
agacgtgtta aaatcagcac tcctggactg gaaattaaag attgaaaggg tagactactt 2580
ttcttttttt tactcaaaag tttagagaat ctctgtttct ttccatttta aaaacatatt 2640
ttaagataat agcataaaga ctttaaaaaa gttcctcccc tccatcttcc cacaccaggt 2700
caccagcact gtatttttctg tcaccaagac aatgatttct tgttattgag gctgttgctt 2760
ttgtggatgt gtgattttta ttttcaataa acttttgcatt cttgggtttta aagaaa 2816

```

<210> 314

<211> 499

<212> PRT

<213> Homo sapiens

<400> 314

```

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
  1              5              10              15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
  20              25              30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
  35              40              45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
  50              55              60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
  65              70              75              80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
  85              90              95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
  100             105             110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
  115             120             125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
  130             135             140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
  145             150             155             160

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg

```

268/299

165					170					175					
Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Asp	Val	Val	Lys
			180					185					190		
Arg	Cys	Pro	Asn	His	Glu	Leu	Gly	Arg	Asp	Phe	Asn	Glu	Gly	Gln	Ser
		195					200					205			
Ala	Pro	Ala	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Asn	Leu	Ser	Gln
	210					215					220				
Tyr	Val	Asp	Asp	Pro	Val	Thr	Gly	Arg	Gln	Ser	Val	Val	Val	Pro	Tyr
225					230					235					240
Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Ile	Leu	Tyr	Asn	Phe
			245						250					255	
Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu
			260					265					270		
Ile	Ile	Ile	Thr	Leu	Glu	Met	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg
		275					280					285			
Ser	Phe	Glu	Gly	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala
	290					295					300				
Asp	Glu	Asp	His	Tyr	Arg	Glu	Gln	Gln	Ala	Leu	Asn	Glu	Ser	Ser	Ala
305					310					315					320
Lys	Asn	Gly	Ala	Ala	Ser	Lys	Arg	Ala	Phe	Lys	Gln	Ser	Pro	Pro	Ala
			325						330					335	
Val	Pro	Ala	Leu	Gly	Ala	Gly	Val	Lys	Lys	Arg	Arg	His	Gly	Asp	Glu
		340						345					350		
Asp	Thr	Tyr	Tyr	Leu	Gln	Val	Arg	Gly	Arg	Glu	Asn	Phe	Glu	Ile	Leu
	355					360					365				
Met	Lys	Leu	Lys	Glu	Ser	Leu	Glu	Leu	Met	Glu	Leu	Val	Pro	Gln	Pro
	370					375					380				
Leu	Val	Asp	Ser	Tyr	Arg	Gln	Gln	Gln	Gln	Leu	Leu	Gln	Arg	Pro	Ser
385					390					395					400
His	Leu	Gln	Pro	Pro	Ser	Tyr	Gly	Pro	Val	Leu	Ser	Pro	Met	Asn	Lys
			405					410						415	
Val	His	Gly	Gly	Met	Asn	Lys	Leu	Pro	Ser	Val	Asn	Gln	Leu	Val	Gly
		420						425					430		
Gln	Pro	Pro	Pro	His	Ser	Ser	Ala	Ala	Thr	Pro	Asn	Leu	Gly	Pro	Val
		435					440					445			
Gly	Pro	Gly	Met	Leu	Asn	Asn	His	Gly	His	Ala	Val	Pro	Ala	Asn	Gly
	450					455					460				
Glu	Met	Ser	Ser	Ser	His	Ser	Ala	Gln	Ser	Met	Val	Ser	Gly	Ser	His
465					470					475					480

269/299

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr
 485 490 495

Trp Gly Pro

<210> 315

<211> 636

<212> PRT

<213> Homo sapiens

<400> 315

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
 1 5 10 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
 20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
 35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
 50 55 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
 65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
 85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
 100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
 115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
 130 135 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
 145 150 155 160

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg
 165 170 175

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
 180 185 190

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
 195 200 205

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
 210 215 220

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr
 225 230 235 240

270/299

Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Ile	Leu	Tyr	Asn	Phe	
				245					250					255		
Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	
				260					265					270		
Ile	Ile	Ile	Thr	Leu	Glu	Met	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg	
				275					280					285		
Ser	Phe	Glu	Gly	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala	
				290					295					300		
Asp	Glu	Asp	His	Tyr	Arg	Glu	Gln	Gln	Ala	Leu	Asn	Glu	Ser	Ser	Ala	
				305					310					315		
Lys	Asn	Gly	Ala	Ala	Ser	Lys	Arg	Ala	Phe	Lys	Gln	Ser	Pro	Pro	Ala	
				325					330					335		
Val	Pro	Ala	Leu	Gly	Ala	Gly	Val	Lys	Lys	Arg	Arg	His	Gly	Asp	Glu	
				340					345					350		
Asp	Thr	Tyr	Tyr	Leu	Gln	Val	Arg	Gly	Arg	Glu	Asn	Phe	Glu	Ile	Leu	
				355					360					365		
Met	Lys	Leu	Lys	Glu	Ser	Leu	Glu	Leu	Met	Glu	Leu	Val	Pro	Gln	Pro	
				370					375					380		
Leu	Val	Asp	Ser	Tyr	Arg	Gln	Gln	Gln	Gln	Leu	Leu	Gln	Arg	Pro	Ser	
				385					390					395		
His	Leu	Gln	Pro	Pro	Ser	Tyr	Gly	Pro	Val	Leu	Ser	Pro	Met	Asn	Lys	
				405					410					415		
Val	His	Gly	Gly	Met	Asn	Lys	Leu	Pro	Ser	Val	Asn	Gln	Leu	Val	Gly	
				420					425					430		
Gln	Pro	Pro	Pro	His	Ser	Ser	Ala	Ala	Thr	Pro	Asn	Leu	Gly	Pro	Val	
				435					440					445		
Gly	Pro	Gly	Met	Leu	Asn	Asn	His	Gly	His	Ala	Val	Pro	Ala	Asn	Gly	
				450					455					460		
Glu	Met	Ser	Ser	Ser	His	Ser	Ala	Gln	Ser	Met	Val	Ser	Gly	Ser	His	
				465					470					475		
Cys	Thr	Pro	Pro	Pro	Pro	Tyr	His	Ala	Asp	Pro	Ser	Leu	Val	Ser	Phe	
				485					490					495		
Leu	Thr	Gly	Leu	Gly	Cys	Pro	Asn	Cys	Ile	Glu	Tyr	Phe	Thr	Ser	Gln	
				500					505					510		
Gly	Leu	Gln	Ser	Ile	Tyr	His	Leu	Gln	Asn	Leu	Thr	Ile	Glu	Asp	Leu	
				515					520					525		
Gly	Ala	Leu	Lys	Ile	Pro	Glu	Gln	Tyr	Arg	Met	Thr	Ile	Trp	Arg	Gly	
				530					535					540		
Leu	Gln	Asp	Leu	Lys	Gln	Gly	His	Asp	Tyr	Ser	Thr	Ala	Gln	Gln	Leu	

271/299

545 550 555 560
 Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu
 565 570 575
 Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His
 580 585 590
 Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu
 595 600 605
 Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln
 610 615 620
 Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His
 625 630 635

<210> 316

<211> 588

<212> PRT

<213> Homo sapiens

<400> 316

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
 1 5 10 15
 Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
 20 25 30
 Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
 35 40 45
 Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
 50 55 60
 Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
 65 70 75 80
 Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
 85 90 95
 Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
 100 105 110
 Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg
 115 120 125
 Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
 130 135 140
 Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
 145 150 155 160
 Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
 165 170 175
 Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr

272/299

180					185					190					
Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Ile	Leu	Tyr	Asn	Phe
		195					200					205			
Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu
	210					215					220				
Ile	Ile	Ile	Thr	Leu	Glu	Met	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg
225						230					235				240
Ser	Phe	Glu	Gly	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala
				245					250					255	
Asp	Glu	Asp	His	Tyr	Arg	Glu	Gln	Gln	Ala	Leu	Asn	Glu	Ser	Ser	Ala
			260					265					270		
Lys	Asn	Gly	Ala	Ala	Ser	Lys	Arg	Ala	Phe	Lys	Gln	Ser	Pro	Pro	Ala
		275					280					285			
Val	Pro	Ala	Leu	Gly	Ala	Gly	Val	Lys	Lys	Arg	Arg	His	Gly	Asp	Glu
	290					295					300				
Asp	Thr	Tyr	Tyr	Leu	Gln	Val	Arg	Gly	Arg	Glu	Asn	Phe	Glu	Ile	Leu
305						310					315				320
Met	Lys	Leu	Lys	Glu	Ser	Leu	Glu	Leu	Met	Glu	Leu	Val	Pro	Gln	Pro
				325					330					335	
Leu	Val	Asp	Ser	Tyr	Arg	Gln	Gln	Gln	Gln	Leu	Leu	Gln	Arg	Pro	Ser
			340					345					350		
His	Leu	Gln	Pro	Pro	Ser	Tyr	Gly	Pro	Val	Leu	Ser	Pro	Met	Asn	Lys
		355					360					365			
Val	His	Gly	Gly	Met	Asn	Lys	Leu	Pro	Ser	Val	Asn	Gln	Leu	Val	Gly
	370					375					380				
Gln	Pro	Pro	Pro	His	Ser	Ser	Ala	Ala	Thr	Pro	Asn	Leu	Gly	Pro	Val
385						390					395				400
Gly	Pro	Gly	Met	Leu	Asn	Asn	His	Gly	His	Ala	Val	Pro	Ala	Asn	Gly
				405					410					415	
Glu	Met	Ser	Ser	Ser	His	Ser	Ala	Gln	Ser	Met	Val	Ser	Gly	Ser	His
			420					425					430		
Cys	Thr	Pro	Pro	Pro	Tyr	His	Ala	Asp	Pro	Ser	Leu	Val	Ser	Phe	
		435				440					445				
Leu	Thr	Gly	Leu	Gly	Cys	Pro	Asn	Cys	Ile	Glu	Tyr	Phe	Thr	Ser	Gln
	450					455					460				
Gly	Leu	Gln	Ser	Ile	Tyr	His	Leu	Gln	Asn	Leu	Thr	Ile	Glu	Asp	Leu
465						470					475				480
Gly	Ala	Leu	Lys	Ile	Pro	Glu	Gln	Tyr	Arg	Met	Thr	Ile	Trp	Arg	Gly
				485					490					495	

273/299

Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu
500 505 510

Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu
515 520 525

Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His
530 535 540

Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu
545 550 555 560

Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln
565 570 575

Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His
580 585

<210> 317

<211> 2234

<212> DNA

<213> Homo sapiens

<400> 317

aggggacgca gcgaaaccgg ggcccgcgcc agggcagccg ggacggacgc cgatgcccgg 60
ggctgcgacg gctgcagagc gagctgccct cggaggccgg cgtggggaag atggcccagt 120
ccaccgccac ctcccctgat gggggcacca cgtttgagca cctctggagc tctctggaac 180
cagacagcac ctacttcgac cttccccagt caagccgggg gaataatgag gtggtgggcg 240
gaacggattc cagcatggac gtcttccacc tggagggcag gactacatct gtcatggccc 300
agttcaatct gctgagcagc accatggacc agatgagcag ccgcgcggcc tcggccagcc 360
cctacacccc agagcacgcc gccagcgtgc ccaccactc gccctacgca caaccagct 420
ccaccttcga caccatgtcg ccggcgccctg tcatcccctc caacaccgac taccgccgac 480
cccaccactt tgaggtcact ttccagcagt ccagcacggc caagtcagcc acctggacgt 540
actccccgct cttgaagaaa ctctactgcc agatgcgcaa gacatgcccc atccagatca 600
aggtgtccac cccgccaccc ccaggcactg ccatecgggc catgcctgtt tacaagaaag 660
cggagcacgt gaccgacgtc gtgaaacgct gccccaacca cgagctcggg agggacttca 720
acgaaggaca gtctgctcca gccagccacc tcatccgctg ggaaggcaat aatctctcgc 780
agtatgtgga tgaccctgtc accggcaggc agagcgtcgt ggtgccctat gagccaccac 840
aggtggggac ggaattcacc accatcctgt acaacttcat gtgtaacagc agctgtgtag 900
ggggcatgaa ccggcggccc atcctcatca tcatcaccct ggagatgcgg gatgggcagg 960
tgctggggcg ccggctcctt gagggccgca tctgcgcctg tcctggccgc gaccgaaaag 1020
ctgatgagga ccactaccgg gagcagcagg ccctgaacga gagctccgcc aagaacgggg 1080
ccgccagcaa gcgtgccttc aagcagagcc cccctgccgt ccccgccctt ggtgccgggtg 1140
tgaagaagcg gcggcatgga gacgaggaca cgtactacct tcaggtgcga ggccgggaga 1200
actttgagat cctgatgaag ctgaaagaga gcctggagct gatggagtgt gtgccgcagc 1260
cactggtgga ctctatcgg cagcagcagc agctcctaca gaggccgagt cacctacagc 1320
ccccgtccta cgggcgggtc ctctcgccca tgaacaaggc gcacgggggc atgaacaagc 1380
tgccctccgt caaccagctg gtgggcccagc ctcccccgca cagttcggca gctacaccca 1440
acctggggcc cgtggggccc gggatgctca acaaccatgg ccacgcagtg ccagccaacg 1500
gcgagatgag cagcagccac agcgcgccagt ccattggtctc ggggtcccac tgactccgc 1560
caccccccta ccacgcgcag cccagcctcg tcagtttttt aacaggattg ggggtgtccaa 1620
actgcacgca gtatttcacc tcccaagggt tacagagcat ttaccacctg cagaacctga 1680
ccattgagga cctggggggc ctgaagatcc ccgagcagta ccgcatgacc atctggcggg 1740
gcctgcagga cctgaagcag ggccacgact acagcaccgc gcagcagctg ctccgctcta 1800
gcaacgcggc caccatctcc atcggcggtc agggggaact gcagcgccag cgggtcatgg 1860
aggcgtgca cttccgcgtg cgccacacca tcaccatccc caaccgcggc ggcccaggcg 1920

274/299

```

gcggccctga cgagtgggcg gacttcgggt tcgacctgcc cgactgcaag gcccgcaagc 1980
agcccatcaa ggaggagttc acggaggccg agatccactg agggcctcgc ctggctgcag 2040
cctgcgccac cgcccagaga cccaagctgc ctcccctctc cttcctgtgt gtccaaaact 2100
gcctcaggag gcaggacctt cgggctgtgc ccggggaaag gcaaggtcgc gcccatcccc 2160
aggcacctca caggccccag gaaaggccca gccaccgaag ccgcctgtgg acagcctgag 2220
tcacctgcag aacc                                     2234

```

<210> 318

<211> 732

<212> PRT

<213> Homo sapiens

<400> 318

```

Met Pro Glu Glu Thr Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu
  1                      5                      10                      15

Val Glu Thr Phe Ala Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu
                20                      25                      30

Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu
                35                      40                      45

Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Thr Leu
                50                      55                      60

Thr Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu
  65                      70                      75                      80

Ile Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile
                85                      90                      95

Gly Met Thr Lys Ala Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys
                100                      105                      110

Ser Gly Thr Lys Ala Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile
                115                      120                      125

Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val
                130                      135                      140

Ala Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr
                145                      150                      155                      160

Ala Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr
                165                      170                      175

Gly Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu
                180                      185                      190

Asp Gln Thr Glu Tyr Leu Glu Glu Arg Arg Ile Lys Glu Ile Val Lys
                195                      200                      205

Lys His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys
                210                      215                      220

Glu Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp
                225                      230                      235                      240

```

275/299

Lys Glu Glu Glu Lys Glu Lys Glu Glu Lys Glu Ser Glu Asp Lys Pro
 245 250 255
 Glu Ile Glu Asp Val Gly Ser Asp Glu Glu Glu Glu Lys Lys Asp Gly
 260 265 270
 Asp Lys Lys Lys Lys Lys Lys Ile Lys Glu Lys Tyr Ile Asp Gln Glu
 275 280 285
 Glu Leu Asn Lys Thr Lys Pro Ile Trp Thr Arg Asn Pro Asp Asp Ile
 290 295 300
 Thr Asn Glu Glu Tyr Gly Glu Phe Tyr Lys Ser Leu Thr Asn Asp Trp
 305 310 315 320
 Glu Asp His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu Glu
 325 330 335
 Phe Arg Ala Leu Leu Phe Val Pro Arg Arg Ala Pro Phe Asp Leu Phe
 340 345 350
 Glu Asn Arg Lys Lys Lys Asn Asn Ile Lys Leu Tyr Val Arg Arg Val
 355 360 365
 Phe Ile Met Asp Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Asn Phe
 370 375 380
 Ile Arg Gly Val Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser Arg
 385 390 395 400
 Glu Met Leu Gln Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn Leu
 405 410 415
 Val Lys Lys Cys Leu Glu Leu Phe Thr Glu Leu Ala Glu Asp Lys Glu
 420 425 430
 Asn Tyr Lys Lys Phe Tyr Glu Gln Phe Ser Lys Asn Ile Lys Leu Gly
 435 440 445
 Ile His Glu Asp Ser Gln Asn Arg Lys Lys Leu Ser Glu Leu Leu Arg
 450 455 460
 Tyr Tyr Thr Ser Ala Ser Gly Asp Glu Met Val Ser Leu Lys Asp Tyr
 465 470 475 480
 Cys Thr Arg Met Lys Glu Asn Gln Lys His Ile Tyr Tyr Ile Thr Gly
 485 490 495
 Glu Thr Lys Asp Gln Val Ala Asn Ser Ala Phe Val Glu Arg Leu Arg
 500 505 510
 Lys His Gly Leu Glu Val Ile Tyr Met Ile Glu Pro Ile Asp Glu Tyr
 515 520 525
 Cys Val Gln Gln Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Ser Val
 530 535 540

276/299

Thr Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Glu Lys Lys Lys
 545 550 555 560
 Gln Glu Glu Lys Lys Thr Lys Phe Glu Asn Leu Cys Lys Ile Met Lys
 565 570 575
 Asp Ile Leu Glu Lys Lys Val Glu Lys Val Val Val Ser Asn Arg Leu
 580 585 590
 Val Thr Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala
 595 600 605
 Asn Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr
 610 615 620
 Met Gly Tyr Met Ala Ala Lys Lys His Leu Glu Ile Asn Pro Asp His
 625 630 635 640
 Ser Ile Ile Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp
 645 650 655
 Lys Ser Val Lys Asp Leu Val Ile Leu Leu Tyr Glu Thr Ala Leu Leu
 660 665 670
 Ser Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg Ile
 675 680 685
 Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro Thr
 690 695 700
 Ala Asp Asp Thr Ser Ala Ala Val Thr Glu Glu Met Pro Pro Leu Glu
 705 710 715 720
 Gly Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp
 725 730

<210> 319

<211> 249

<212> PRT

<213> Homo sapiens

<400> 319

Met Lys Glu Thr Gln Lys Ser Thr Tyr Tyr Ile Thr Gly Glu Ser Lys
 1 5 10 15
 Glu Gln Val Ala Asn Ser Ala Phe Val Glu Arg Val Arg Lys Gln Gly
 20 25 30
 Phe Glu Val Val Tyr Met Thr Glu Pro Ile Asp Glu Tyr Cys Val Gln
 35 40 45
 Gln Leu Lys Glu Phe Asp Gly Lys Ser Leu Val Ser Val Thr Lys Glu
 50 55 60
 Gly Leu Glu Leu Pro Glu Asp Glu Glu Glu Lys Lys Lys Met Glu Glu
 65 70 75 80

277/299

Ser Lys Glu Lys Phe Glu Asn Leu Cys Lys Leu Met Lys Glu Ile Leu
85 90 95

Asp Lys Lys Val Glu Lys Val Thr Ile Ser Asn Arg Leu Val Ser Ser
100 105 110

Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala Asn Met Glu
115 120 125

Gln Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr Met Gly Tyr
130 135 140

Met Met Ala Lys Lys His Leu Glu Ile Asn Pro Asp His Pro Ile Met
145 150 155 160

Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp Lys Ala Val
165 170 175

Lys Asp Leu Val Val Leu Leu Phe Glu Thr Ala Leu Leu Ser Ser Gly
180 185 190

Phe Ser Leu Glu Asp Pro Gln Thr His Ser Asn His Ile Tyr His Met
195 200 205

Ile Lys Leu Gly Leu Gly Thr Asp Glu Asp Glu Val Ala Ala Glu Glu
210 215 220

Pro Ser Asp Ala Val Pro Asp Glu Ile Pro Pro Leu Glu Gly Asp Glu
225 230 235 240

Asp Ala Ser Arg Met Glu Glu Val Asp
245

<210> 320

<211> 1313

<212> DNA

<213> Homo sapiens

<400> 320

tggtgtggtt gactctgagg atctgccctt gaacatctgc cgagagatgc tccagcagag 60
caaaatcttg aaagtcattc gcaaaaacat tgtaagaag tgccttgagc tcttctctga 120
gctggcagaa gacaaggaga ttataagaaa ttctatgagg cattttctaa aaatctcaag 180
cttggaatcc acgaagactc cactaaccgc caccgcctgt ctgagctgct gcgctgtcac 240
acctcccagt ctggagatga gatgacatct ctgtcgtagt atgtttctca catgaaggag 300
acacagaagt ccacctatta catcactggt gagagcaaag agcagggtggc caactctgct 360
tttgtggagc gagtgcggaa acagggttc gaggtggtat atatgactga gccattgac 420
gagtactgtg tgcagcagct caaggagttt gatgggaaaa gcctggtctc agttaccaag 480
gagggtctgg agctacctga ggatgaggag gagaagaaga agatggaaga aagcaaggaa 540
aagtttgaga acctctgcaa gctcatgaaa gaaatcttag ataagaaggt tgagaagggtg 600
acaatctcca atagacttgt gtcttcaccc tgctgcattg tgaccagcac ctacggctgg 660
acagccaata tggagcagat catgaaagcc caggcacttc gggacaactc caccatgggc 720
tatatgatgg ccaaaaagca cctggagatc aaccccgacc accccatcat ggagacgctg 780
cggcagaagg ctgaggccga caagaatgat aaggcagtta aggacctggt ggtgctgctg 840
tttgaaaccg ccctgctatc ttctggcttt tcccttgagg atccccagac ccactccaac 900
cacatctacc acatgatcaa gctaggtcta ggtactgatg aagatgaagt ggcagcagag 960
gaacccagtg atgcagttcc tgatgagatc cccctcttg aggtgatga ggatgcgtct 1020
cgcatggaag aagtcgatta ggagttcata gttggaaaac ttgtgccctt gtatagtgtc 1080

278/299

```

cccatggctc ccactgcagc ctcgagtgcc cctgtccac ctggctgctg gtgtctagtg 1140
tttttttccc tctcctgtcc ttgtgttgaa ggcaggaaac caagggtgtc aagccccatt 1200
ccctctctac tcttgacagc aggattggat gttgtgtatt gtggtttatt ttattttctt 1260
cattttgttc tgaaattaaa gaatgtaaaa taaagaatat gccgttttta tac 1313

```

<210> 321

<211> 724

<212> PRT

<213> Mus musculus

<400> 321

```

Met Pro Glu Glu Val His His Gly Glu Glu Glu Val Glu Thr Phe Ala
  1              5              10              15

Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe
      20              25              30

Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser
      35              40              45

Asp Ala Leu Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Ser Lys
      50              55              60

Leu Asp Ser Gly Lys Glu Leu Lys Ile Asp Ile Leu Pro Asn Pro Gln
      65              70              75              80

Glu Arg Thr Leu Thr Leu Val Asp Thr Gly Ile Gly Met Thr Lys Ala
      85              90              95

Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Lys Ala
      100             105             110

Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile Ser Met Ile Gly Gln
      115             120             125

Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val Ala Glu Lys Val Val
      130             135             140

Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr Ala Trp Glu Ser Ser
      145             150             155             160

Ala Gly Gly Ser Phe Thr Val Arg Ala Asp His Gly Glu Pro Ile Gly
      165             170             175

Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu Asp Gln Thr Glu Tyr
      180             185             190

Leu Glu Glu Arg Arg Val Lys Glu Val Val Lys Lys His Ser Gln Phe
      195             200             205

Ile Gly Tyr Pro Ile Thr Leu Tyr Leu Glu Lys Glu Arg Glu Lys Glu
      210             215             220

Ile Ser Asp Asp Glu Ala Glu Glu Glu Lys Gly Glu Lys Glu Glu Glu
      225             230             235             240

Asp Lys Glu Asp Glu Glu Lys Pro Lys Ile Glu Asp Val Gly Ser Asp

```

245

255

Glu	Glu	Asp	Asp	Ser	Gly	Lys	Asp	Lys	Lys	Lys	Lys	Thr	Lys	Lys	Ile	
			260				265						270			
Lys	Glu	Lys	Tyr	Ile	Asp	Gln	Glu	Glu	Leu	Asn	Lys	Thr	Lys	Pro	Ile	
			275				280						285			
Trp	Thr	Arg	Asn	Pro	Asp	Asp	Ile	Thr	Gln	Glu	Glu	Tyr	Gly	Glu	Phe	
			290				295						300			
Tyr	Lys	Ser	Leu	Thr	Asn	Asp	Trp	Glu	Asp	His	Leu	Ala	Val	Lys	His	
			305				310						315			
Phe	Ser	Val	Glu	Gly	Gln	Leu	Glu	Phe	Arg	Ala	Phe	Leu	Phe	Ile	Pro	
			325						330						335	
Arg	Arg	Ala	Pro	Phe	Asp	Leu	Phe	Glu	Asn	Lys	Lys	Lys	Lys	Asn	Asn	
			340						345						350	
Ile	Lys	Leu	Tyr	Val	Arg	Arg	Val	Phe	Ile	Met	Asp	Ser	Cys	Asp	Glu	
			355						360						365	
Leu	Ile	Pro	Glu	Tyr	Leu	Asn	Phe	Ile	Arg	Gly	Val	Val	Asp	Ser	Glu	
			370						375						380	
Asp	Leu	Pro	Leu	Asn	Ile	Ser	Arg	Glu	Met	Leu	Gln	Gln	Ser	Lys	Ile	
			385						390						395	400
Leu	Lys	Val	Ile	Arg	Lys	Asn	Ile	Val	Lys	Lys	Cys	Leu	Glu	Leu	Phe	
			405						410						415	
Ser	Glu	Leu	Ala	Glu	Asp	Lys	Glu	Asn	Tyr	Lys	Lys	Phe	Tyr	Glu	Ala	
			420						425						430	
Phe	Ser	Lys	Asn	Leu	Lys	Leu	Gly	Ile	His	Glu	Asp	Ser	Thr	Asn	Arg	
			435						440						445	
Arg	Arg	Leu	Ser	Glu	Leu	Leu	Arg	Tyr	His	Thr	Ser	Gln	Ser	Gly	Asp	
			450						455						460	
Glu	Met	Thr	Ser	Leu	Ser	Glu	Tyr	Val	Ser	Arg	Met	Lys	Glu	Thr	Gln	
			465						470						475	480
Lys	Ser	Ile	Tyr	Tyr	Ile	Thr	Gly	Glu	Ser	Lys	Glu	Gln	Val	Ala	Asn	
			485						490						495	
Pro	Ala	Phe	Val	Glu	Arg	Val	Arg	Lys	Arg	Gly	Phe	Glu	Val	Val	Tyr	
			500						505						510	
Met	Thr	Glu	Pro	Ile	Asp	Glu	Tyr	Cys	Val	Gln	Gln	Leu	Lys	Glu	Phe	
			515						520						525	
Asp	Gly	Lys	Ser	Leu	Val	Ser	Val	Thr	Lys	Glu	Gly	Leu	Glu	Leu	Pro	
			530						535						540	
Glu	Asp	Glu	Glu	Glu	Lys	Lys	Lys	Met	Glu	Glu	Ser	Lys	Ala	Lys	Phe	
			545						550						555	560

280/299

Glu Asn Leu Cys Lys Leu Met Lys Glu Ile Leu Asp Lys Lys Val Glu
 565 570 575
 Lys Val Thr Ile Ser Asn Arg Leu Val Ser Ser Pro Cys Cys Ile Val
 580 585 590
 Thr Ser Thr Tyr Gly Trp Thr Ala Asn Met Glu Arg Ile Met Lys Ala
 595 600 605
 Gln Ala Leu Arg Asp Asn Ser Thr Met Gly Tyr Met Met Ala Lys Lys
 610 615 620
 His Leu Glu Ile Asn Pro Asp His Pro Ile Val Glu Thr Leu Arg Gln
 625 630 635 640
 Lys Ala Glu Ala Asp Lys Asn Asp Lys Ala Val Lys Asp Leu Val Val
 645 650 655
 Leu Leu Phe Glu Thr Ala Leu Leu Ser Ser Gly Phe Ser Leu Glu Asp
 660 665 670
 Pro Gln Thr His Ser Asn Arg Ile Tyr Arg Met Ile Lys Leu Gly Leu
 675 680 685
 Gly Ile Asp Glu Asp Glu Val Thr Ala Glu Glu Pro Ser Ala Ala Val
 690 695 700
 Pro Asp Glu Ile Pro Pro Leu Glu Gly Asp Glu Asp Ala Ser Arg Met
 705 710 715 720
 Glu Glu Val Asp

<210> 322
 <211> 724
 <212> PRT
 <213> Rattus sp.

<400> 322
 Met Pro Glu Glu Val His His Gly Glu Glu Glu Val Glu Thr Phe Ala
 1 5 10 15
 Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe
 20 25 30
 Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser
 35 40 45
 Asp Ala Leu Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Ser Lys
 50 55 60
 Leu Asp Ser Gly Lys Glu Leu Lys Ile Asp Ile Ile Pro Asn Pro Gln
 65 70 75 80
 Glu Ala Thr Leu Thr Leu Val Asp Thr Gly Ile Gly Met Thr Lys Ala
 85 90 95

281/299

Asp	Leu	Ile	Asn	Asn	Leu	Gly	Thr	Ile	Ala	Lys	Ser	Gly	Thr	Lys	Ala	100	105	110
Phe	Met	Glu	Ala	Leu	Gln	Ala	Gly	Ala	Asp	Ile	Ser	Met	Ile	Gly	Gln	115	120	125
Phe	Gly	Val	Gly	Phe	Tyr	Ser	Ala	Tyr	Leu	Val	Ala	Glu	Lys	Val	Val	130	135	140
Val	Ile	Thr	Lys	His	Asn	Asp	Asp	Glu	Gln	Tyr	Ala	Trp	Glu	Ser	Ser	145	150	155
Ala	Gly	Gly	Ser	Phe	Thr	Val	Arg	Ala	Asp	His	Gly	Glu	Pro	Ile	Gly	165	170	175
Arg	Gly	Thr	Lys	Val	Ile	Leu	His	Leu	Lys	Glu	Asp	Gln	Thr	Glu	Tyr	180	185	190
Leu	Glu	Glu	Arg	Arg	Val	Lys	Glu	Val	Val	Lys	Lys	His	Ser	Gln	Phe	195	200	205
Ile	Gly	Tyr	Pro	Ile	Thr	Leu	Tyr	Leu	Glu	Lys	Glu	Arg	Glu	Lys	Glu	210	215	220
Ile	Ser	Asp	Asp	Glu	Ala	Glu	Glu	Glu	Lys	Gly	Glu	Lys	Glu	Glu	Glu	225	230	235
Asp	Lys	Glu	Asp	Glu	Glu	Lys	Pro	Lys	Ile	Glu	Asp	Val	Gly	Ser	Asp	245	250	255
Glu	Glu	Asp	Asp	Ser	Gly	Lys	Asp	Lys	Lys	Lys	Lys	Thr	Lys	Lys	Ile	260	265	270
Lys	Glu	Lys	Tyr	Ile	Asp	Gln	Glu	Glu	Leu	Asn	Lys	Thr	Lys	Pro	Ile	275	280	285
Trp	Thr	Arg	Asn	Pro	Asp	Asp	Ile	Thr	Gln	Glu	Glu	Tyr	Gly	Glu	Phe	290	295	300
Tyr	Lys	Ser	Leu	Thr	Asn	Asp	Trp	Glu	Asp	His	Leu	Ala	Val	Lys	His	305	310	315
Phe	Ser	Val	Glu	Gly	Gln	Leu	Glu	Phe	Arg	Ala	Leu	Leu	Phe	Ile	Pro	325	330	335
Arg	Arg	Ala	Pro	Phe	Asp	Leu	Phe	Glu	Asn	Lys	Lys	Lys	Lys	Asn	Asn	340	345	350
Ile	Lys	Leu	Tyr	Val	Arg	Arg	Val	Phe	Ile	Met	Asp	Ser	Cys	Asp	Asp	355	360	365
Leu	Ile	Pro	Glu	Tyr	Leu	Asn	Phe	Ile	Arg	Gly	Val	Val	Asp	Ser	Glu	370	375	380
Asp	Leu	Pro	Leu	Asn	Ile	Ser	Arg	Glu	Met	Leu	Gln	Gln	Ser	Lys	Ile	385	390	395
Leu	Lys	Val	Ile	Arg	Lys	Asn	Ile	Val	Lys	Lys	Cys	Leu	Glu	Leu	Phe			

282/299

405	410	415
Ser Glu Leu Ala Glu Asp Lys Glu Asn Tyr Lys Lys Phe Tyr Glu Ala		
420	425	430
Phe Ser Lys Asn Leu Lys Leu Gly Ile His Glu Asp Ser Thr Asn Arg		
435	440	445
Arg Arg Leu Ser Glu Leu Leu Arg Tyr His Thr Ser Gln Ser Gly Asp		
450	455	460
Glu Met Thr Ser Leu Ser Glu Tyr Val Ser Arg Met Lys Glu Thr Gln		
465	470	480
Lys Ser Ile Tyr Tyr Ile Thr Gly Glu Ser Lys Glu Gln Val Ala Asn		
485	490	495
Ser Ala Phe Val Glu Arg Val Arg Lys Arg Gly Phe Glu Val Val Tyr		
500	505	510
Met Thr Glu Pro Ile Asp Glu Tyr Cys Val Gln Gln Leu Lys Glu Phe		
515	520	525
Asp Gly Lys Ser Leu Val Ser Val Thr Lys Glu Gly Leu Glu Leu Pro		
530	535	540
Glu Asp Glu Glu Glu Lys Lys Lys Met Glu Glu Ser Lys Ala Arg Phe		
545	550	560
Glu Asn Leu Cys Lys Leu Met Lys Glu Ile Leu Asp Lys Lys Val Glu		
565	570	575
Lys Val Thr Ile Ser Asn Arg Leu Val Ser Ser Pro Cys Cys Ile Val		
580	585	590
Thr Ser Thr Tyr Gly Trp Thr Ala Asn Met Glu Arg Ile Met Lys Ala		
595	600	605
Gln Ala Leu Arg Asp Asn Ser Thr Met Gly Tyr Met Met Ala Lys Lys		
610	615	620
His Leu Glu Ile Asn Pro Asp His Pro Ile Val Glu Thr Leu Arg Gln		
625	630	635
Lys Ala Glu Ala Asp Lys Asn Asp Lys Ala Val Lys Asp Leu Val Val		
645	650	655
Leu Leu Phe Glu Thr Ala Leu Ser Ser Leu Ala Ser His Phe Arg Arg		
660	665	670
Pro Lys Thr His Ser Asn Arg Ile Tyr Arg Met Ile Lys Leu Gly Leu		
675	680	685
Gly Ile Asp Glu Asp Glu Val Thr Ala Glu Glu Pro Ser Ala Ala Val		
690	695	700
Pro Asp Glu Ile Pro Pro Leu Glu Gly Asp Glu Asp Ala Ser Arg Met		
705	710	715
		720

283/299

Glu Glu Val Asp

<210> 323

<211> 733

<212> PRT

<213> *Cricetulus griseus*

<400> 323

```

Met Pro Glu Glu Thr Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu
  1              5              10              15

Val Glu Thr Phe Ala Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu
      20              25              30

Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu
      35              40              45

Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Ser Leu
      50              55              60

Thr Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Ile
      65              70              75              80

Ile Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile
      85              90              95

Gly Met Thr Lys Ala Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys
      100             105             110

Ser Gly Thr Lys Ala Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile
      115             120             125

Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Thr Ala Tyr Leu Val
      130             135             140

Ala Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr
      145             150             155             160

Ala Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr
      165             170             175

Gly Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu
      180             185             190

Asp Gln Thr Glu Tyr Met Glu Glu Arg Arg Ile Lys Glu Ile Val Lys
      195             200             205

Lys His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys
      210             215             220

Glu Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp
      225             230             235             240

Lys Glu Glu Glu Lys Glu Lys Glu Glu Lys Gly Ile Asp Asp Lys Pro
      245             250             255

```

284/299

Glu Ile Glu Asp Val Gly Ser Asp Glu Glu Glu Glu Glu Lys Lys Asp
 260 265 270
 Gly Asp Lys Lys Lys Lys Lys Lys Ile Lys Glu Lys Tyr Ile Asp Gln
 275 280 285
 Glu Glu Leu Asn Lys Thr Lys Pro Ile Trp Thr Arg Asn Pro Asp Asp
 290 295 300
 Ile Thr Asn Glu Glu Tyr Gly Glu Phe Tyr Lys Ser Leu Thr Asn Asp
 305 310 315 320
 Trp Glu Glu His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu
 325 330 335
 Glu Phe Arg Ala Leu Leu Phe Val Pro Arg Arg Ala Pro Phe Asp Leu
 340 345 350
 Phe Glu Asn Arg Lys Lys Lys Asn Asn Ile Lys Leu Tyr Val Arg Arg
 355 360 365
 Val Phe Ile Met Asp Asn Cys Glu Glu Leu Phe Pro Glu Tyr Leu Asn
 370 375 380
 Phe Ile Arg Gly Val Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser
 385 390 395 400
 Arg Glu Ile Leu Gln Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn
 405 410 415
 Leu Val Arg Lys Cys Leu Glu Leu Phe His Glu Leu Ala Glu Asp Lys
 420 425 430
 Glu Asn Tyr Lys Lys Phe Tyr Glu Gln Phe Ser Lys Asn Ile Lys Leu
 435 440 445
 Gly Ile His Glu Asp Ser Gln Asn Arg Lys Lys Leu Ser Glu Leu Leu
 450 455 460
 Arg Tyr Tyr Thr Ser Ala Ser Gly Asp Glu Met Val Ser Leu Lys Asp
 465 470 475 480
 Tyr Cys Thr Arg Met Lys Glu Asn Gln Lys His Ile Tyr Phe Ile Thr
 485 490 495
 Gly Glu Thr Lys Asp Gln Val Ala Asn Ser Ala Phe Val Glu Arg Leu
 500 505 510
 Arg Lys His Gly Leu Glu Val Ile Tyr Met Ile Glu Pro Ile Asp Glu
 515 520 525
 Tyr Cys Val Gln Gln Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Ser
 530 535 540
 Val Thr Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Glu Lys Lys
 545 550 555 560
 Lys Gln Glu Glu Lys Lys Thr Lys Phe Glu Asn Leu Cys Lys Ile Met

285/299

565	570	575
Lys Asp Ile Leu Glu Lys Lys Val Glu Lys Val Val Val Ser Asn Arg		
580	585	590
Leu Val Thr Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr		
595	600	605
Ala Asn Met Glu Arg Ile Ile Lys Ala Gln Ala Leu Arg Asp Asn Ser		
610	615	620
Thr Met Gly Tyr Met Ala Ala Lys Lys His Leu Glu Ile Asn Pro Asp		
625	630	635
His Ser Ile Ile Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn		
645	650	655
Asp Lys Ser Val Lys Asp Leu Val Ile Leu Leu Tyr Glu Thr Ala Leu		
660	665	670
Leu Ser Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg		
675	680	685
Ile Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro		
690	695	700
Thr Val Asp Asp Thr Ser Ala Ala Val Thr Glu Glu Met Pro Pro Leu		
705	710	715
Glu Gly Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp		
725	730	

<210> 324

<211> 725

<212> PRT

<213> Gallus gallus

<400> 324

Met Pro Glu Gln Val Gln His Gly Glu Asp Glu Val Glu Thr Phe Ala
1 5 10 15
Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe
20 25 30
Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser
35 40 45
Asp Ala Leu Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Ser Lys
50 55 60
Leu Asp Thr Gly Lys Asp Leu Lys Ile Asp Ile Val Pro Asn Pro Arg
65 70 75 80
Asp Pro Thr Leu Thr Leu Leu Asp Thr Gly Ile Gly Met Thr Lys Ala
85 90 95
Asp Leu Val Asn Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Lys Ala

286/299

100	105	110
Phe Met Glu Ala Leu Gln Ala Gly	Ala Asp Ile Ser Met	Ile Gly Gln
115	120	125
Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val Ala Glu Lys Val Val		
130	135	140
Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr Ala Trp Glu Ser Ser		
145	150	155
Ala Gly Gly Ser Phe Thr Val Arg Thr Asp His Gly Glu Pro Ile Gly		
165	170	175
Arg Gly Thr Lys Val Ile Leu Tyr Leu Lys Glu Asp Gln Thr Glu Tyr		
180	185	190
Leu Glu Glu Arg Arg Val Lys Glu Val Val Lys Lys His Ser Gln Phe		
195	200	205
Ile Gly Tyr Pro Ile Thr Leu Tyr Val Glu Lys Glu Arg Glu Lys Glu		
210	215	220
Val Ser Asp Asp Glu Ala Glu Glu Glu Lys Val Glu Lys Glu Glu Glu		
225	230	235
Glu Ser Lys Asp Glu Glu Lys Pro Lys Ile Glu Asp Val Gly Ser Asp		
245	250	255
Glu Glu Glu Glu Glu Gly Glu Lys Ser Lys Lys Lys Lys Thr Lys Lys		
260	265	270
Ile Lys Glu Lys Tyr Ile Asp Gln Glu Glu Leu Asn Lys Thr Lys Pro		
275	280	285
Ile Trp Thr Arg Asn Pro Asp Asp Ile Thr Gln Glu Glu Tyr Gly Glu		
290	295	300
Phe Tyr Lys Ser Leu Thr Asn Asp Trp Glu Asp His Leu Ala Val Lys		
305	310	315
His Phe Ser Val Glu Gly Gln Leu Glu Phe Arg Ala Leu Leu Phe Ile		
325	330	335
Pro Arg Arg Ala Pro Phe Asp Leu Phe Glu Asn Lys Lys Lys Lys Asn		
340	345	350
Asn Ile Lys Leu Tyr Val Arg Arg Val Phe Ile Met Asp Ser Cys Asp		
355	360	365
Glu Leu Ile Pro Glu Tyr Leu Asn Phe Ile Arg Gly Val Val Asp Ser		
370	375	380
Glu Asp Leu Pro Leu Asn Ile Ser Arg Glu Met Leu Gln Gln Ser Lys		
385	390	395
Ile Leu Lys Val Ile Arg Lys Asn Ile Val Lys Lys Cys Leu Glu Leu		
405	410	415

287/299

Phe Thr Glu Leu Ala Glu Asp Lys Glu Asn Tyr Lys Lys Phe Tyr Glu	420	425	430
Ala Phe Ser Lys Asn Leu Lys Leu Gly Ile His Glu Asp Ser Thr Asn	435	440	445
Arg Lys Arg Leu Ser Glu Leu Leu Arg Tyr His Thr Ser Gln Ser Gly	450	455	460
Asp Glu Met Thr Ser Leu Ser Glu Tyr Val Ser Arg Met Lys Glu Ser	465	470	475
Gln Lys Ser Ile Tyr Tyr Ile Thr Gly Glu Ser Lys Glu Gln Val Ala	485	490	495
Asn Ser Ala Phe Val Glu Arg Val Arg Lys Arg Gly Phe Glu Val Val	500	505	510
Tyr Met Thr Glu Pro Ile Asp Glu Tyr Cys Val Gln Gln Leu Lys Glu	515	520	525
Phe Asp Gly Lys Thr Leu Val Ser Val Thr Lys Glu Gly Leu Glu Leu	530	535	540
Pro Glu Asp Glu Glu Glu Lys Lys Asn Met Glu Glu Ser Lys Ala Lys	545	550	555
Phe Glu Thr Leu Cys Lys Leu Met Lys Glu Ile Leu Asp Lys Lys Val	565	570	575
Glu Lys Val Thr Ile Ser Asn Arg Leu Val Ser Ser Pro Cys Cys Ile	580	585	590
Val Thr Ser Thr Tyr Gly Trp Thr Ala Asn Met Glu Arg Ile Met Lys	595	600	605
Ala Gln Ala Leu Arg Asp Asn Ser Thr Met Gly Tyr Met Met Ala Lys	610	615	620
Lys His Leu Glu Ile Asn Pro Asp His Pro Ile Val Glu Thr Leu Arg	625	630	635
Gln Lys Ala Asp Ala Asn Lys Asn Asp Lys Ala Val Lys Asp Leu Val	645	650	655
Val Leu Leu Phe Glu Thr Ala Leu Leu Ser Ser Gly Phe Ser Leu Glu	660	665	670
Asp Pro Gln Thr His Ser Asn Arg Ile Tyr Arg Met Ile Lys Leu Gly	675	680	685
Leu Gly Ile Asp Glu Asp Glu Val Ile Ala Glu Glu Ser Ser Ile Ala	690	695	700
Pro Pro Asp Glu Ile Pro Pro Leu Glu Gly Asp Glu Asp Thr Ser Arg	705	710	715
			720

288/299

Met Glu Glu Val Asp
725

<210> 325

<211> 233

<212> PRT

<213> *Sarcophaga crassipalpis*

<400> 325

Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val Ala Asp Lys Val Thr
1 5 10 15

Val Thr Ser Lys His Asn Asp Asp Glu Gln Tyr Ile Trp Glu Ser Ser
20 25 30

Ala Gly Gly Ser Phe Thr Val Lys Pro Asp Ser Ser Glu Pro Leu Gly
35 40 45

Arg Gly Thr Lys Ile Val Leu Tyr Ile Lys Glu Asp Gln Thr Glu Tyr
50 55 60

Leu Glu Glu Ser Lys Ile Lys Glu Ile Val Asn Lys His Ser Gln Phe
65 70 75 80

Ile Gly Tyr Pro Ile Lys Leu Leu Val Gln Lys Glu Arg Asp Gln Glu
85 90 95

Val Ser Asp Asp Glu Ala Glu Glu Glu Lys Lys Glu Met Asp Thr Asp
100 105 110

Glu Pro Lys Ile Glu Asp Val Gly Glu Asp Glu Asp Ala Asp Lys Lys
115 120 125

Asp Lys Asp Gly Lys Lys Lys Lys Thr Ile Lys Val Ala Tyr Thr Glu
130 135 140

Asp Glu Glu Leu Asn Lys Thr Lys Pro Ile Trp Thr Arg Asn Pro Asp
145 150 155 160

Asp Ile Thr Gln Ala Glu Tyr Gly Asp Phe Tyr Lys Ser Leu Thr Asn
165 170 175

Asp Trp Glu Asp His Leu Ala Val Lys His Phe Pro Leu Lys Gly Gln
180 185 190

Leu Glu Phe Arg Ala Leu Leu Phe Ile Pro Arg Arg Thr Pro Phe Asp
195 200 205

Leu Phe Glu Asn Gln Lys Lys Arg Asn Asn Ile Lys Leu Tyr Val Pro
210 215 220

Arg Val Phe Ile Met Asp Asn Cys Glu
225 230

<210> 326

<211> 724

289/299

<212> PRT

<213> Danio rerio

<400> 326

```

Met Pro Glu Glu Met Arg Gln Glu Glu Glu Ala Glu Thr Phe Ala Phe
  1             5             10             15

Gln Ala Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe Tyr
      20             25             30

Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Val Ser Asn Ala Ser Asp
      35             40             45

Ala Leu Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Thr Lys Leu
      50             55             60

Asp Ser Gly Lys Asp Leu Lys Ile Asp Ile Ile Pro Asn Val Gln Glu
      65             70             75             80

Arg Thr Leu Thr Leu Ile Asp Thr Gly Ile Gly Met Thr Lys Ala Asp
      85             90             95

Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Lys Ala Phe
      100            105            110

Met Glu Ala Leu Gln Ala Gly Ala Asp Ile Ser Met Ile Gly Gln Phe
      115            120            125

Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val Ala Glu Lys Val Thr Val
      130            135            140

Ile Thr Lys His Asn Asp Asp Glu Gln Tyr Ala Trp Glu Ser Ser Ala
      145            150            155            160

Gly Gly Ser Phe Thr Val Lys Val Asp His Gly Glu Pro Ile Gly Arg
      165            170            175

Gly Thr Lys Val Ile Leu His Leu Lys Glu Asp Gln Thr Glu Tyr Ile
      180            185            190

Glu Glu Lys Arg Val Lys Glu Val Val Lys Lys His Ser Gln Phe Ile
      195            200            205

Gly Tyr Pro Ile Thr Leu Tyr Val Glu Lys Glu Arg Asp Lys Glu Ile
      210            215            220

Ser Asp Asp Glu Ala Glu Glu Glu Lys Ala Glu Lys Glu Glu Lys Glu
      225            230            235            240

Glu Glu Gly Glu Asp Lys Pro Lys Ile Glu Asp Val Gly Ser Asp Asp
      245            250            255

Glu Glu Asp Thr Lys Asp Lys Asp Lys Lys Lys Lys Lys Lys Ile Lys
      260            265            270

Glu Lys Tyr Ile Asp Gln Glu Glu Leu Asn Lys Thr Lys Pro Ile Trp
      275            280            285

```


290/299

Thr Arg Asn Pro Asp Asp Ile Ser Asn Glu Glu Tyr Gly Glu Phe Tyr
 290 295 300
 Lys Ser Leu Thr Asn Asp Trp Glu Asp His Leu Ala Val Lys His Phe
 305 310 315 320
 Ser Val Glu Gly Gln Leu Glu Phe Arg Ala Leu Leu Phe Ile Pro Arg
 325 330 335
 Arg Ala Pro Phe Asp Leu Phe Glu Asn Lys Lys Lys Lys Asn Asn Ile
 340 345 350
 Lys Leu Tyr Val Arg Arg Val Phe Ile Met Asp Asn Cys Glu Glu Leu
 355 360 365
 Ile Pro Glu Tyr Leu Asn Phe Ile Arg Gly Val Val Asp Ser Glu Asp
 370 375 380
 Leu Pro Leu Asn Ile Ser Arg Glu Met Leu Gln Gln Ser Lys Ile Leu
 385 390 395 400
 Lys Val Ile Arg Lys Asn Ile Val Lys Lys Cys Leu Glu Leu Phe Ala
 405 410 415
 Asp Val Ala Glu Asp Lys Asp Asn Tyr Lys Lys Phe Tyr Asp Ala Phe
 420 425 430
 Ser Lys Asn Leu Lys Leu Gly Ile His Glu Asp Ser Gln Asn Arg Arg
 435 440 445
 Lys Leu Ser Glu Leu Leu Arg Tyr Gln Ser Ser Gln Ser Gly Tyr Glu
 450 455 460
 Met Thr Ser Leu Thr Glu Tyr Val Ser Arg Met Lys Glu Asn Gln Lys
 465 470 475 480
 Ser Ile Tyr Tyr Ile Thr Gly Glu Ser Lys Asp Gln Val Ala His Ser
 485 490 495
 Ala Phe Val Glu Arg Val Cys Lys Arg Gly Phe Glu Val Leu Tyr Met
 500 505 510
 Thr Glu Pro Ile Asp Glu Tyr Cys Val Gln Gln Leu Lys Asp Phe Asp
 515 520 525
 Gly Lys Ser Leu Val Ser Val Thr Lys Glu Gly Leu Glu Leu Pro Glu
 530 535 540
 Asp Glu Asp Glu Lys Lys Lys Met Glu Glu Asp Lys Ala Lys Phe Glu
 545 550 555 560
 Asn Leu Cys Lys Leu Met Lys Glu Ile Leu Asp Lys Lys Val Glu Lys
 565 570 575
 Val Thr Val Ser Asn Arg Leu Val Ser Ser Pro Cys Cys Ile Val Thr
 580 585 590
 Ser Thr Tyr Gly Trp Thr Ala Asn Met Glu Arg Ile Met Lys Ala Gln

291/299

595 600 605
 Ala Leu Arg Asp Asn Ser Thr Met Gly Tyr Met Met Ala Lys Lys His
 610 615 620
 Leu Glu Ile Asn Pro Asp His Pro Ile Met Glu Thr Leu Arg Gln Lys
 625 630 635 640
 Ala Glu Ala Asp Lys Asn Asp Lys Ala Val Lys Asp Leu Val Ile Leu
 645 650 655
 Leu Phe Glu Thr Ala Leu Leu Ser Ser Gly Phe Ser Leu Asp Asp Pro
 660 665 670
 Gln Thr His Ser Asn Arg Ile Tyr Arg Met Ile Lys Leu Gly Leu Gly
 675 680 685
 Ile Asp Glu Asp Glu Asp Val Pro Val Glu Glu Pro Ser Ser Ala Ala
 690 695 700
 Pro Glu Asp Ile Pro Pro Leu Glu Gly Asp Asp Asp Ala Ser Arg Met
 705 710 715 720
 Glu Glu Val Asp

<210> 327

<211> 722

<212> PRT

<213> Salmo salar

<400> 327

Met Pro Glu Glu Met Arg Gln Glu Glu Glu Ala Glu Thr Phe Ala Phe
 1 5 10 15
 Gln Ala Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe Tyr
 20 25 30
 Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp
 35 40 45
 Ala Leu Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Thr Lys Leu
 50 55 60
 Asp Asn Gly Lys Glu Leu Lys Ile Asp Val Ile Pro Asn Val Glu Glu
 65 70 75 80
 Arg Thr Leu Thr Leu Ile Asp Thr Gly Ile Gly Met Thr Lys Ala Asp
 85 90 95
 Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Lys Ala Phe
 100 105 110
 Met Glu Ala Leu Gln Ala Gly Ala Asp Ile Ser Met Ile Gly Gln Phe
 115 120 125
 Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val Ala Glu Arg Val Thr Val
 130 135 140

292/299

Ile	Thr	Lys	His	Asn	Asp	Asp	Glu	Gln	Tyr	Ile	Trp	Glu	Ser	Ser	Ala	145	150	155	160
Gly	Gly	Ser	Phe	Thr	Val	Lys	Val	Asp	Thr	Gly	Glu	Pro	Met	Leu	Arg	165	170	175	
Gly	Thr	Lys	Val	Ile	Leu	His	Met	Lys	Glu	Asp	Gln	Thr	Glu	Tyr	Val	180	185	190	
Glu	Glu	Lys	Arg	Val	Lys	Glu	Val	Val	Lys	Lys	His	Ser	Gln	Phe	Ile	195	200	205	
Gly	Tyr	Pro	Ile	Thr	Leu	Phe	Val	Glu	Lys	Glu	Arg	Glu	Lys	Glu	Ile	210	215	220	
Ser	Asp	Asp	Glu	Glu	Glu	Lys	Ala	Glu	Glu	Glu	Lys	Glu	Glu	Lys	Glu	225	230	235	240
Ala	Glu	Asp	Lys	Pro	Lys	Ile	Glu	Asp	Val	Gly	Ser	Asp	Asp	Glu	Glu	245	250	255	
Asp	Ser	Lys	Asp	Lys	Asp	Lys	Lys	Lys	Thr	Lys	Lys	Ile	Lys	Glu	Lys	260	265	270	
Tyr	Ile	Asp	Gln	Glu	Glu	Leu	Asn	Lys	Thr	Lys	Pro	Ile	Trp	Thr	Arg	275	280	285	
Asn	Pro	Asp	Asp	Ile	Thr	Met	Glu	Glu	Tyr	Gly	Glu	Phe	Tyr	Lys	Ser	290	295	300	
Leu	Thr	Asn	Asp	Trp	Glu	Glu	His	Leu	Ala	Val	Lys	His	Phe	Ser	Val	305	310	315	320
Glu	Gly	Gln	Leu	Glu	Phe	Arg	Ala	Leu	Leu	Phe	Ile	Pro	Arg	Arg	Ala	325	330	335	
Pro	Phe	Asp	Leu	Phe	Glu	Asn	Lys	Lys	Lys	Lys	Asn	Asn	Ile	Lys	Leu	340	345	350	
Tyr	Val	Arg	Arg	Val	Phe	Ile	Met	Asp	Ser	Cys	Glu	Glu	Leu	Ile	Pro	355	360	365	
Glu	Tyr	Leu	Asn	Phe	Val	Arg	Gly	Val	Val	Asp	Ser	Glu	Asp	Leu	Pro	370	375	380	
Leu	Asn	Ile	Ser	Arg	Glu	Met	Leu	Gln	Gln	Ser	Lys	Ile	Leu	Lys	Val	385	390	395	400
Ile	Arg	Lys	Asn	Ile	Val	Lys	Lys	Cys	Met	Glu	Leu	Phe	Gly	Glu	Leu	405	410	415	
Ala	Glu	Asp	Arg	Glu	Asn	Tyr	Asn	Lys	Phe	Tyr	Asp	Gly	Phe	Ser	Lys	420	425	430	
Asn	Leu	Lys	Leu	Gly	Ile	His	Glu	Asp	Ser	Gln	Asn	Arg	Lys	Lys	Leu	435	440	445	

293/299

Ser Glu Leu Leu Arg Tyr His Ser Ser Gln Ser Gly Asp Glu Leu Thr
 450 455 460
 Ser Leu Thr Glu Tyr Leu Thr Arg Met Lys Asp Asn Gln Lys Ser Ile
 465 470 475 480
 Tyr Tyr Ile Thr Gly Glu Ser Lys Asp Gln Val Ala Asn Ser Ala Phe
 485 490 495
 Val Glu Arg Val Arg Lys Arg Gly Phe Glu Val Leu Tyr Met Thr Glu
 500 505 510
 Pro Ile Asp Glu Tyr Cys Val Gln Gln Leu Lys Glu Phe Asp Gly Lys
 515 520 525
 Thr Leu Val Ser Val Thr Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu
 530 535 540
 Glu Glu Lys Lys Lys Met Asp Glu Asp Lys Thr Lys Phe Glu Asn Leu
 545 550 555 560
 Cys Lys Leu Met Lys Glu Ile Leu Asp Lys Lys Val Glu Lys Val Thr
 565 570 575
 Val Ser Asn Arg Leu Val Ser Ser Pro Cys Cys Ile Val Thr Ser Thr
 580 585 590
 Tyr Gly Trp Thr Ala Asn Met Glu Arg Ile Met Lys Ala Gln Ala Leu
 595 600 605
 Arg Asp Asn Ser Thr Met Gly Tyr Met Met Ala Lys Lys His Leu Glu
 610 615 620
 Ile Asn Pro Asp His Pro Ile Val Glu Thr Leu Arg Gln Lys Ala Asp
 625 630 635 640
 Leu Asp Lys Asn Asp Lys Ala Val Lys Asp Leu Val Ile Leu Leu Phe
 645 650 655
 Glu Thr Ala Leu Leu Ser Ser Gly Phe Ser Leu Asp Asp Pro Gln Thr
 660 665 670
 His Ser Asn Arg Ile Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp
 675 680 685
 Asp Asp Glu Val Ile Pro Glu Glu Pro Thr Ser Ala Pro Ala Pro Asp
 690 695 700
 Glu Ile Pro Pro Leu Glu Gly Asp Asp Asp Ala Ser Arg Met Glu Glu
 705 710 715 720

Val Asp

<210> 328

<211> 733

<212> PRT

<213> Sus scrofa

294/299

<400> 328

```

Met Pro Glu Glu Thr Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu
 1           5           10           15

Val Glu Thr Phe Ala Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu
      20           25           30

Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu
      35           40           45

Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Ser Leu
      50           55           60

Thr Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu
      65           70           75           80

Ile Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile
      85           90           95

Gly Met Thr Lys Ala Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys
      100           105           110

Ser Gly Thr Lys Ala Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile
      115           120           125

Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val
      130           135           140

Ala Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr
      145           150           155           160

Ala Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr
      165           170           175

Gly Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu
      180           185           190

Asp Gln Thr Glu Tyr Leu Glu Glu Arg Arg Ile Lys Glu Ile Val Lys
      195           200           205

Lys His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys
      210           215           220

Glu Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp
      225           230           235           240

Lys Glu Glu Glu Lys Glu Lys Glu Glu Lys Glu Ser Glu Asp Lys Pro
      245           250           255

Glu Ile Glu Asp Val Gly Ser Asp Glu Glu Glu Glu Glu Lys Lys Asp
      260           265           270

Gly Asp Lys Lys Lys Lys Lys Lys Ile Lys Glu Lys Tyr Ile Asp Gln
      275           280           285

Glu Glu Leu Asn Lys Thr Lys Pro Ile Trp Thr Arg Asn Pro Asp Asp
      290           295           300

```

295/299

Ile Thr Asn Glu Glu Tyr Gly Glu Phe Tyr Lys Ser Leu Thr Asn Asp		
305	310	315 320
Trp Glu Asp His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu		
	325	330 335
Glu Phe Arg Ala Leu Leu Phe Val Pro Arg Arg Ala Pro Phe Asp Leu		
	340	345 350
Phe Glu Asn Arg Lys Lys Lys Asn Asn Ile Lys Leu Tyr Val Arg Arg		
	355	360 365
Val Phe Ile Met Asp Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Asn		
	370	375 380
Phe Ile Arg Gly Val Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser		
385	390	395 400
Arg Glu Met Leu Gln Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn		
	405	410 415
Leu Val Lys Lys Cys Leu Glu Leu Phe Thr Glu Leu Ala Glu Asp Lys		
	420	425 430
Glu Asn Tyr Lys Lys Phe Tyr Glu Gln Phe Ser Lys Asn Ile Lys Leu		
	435	440 445
Gly Ile His Glu Asp Ser Gln Asn Arg Lys Lys Leu Ser Glu Leu Leu		
450	455	460
Arg Tyr Tyr Thr Ser Ala Ser Gly Asp Glu Met Val Ser Leu Lys Asp		
465	470	475 480
Tyr Cys Thr Arg Met Lys Glu Asn Gln Lys His Ile Tyr Tyr Ile Thr		
	485	490 495
Gly Glu Thr Lys Asp Gln Val Ala Asn Ser Ala Phe Val Glu Arg Leu		
	500	505 510
Arg Lys His Gly Leu Glu Val Ile Tyr Met Ile Glu Pro Ile Asp Glu		
	515	520 525
Tyr Cys Val Gln Gln Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Ser		
	530	535 540
Val Thr Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Glu Lys Lys		
545	550	555 560
Lys Gln Glu Glu Lys Lys Thr Lys Phe Glu Asn Leu Cys Lys Ile Met		
	565	570 575
Lys Asp Ile Leu Glu Lys Lys Val Glu Lys Val Val Val Ser Asn Arg		
	580	585 590
Leu Val Thr Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr		
	595	600 605

296/299

Ala Asn Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser
 610 615 620

Thr Met Gly Tyr Met Ala Ala Lys Lys His Leu Glu Ile Asn Pro Asp
 625 630 635 640

His Ser Ile Ile Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn
 645 650 655

Asp Lys Ser Val Lys Asp Leu Val Ile Leu Leu Tyr Glu Thr Ala Leu
 660 665 670

Leu Ser Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg
 675 680 685

Ile Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro
 690 695 700

Thr Ala Asp Asp Ser Ser Ala Ala Val Thr Glu Glu Met Pro Pro Leu
 705 710 715 720

Glu Gly Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp
 725 730

<210> 329

<211> 709

<212> PRT.

<213> *Saccharomyces cerevisiae*

<400> 329

Met Ala Ser Glu Thr Phe Glu Phe Gln Ala Glu Ile Thr Gln Leu Met
 1 5 10 15

Ser Leu Ile Ile Asn Thr Val Tyr Ser Asn Lys Glu Ile Phe Leu Arg
 20 25 30

Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Asp Lys Ile Arg Tyr Lys
 35 40 45

Ser Leu Ser Asp Pro Lys Gln Leu Glu Thr Glu Pro Asp Leu Phe Ile
 50 55 60

Arg Ile Thr Pro Lys Pro Glu Gln Lys Val Leu Glu Ile Arg Asp Ser
 65 70 75 80

Gly Ile Gly Met Thr Lys Ala Glu Leu Ile Asn Asn Leu Gly Thr Ile
 85 90 95

Ala Lys Ser Gly Thr Lys Ala Phe Met Glu Ala Leu Ser Ala Gly Ala
 100 105 110

Asp Val Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Leu Phe
 115 120 125

Leu Val Ala Asp Arg Val Gln Val Ile Ser Lys Ser Asn Asp Asp Glu
 130 135 140

297/299

Gln	Tyr	Ile	Trp	Glu	Ser	Asn	Ala	Gly	Gly	Ser	Phe	Thr	Val	Thr	Leu	145	150	155	160
Asp	Glu	Val	Asn	Glu	Arg	Ile	Gly	Arg	Gly	Thr	Ile	Leu	Arg	Leu	Phe	165	170	175	
Leu	Lys	Asp	Asp	Gln	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Arg	Ile	Lys	Glu	180	185	190	
Val	Ile	Lys	Arg	His	Ser	Glu	Phe	Val	Ala	Tyr	Pro	Ile	Gln	Leu	Val	195	200	205	
Val	Thr	Lys	Glu	Val	Glu	Lys	Glu	Val	Pro	Ile	Pro	Glu	Glu	Glu	Lys	210	215	220	
Lys	Asp	Glu	Glu	Lys	Lys	Asp	Glu	Glu	Lys	Lys	Asp	Glu	Asp	Asp	Lys	225	230	235	240
Lys	Pro	Lys	Leu	Glu	Glu	Val	Asp	Glu	Glu	Glu	Lys	Lys	Pro	Lys	245	250	255		
Thr	Lys	Lys	Val	Lys	Glu	Glu	Val	Gln	Glu	Ile	Glu	Glu	Leu	Asn	Lys	260	265	270	
Thr	Lys	Pro	Leu	Trp	Thr	Arg	Asn	Pro	Ser	Asp	Ile	Thr	Gln	Glu	Glu	275	280	285	
Tyr	Asn	Ala	Phe	Tyr	Lys	Ser	Ile	Ser	Asn	Asp	Trp	Glu	Asp	Pro	Leu	290	295	300	
Tyr	Val	Lys	His	Phe	Ser	Val	Glu	Gly	Gln	Leu	Glu	Phe	Arg	Ala	Ile	305	310	315	320
Leu	Phe	Ile	Pro	Lys	Arg	Ala	Pro	Phe	Asp	Leu	Phe	Glu	Ser	Lys	Lys	325	330	335	
Lys	Lys	Asn	Asn	Ile	Lys	Leu	Tyr	Val	Arg	Arg	Val	Phe	Ile	Thr	Asp	340	345	350	
Glu	Ala	Glu	Asp	Leu	Ile	Pro	Glu	Trp	Leu	Ser	Phe	Val	Lys	Gly	Val	355	360	365	
Val	Asp	Ser	Glu	Asp	Leu	Pro	Leu	Asn	Leu	Ser	Arg	Glu	Met	Leu	Gln	370	375	380	
Gln	Asn	Lys	Ile	Met	Lys	Val	Ile	Arg	Lys	Asn	Ile	Val	Lys	Lys	Leu	385	390	395	400
Ile	Glu	Ala	Phe	Asn	Glu	Ile	Ala	Glu	Asp	Ser	Glu	Gln	Phe	Glu	Lys	405	410	415	
Phe	Tyr	Ser	Ala	Phe	Ser	Lys	Asn	Ile	Lys	Leu	Gly	Val	His	Glu	Asp	420	425	430	
Thr	Gln	Asn	Arg	Ala	Ala	Leu	Ala	Lys	Leu	Leu	Arg	Tyr	Asn	Ser	Thr	435	440	445	
Lys	Ser	Val	Asp	Glu	Leu	Thr	Ser	Leu	Thr	Asp	Tyr	Val	Thr	Arg	Met				

298/299

450	455	460
Pro Glu His Gln Lys Asn Ile Tyr Tyr Ile Thr Gly Glu Ser Leu Lys		
465	470	475 480
Ala Val Glu Lys Ser Pro Phe Leu Asp Ala Leu Lys Ala Lys Asn Phe		
	485	490 495
Glu Val Leu Phe Leu Thr Asp Pro Ile Asp Glu Tyr Ala Phe Thr Gln		
	500	505 510
Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Asp Ile Thr Lys Asp Phe		
	515	520 525
Glu Leu Glu Glu Thr Asp Glu Glu Lys Ala Glu Arg Glu Lys Glu Ile		
	530	535 540
Lys Glu Tyr Glu Pro Leu Thr Lys Ala Leu Lys Glu Ile Leu Gly Asp		
	545	550 555 560
Gln Val Glu Lys Val Val Val Ser Tyr Lys Leu Leu Asp Ala Pro Ala		
	565	570 575
Ala Ile Arg Thr Gly Gln Phe Gly Trp Ser Ala Asn Met Glu Arg Ile		
	580	585 590
Met Lys Ala Gln Ala Leu Arg Asp Ser Ser Met Ser Ser Tyr Met Ser		
	595	600 605
Ser Lys Lys Thr Phe Glu Ile Ser Pro Lys Ser Pro Ile Ile Lys Glu		
	610	615 620
Leu Lys Lys Arg Val Asp Glu Gly Gly Ala Gln Asp Lys Thr Val Lys		
	625	630 635 640
Asp Leu Thr Lys Leu Leu Tyr Glu Thr Ala Leu Leu Thr Ser Gly Phe		
	645	650 655
Ser Leu Asp Glu Pro Thr Ser Phe Ala Ser Arg Ile Asn Arg Leu Ile		
	660	665 670
Ser Leu Gly Leu Asn Ile Asp Glu Asp Glu Glu Thr Glu Thr Ala Pro		
	675	680 685
Glu Ala Ser Thr Ala Ala Pro Val Glu Glu Val Pro Ala Asp Thr Glu		
	690	695 700
Met Glu Glu Val Asp		
705		

<210> 330

<211> 260

<212> PRT

<213> Rana esculenta

<400> 330

Glu Met Ala Ser Leu Ser Glu Tyr Val Ser Arg Met Lys Glu Thr Gln

299/299

1	5	10	15
Lys Ser Ile Tyr Tyr Ile Thr Gly Glu Ser Lys Glu Gln Val Ala Asn	20	25	30
Ser Ala Phe Val Glu Arg Val Arg Lys Arg Gly Phe Glu Val Val Tyr	35	40	45
Met Thr Glu Pro Ile Asp Glu Tyr Cys Val Gln Gln Leu Lys Glu Phe	50	55	60
Asp Gly Lys Thr Leu Val Ser Val Thr Lys Glu Gly Leu Glu Leu Pro	65	70	75
Glu Asp Asp Glu Glu Lys Lys Lys Met Glu Glu Asn Lys Thr Lys Phe	85	90	95
Glu Gly Leu Cys Lys Leu Met Lys Glu Ile Leu Asp Lys Lys Val Glu	100	105	110
Lys Val Thr Val Ser Asn Arg Leu Val Ser Ser Pro Cys Cys Ile Val	115	120	125
Thr Ser Thr Tyr Gly Trp Thr Ala Asn Met Glu Arg Ile Met Lys Ala	130	135	140
Gln Ala Leu Arg Asp Asn Ser Thr Met Gly Tyr Met Met Ala Lys Lys	145	150	155
His Leu Glu Ile Asn Pro Glu His Pro Ile Val Glu Thr Leu Arg Gln	165	170	175
Lys Ala Glu Ala Asp Lys Asn Asp Lys Ala Val Lys Asp Leu Val Val	180	185	190
Leu Leu Phe Glu Thr Ala Leu Leu Ser Ser Gly Phe Ser Leu Asp Asp	195	200	205
Pro Gln Thr His Ser Asn Arg Ile Tyr Arg Met Ile Lys Leu Gly Leu	210	215	220
Gly Ile Asp Glu Asp Glu Pro Ala Ile Glu Glu Thr Thr Ala Ala Val	225	230	235
Pro Asp Asp Ile Pro Pro Leu Glu Gly Glu Glu Asp Ala Ser Arg Met	245	250	255
Glu Glu Val Asp	260		